Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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young liver	GIBCO	ALVOOI	5-8 11 20-21 46 50-51 58 65-66 75 79 82 93 97 102-103 108 110 116 139 143-144 148-149 171-172 174 187-189 194-195 198 209 214- 215 230 250 258 267-269 280-281 306 309 342 351 356 359 362 372 374 392 394 398 401 407-408 410 414 431 444 455 459 476 478 483 493 510-512 516 520 522 526 536 549 571 574-577 585 592 601-602 607 621-624 628-630 632-633 637 648 660 666-667 678 697-698 700 717 719 728 730 734 738 744-745 766 770 773 779 788 800 808 812 814 841 849-851 871 874 879 887 893 898-900 902-904 906-907 911 919 922 924 934 953 957 963 965 970 984 986 997 1001 1004 1007 1012 1029-1030 1033-1034 1052 1061 1066 1070 1076 1086 1089 1093 1099-1102 1110-1112 1116- 1117 1119 1121 1125 1136-1137 1144-1145 1156-1157 1159 1196 1199-1200 1209 1211 1219-1220 1241 1244 1262 1270 1275 1279 1283 1295 1317-1320 1332 1339 1344 1359 1362-1363 1379 1383- 1384 1403 1415 1430-1431 1437 1450 1467 1475-1476 1483-1484 1494-1495 1498 1505 1512 1516 1518-1519 1526 1529 1547 1550- 1552 1557-1559 1565 1583 1587 1597 1609 1614 1620 1631 1637 1644 1654-1655 1662 1667 1669 1684 1691-1692 1702 1711 1725 1738 1741 1743-1744 1758
adult liver	Invitrogen	ALV002	1760-1761 1763-1765 1769 5-8 17 20-21 32-33 41 55 58 64
			75 77 86 89 102 108 117 119 175- 176 198 200 209 231 235-236 250 272 275-276 284 306 316 321 325 333 356 359 374 376 398 401 408 414 428 430 433-435 454 476 494 503-505 517-518 528 534 544 552 561-563 567 578 581 608-609 630 632 637 644 650 661 665 672 702 707 710 721-722 750 753 778 782 794 814 820 826 834-837 847 849- 850 858 861 874 879 893 898 904 911 918 921-922 926 946 948 972 978 986 996 1020 1027 1031 1034 1053 1063 1068 1070 1073 1086 1089 1093 1097 1113 1119 1156 1159 1195 1198-1199 1208 1220 1227 1241 1261 1272-1273 1277 1285 1308 1315 1320 1324-1325 1330 1362-1363 1375 1403 1408- 1409 1415 1431-1432 1435 1467 1469 1482 1504 1524 1542 1547

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adult liver	Clontech	ALV003	1765 1772 1774 29 676 997 1063 1119 1536 1766
adult liver	Invitrogen	ADV001	1 4-18 20-23 29 35-40 42-48 50-
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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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adult placenta	Clontech	APLC01	5-8 44-45 90-91 107-108 159 178
ļ			311 351 414 476 503 545 574 624
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adult spleen	GIBCO	ASP001	3 5-8 12 15-16 19-21 24 29 34-36
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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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	}	}	738 744 746 773 780 784 788-789
}	ì]	802 804 809 811 814 826 831 837
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Conomic DVA	Pagestah	PACO01	1767 1779 686 1352 1412
Genomic DNA from BAC 63I18	Research Genetics	BAC001	000 1354 1414
TYOU DAC 93119	(CITE BAC]	1
	Library)]	
Genomic DNA	Research	BAC002	1411-1412
from BAC 39316	Genetics	DACOUZ	
	(CITE BAC		
	Library)	1	
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Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
Genomic DNA from BAC 39316	Research Genetics (CITB BAC Library)	BAC003	1352
adult bladder	Invitrogen	BLD001	5-8 17-18 22-23 33 37-39 56-57 80 93 100 120-121 169 201 237 251-252 272 278 311 348 363 382 413 415 424 430 443 483 502 542- 543 562 564 607 616-617 626 635 652 667 671 710 727 755-756 762 773 786 788 837 840 866 893 898 909 918 929 966 977 983 1016 1025 1055 1073 1082 1140 1167 1185 1189 1199 1270 1369 1481 1536 1560 1573 1596 1614 1636- 1637 1649-1650 1654-1655 1658 1669 1671 1690 1719 1727 1731- 1732 1739 1741 1760-1761 1779
bone marrow	Clontech	BMD001	3-8 11 13 18 29-31 33 35-36 40 43-45 47-48 50-51 57 60 65-66 75 80 82 85 88-89 94 100 103 107 110 115 118-119 124-125 133-134 136-137 139-141 146 150 152-153 155 161 163 168-170 172 178-180 187 192-193 197-198 203-205 210- 213 215 217 219 222 224-226 233 235-237 242-244 255 258 260 263- 264 266 273 276 278 283 286 290 295 301-302 307 312-313 321 330 333 339 343 352 357-358 370-371 382 384-385 387 389 394 408 410 412 416 421 424-427 429-431 436- 437 439 441-442 445 447 454-456 461-462 471-472 475 477-479 481- 482 485 488 493 498 500 503-506 513 516 519 523-524 526 530 535- 540 542 544-545 549 555 565 567 569-577 581 583-586 588 593 601 603-604 608-609 613-619 621-622 632-633 636-637 642 649-650 656- 660 666 670 672 674-675 679 683 701 708 716 718-720 731 735-736 740-742 744-745 752 761 765 772- 773 775-778 780 785-786 789-791 796 798 802 810-812 823-824 826 830 832-833 837-838 843-844 848- 855 858-859 866-867 869 878-880 883 890-892 896 903 905 908 912- 914 922-924 927 930-931 937 939- 941 952-953 955-958 963 969 973 976 981 985 987 990 992 995 1000 1002 1005-1007 1013 1016 1025 1028-1031 1033 1035 1037 1039 1042 1044 1047 1050 1053-1054 1059 1061 1063 1066 1070-1071 1079 1106 1110-1113 1115-1117 1124 1126 1134-1135 1142 1144- 1145 1163 1172 1178 1197 1199- 1200 1202 1216-1217 1224 1227- 1228 1240 1246 1254 1261 1266 1270 1278 1281 1285 1287 1290- 1291 1293 1299-1301 1308 1314 1317-1320 1327 1331 1339 1343 1346 1349 1353 1356 1361 1367 1369 1372-1374 1379-1380 1394 14400 1403 1406 1408 1413 1417 1419 1423 1425-1427 1430-1431 1443 1445 1446 1449 14459 1459 1463-1464 1482 1486 1493-1494

	DNA Cource	Hyseq	SEQ ID NOS:
Tissue Origin	RNA Source	Library Name	SEQ 15 NOS.
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•		•	1626-1628 1630-1632 1634 1636
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			1713-1714 1717 1720 1722-1723
			1727 1737-1738 1740 1758 1767
			1772 1781-1782 1785-1786
bone marrow	Clontech	BMD002	11 15-16 19 30-31 35-36 68-69 75
}			83-84 93 99 103 108-109 118 137
			139 169-170 174 177 180 190 193
			212-213 219 222 225-226 232 237
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	1	1	569-570 581 583 590-591 597-598
	}		601 616-617 621 641 650 652 656
		l	659 671 674-675 679 684 710 718-
		}	719 728 734 737-738 742 761 765
			774-778 790 811 814 818 830 834-
	1	}	836 854-855 859 866 869 871 878-
			879 884 889 892 904 922-923 932
			990 992 998 1001 1004 1016 1036
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			1088-1089 1106 1112-1114 1155
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	}		1236-1237 1260-1261 1282-1283
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		1	1631 1634 1646 1649 1653 1656
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	1		1786
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bone marrow	Clontech	BMD004	
bone marrow	Clontech	BMD007	95-96 866 1320 1475
adult colon	Invitrogen	CLN001	17 56-58 103 110 117 144 150 171
			179 185 188-189 201 204-206 210 218-221 225-226 231 237 251 277
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	Į		288 310 312 320 333 359 386 388
	1		394 408 420 455 481 485 503 510-
	1		512 590-591 615 635 647-648 665
	1		672 684 697 710 725-726 743 780
			786 788 826-827 848-850 854-855
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		İ	1025 1027 1054-1055 1063 1068-
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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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Mixture of 16	Various	CTL016	401 1490 1686
tissues -	Vendors		
mRNAs			
Mixture of 16	Various	CTL021	312 782 1132-1133 1403 1712 1715
tissues -	Vendors		
mRNAs			
adult cervix	BioChain	CVX001	1 4-8 11 13 18-21 25-26 30-31 33
			37-39 43 46-47 58 61 64-66 71
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	· ·		196 198 201-202 218-219 222 229-
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}			298 301-302 304 307 312-314 324
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	ļ		582 585-586 588-589 593-594 600
			602 604-605 607-609 612 615-619
			623 644 650 654 657-658 662-665
	ļ		670 672 680 683 691-694 698 706
		į	708-709 711 713 720-721 727 729 731-732 737 745-747 753-754 760
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		}	798 800 803 805 818 826 828 831-
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^{*} The 16 tissue-mRNAs and their vendor source, are as follows: 1) Normal adult brain mRNA (Invitrogen), 2) normal adult kidney mRNA (Invitrogen), 3) normal adult liver mRNA (Invitrogen), 4) normal fetal brain mRNA (Invitrogen), 5) normal fetal kidney mRNA (Invitrogen), 6) normal fetal liver mRNA (Invitrogen), 7) normal fetal skin mRNA (Invitrogen), 8) human adrenal gland mRNA (Clontech), 9) human bone marrow mRNA (Clontech), 10) human leukemia lymphablastic mRNA (Clontech), 11) human thymus mRNA (Clontech), 12) human lymph node mRNA (Clontech), 13) human spinal cord mRNA (Clontech), 14) human thyroid mRNA (Clontech), 15) human esophagus mRNA (BioChain), 16) human conceptional umbilical cord mRNA (BioChain).

Tirone Origin	DNA COURCE	Hypen	SEQ ID NOS:
Tissue Origin	RNA Source	Hyseq Library Name	250 10 MO2:
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Genomic clones	Genomic DNA	EPM001	286 686 1297 1303-1304 1352
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chromosome 8	Research	1	
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fetal brain	Clontech	FBR001	62-63 89 112 126 194 322 336-338
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fetal heart	Invitrogen	FHROOT	1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776 1778 1781-1782 1786
fetal heart	Invitrogen	FHR001	1090 1109 1115 1118 1120 1128 1136-1137 1144-1145 1149 1156-1157 1193-1195 1198 1204-1205 1220 1222 1234 1257 1262 1271 1274-1275 1280 1285-1286 1294 1312 1314 1317-1320 1330 1342 1344-1345 1349-1350 1355-1356 1358 1364 1369 1379 1383-1384 1431 1435 1476 1507 1519 1532 1536 1547 1554 1564 1567 1578 1582 1587 1593 1595 1601 1608 1615 1619-1621 1638 1644 1661 1665-1666 1673 1687-1688 1690 1715 1723 1728 1749 1753 1757 1759-1761 1765 1771 1774 1776 1778 1781-1782 1786
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prostate	Clontech	PRT001	9 46 57 71 107 147 171 177 197
			201 229 231 242-243 274 280-281
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			400 430 434-436 461-462 469 477
			489 497 500 505-506 513 521 526
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			871 874 890-891 905 938 945 963-
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Library Name	Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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Tissue Origin	RNA Source	Hyseq Library Name	SEQ ID NOS:
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			100 102 104 110 112 115-117 119 123 127 133 136-137 140 149 152-
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			617 619-623 628-630 634-635 642
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Tissue Origin	RNA Source	Hyseq	SEQ ID NOS:
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SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:	}			SCORE	1
1	Y41736	Homo sapiens	Human PRO1114 protein sequence.	1398	100
2	Y66656	Homo sapiens	Membrane-bound protein PRO943.	2389	99
3	AF113136	Homo sapiens	IL-1 receptor-associated- kinase-M; IRAK-M	3043	100
4	AF017806	Mus musculus	Zn-15 transcription factor	6351	77
5	X02761	Homo sapiens	fibronectin precursor	10535	98
6	X02761	Homo sapiens	fibronectin precursor	8990	89
В	X02761	Homo sapiens	fibronectin precursor	12564	99
9	AJ011679	Homo sapiens	Rab6 GTPase activating protein, GAPCenA	5251	99
10	W88501	Homo sapiens	Human stomach carcinoma clone HP10415-encoded protein.	2381	100
11	AF117754	Homo sapiens	thyroid hormone receptor- associated protein complex component TRAP240	11336	98
12	297630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	896	100
13	Y58620	Homo sapiens	Protein regulating gene expression PRGE-13.	1894	98
14	AF213457	Homo sapiens	triggering receptor expressed on myeloid cells 2	1238	100
16	AF233453	Homo sapiens	RACK-like protein PRKCBP1	3124	99
17	AF201303	Homo sapiens	dhfr oribeta-binding protein	3130	98
18	AF064205	Homo sapiens	dynactin 1 p150 isoform	6377	100
19	U00059	Saccharomyce s cerevisiae	Yhr121wp	174	26
20	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1801	99
21	AB032903	Homo sapiens	guanosine monophosphate reductase isolog	1485	99
22	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	3083	99
23	AF140507	Homo sapiens	Ca2+/calmodulin-dependent protein kinase kinase beta	2300	99
24	AJ289131	Homo sapiens	chondroitin 4-0- sulfotransferase	2211	99
25	U33460	Homo sapiens	DNA-directed RNA polymerase I, largest subunit	8777	98
26	Y44488	Homo sapiens	ACRP30R2 variant protein.	1387	100
27	U43701	Homo sapiens	ribosomal protein L23a	791	100
28	U02032	Homo sapiens	ribosomal protein L23a	767	97
29	Y41324	Homo sapiens	Human secreted protein encoded by gene 17 clone HNFIY77.	1083	99
30	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	715	90
31	W71749	Homo sapiens	Human ubiquitin conjugation system protein 2.	631	82
32	AF231917	Homo sapiens	long-chain 2-hydroxy acid oxidase HAOX2	1811	100
33	Z29481	Homo sapiens	3-hydroxyanthranilic acid dioxygenase	1507	99
34	AB001451	Homo sapiens	Sck	2869	100
35	Y00644	Homo sapiens	precursor polypeptide (AA -34 to 287)	1667	99
36	Y00644	Homo sapiens	precursor polypeptide (AA -34 to 287)	1104	98
37	¥78795	Homo sapiens	Human antizuai-2 (AZ-2) amino acid sequence.	3586	78
38	Y78795	Homo sapiens	Human antizuai-2 (AZ-2) amino acid sequence.	4726	99
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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
39	¥78795	Homo sapiens	Human antizuai-2 (AZ-2) amino acid sequence.	3556	77
40	U93121	Homo sapiens	M-phase phosphoprotein-1	3747	100
41	Y42750	Homo sapiens	Human calcium binding protein 1 (CaBP-1).	795	100
42	AF282626	Homo sapiens	latexin	1189	100
43	G02150	Homo sapiens	Human secreted protein, SEQ ID NO: 6231.	384	94
44	U19617	Mus musculus	Elf-1	2724	88
45	U19617	Mus musculus	Elf-1	2062	86
46	AF100758	Homo sapiens	osteoinductive factor OIF	1538	100
47	Y87591	Homo sapiens	Human SPROUTY-1 protein, SEQ ID NO:24.	1737	99
49	X04145	Homo sapiens	T3 gamma precursor (aa -22 to 160)	942	99
51	X63547	Homo sapiens	oncogene	5845	99
52	M94043	Rattus norvegicus	rab-related GTP-binding protein	1089	96
53	L31783	Mus musculus	uridine kinase	917	71
54	X83973	Homo sapiens	transcription factor	4486	98
55	AF224741	Homo sapiens	chloride channel protein 7	4128	99
56	W74805	Homo sapiens	Human secreted protein encoded by gene 77 clone HOEAS24.	1491	100
57	250907	Homo sapiens	Human TBC-1 cDNA from second transcript.	4824	100
58	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	6089	99
59	D79994	Homo sapiens	similar to ankyrin of Chromatium vinosum.	4014	91
60	Y59738	Homo sapiens	Human normal ovarian tissue derived protein 15.	601	100
61	AB031069	Homo sapiens	protein containing CXXC domain 1	1390	100
62	Y66660	Homo sapiens	Membrane-bound protein PRO783.	2492	99
63	Y66660	Homo sapiens	Membrane-bound protein PRO783.	1709	99
64	S70011	Rattus sp.	tricarboxylate carrier	895	55
65	AF139518	Rattus norvegicus	A-kinase anchor protein	178	24
66	W29666	Homo sapiens	Homo sapiens DH1308_1 clone secreted protein.	157	30
67	AJ245738	Homo sapiens	claudin-15	1206	100
68	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4183	87
69	AF099138	Rattus norvegicus	GLUT4 vesicle protein	4906	86
70	Z82059	Caenorhabdit is elegans	Similarity to Drosophila ring canal protein comes from this gene	1285	44
71	AF224278	Homo sapiens	PMEPAl protein	1282	100
72	AF126426	Homo sapiens	neurotrimin	1809	100
73	Y41652	Homo sapiens	Human MEK2 protein sequence.	2065	99
74	Y41652	Homo sapiens	Human MEK2 protein sequence.	1207	100
75	AF188622	Mus musculus	selectively expressed in embryonic epithelia protein-1	1485	74
76	AE000406	Escherichia coli	putative DNA topoisomerase	950	100
77	X99302	Homo sapiens	Pop1	655	100
78	AL136538	Schizosaccha romyces pombe	similarity to S. cerevisiae ktil2 protein	210	31
•	1	Homo sapiens	G4	1554	99

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:	AL096768	Homo sapiens	dJ858B16.2	SCORE 2033	100
	AL098/88	Homo sapiens	(phosphatidylserine decarboxylase (PSSC, EC	2033	100
	<u> </u>		4.1.1.65))		
81	AL096768	Homo sapiens	dJ858B16.2 (phosphatidylserine decarboxylase (PSSC, EC 4.1.1.65))	1220	96
82	X57351	Homo sapiens	1-8D	677	98
83	AC005594	Homo sapiens	R26984 1	2700	98
84	X73113	Homo sapiens	fast MyBP-C	5959	199
85	AF097330	Homo sapiens	H1 chloride channel; p64H1; CLIC4	1305	99
86	AB018423	Mus musculus	SH2 domain-containing protein	1360	78
87	AF272151	Homo sapiens	adaptor protein CIKS	3084	99
88	AF196329	Homo sapiens	triggering receptor expressed on monocytes 1	1214	100
89	AB016879	Arabidopsis thaliana	contains similarity to pre- mRNA splicing factor-gene_id:MRB17.2	634	36
90	AJ133721	Mus musculus	homeodomain protein	654	57
91	AJ242864	Mus musculus	phtf protein	619	61
92	A61971	unidentified	MCSP	11676	99
93	Y99365	Homo sapiens	Human PRO1250 (UNQ633) amino acid sequence SEQ ID NO:86.	3890	100
94	Y87231	Homo sapiens	Human signal peptide containing protein HSPP-8 SEQ ID NO:8.	1031	100
95	AF227741	Rattus norvegicus	protein kinase WNK1	2428	95
96	AF227741	Rattus norvegicus	protein kinase WNK1	1961	94
97	Y92513	Homo sapiens	Human OXRE-10.	1626	100
98	AL021366	Homo sapiens	cICK0721Q.3 (Kinesin related protein)	3423	100
99	AC005783	Homo sapiens	R33083_1	1974	99
100	Y95293	Homo sapiens	Human GEF containing NEK-like kinase substrate sGNK.	4092	99
101	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein (translation of the cDNA DKFZp566A0946, Em:AL050069))	1509	100
102	AJ006267	Homo sapiens	ClpX-like protein	3233	100
103	AF100753	Homo sapiens	ancient ubiquitous 46 kDa protein AUP1	2042	96
104	AB015982	Homo sapiens	serine/threonine kinase	4718	100
105	AF151074	Homo sapiens	HSPC240	831	64
106	M35522 R99800	Canis familiaris Homo sapiens	GTP-binding protein (rab7)	354	50
107	R99800	Homo Bapiens	NTII-1 nerve protein, facilitates regeneration of nerve cells.	2337	93
108	AF125533	Homo sapiens	NADH-cytochrome b5 reductase isoform	1290	93
109	AC005614	Homo sapiens	F23269_2	3369	99
110	AF064729	Homo sapiens	RAN binding protein 16	3285	100
111	X52425	Homo sapiens	interleukin 4 receptor	4496	100
112	Y41686	Homo sapiens	Human PRO274 protein sequence.	2285	100
113	W15506	Homo sapiens	Mitogen activating protein kinase ERK1.	1991	100
114	Y71071	Homo sapiens	Human membrane transport protein, MTRP-16.	1190	99
115	AL049548	Homo sapiens	dJ398G3.1 (ortholog of rat CPG2)	3497	99
116	AF189817	Mus musculus	evectin-2	1124	90
117	W30891	Homo	Human cytostatin III protein.	715	99

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
	1	sapiens	PRO1038	1469	100
118	AF116618	Homo sapiens	alpha 4 protein	1748	100
119	Y08915	1	List homolog	192	39
120	AF098070	Drosophila melanogaster			
121	AF052432	Homo sapiens	katanin p80 subunit	181	37
122	Y70743	Homo sapiens	PSEQ-1 protein encoded by NSEQ gene associated with matrix remodelling.	2637	98
123	AF083246	Homo sapiens	HSPC028	2132	100
124	Y27096	Homo sapiens	Human viral receptor protein (ACVRP).	833	99
125	M63109	Leishmania major	glycoprotein 96-92	172	27
126	U75467	Drosophila melanogaster	Atu	935	36
127	Z68220	Caenorhabdit is elegans	Similarity to Human ADP/ATP carrier protein	438	43
128	AF095927	Rattus	protein phosphatase 2C	1927	94
136	W92958	Homo sapiens	Human zsig44 protein.	463	100
129 130	AF115391	Lactobacillu s sakei	ribokinase RbsK	508	37
131	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	1250	100
132	X93498	Homo sapiens	21-Glutamic Acid-Rich Protein	916	87
133	W52811	Homo sapiens	Human DBI/ACBP -like protein (DBIH).	705	97
134	Y84444	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	3230	100
135	M69181	Homo sapiens	non-muscle myosin B	189	20
136	W74882	Homo sapiens	Human secreted protein encoded by gene 154 clone HE6FL83.	480	100
137	W78200	Homo sapiens	Human secreted protein encoded by gene 75 clone HHGAU81.	855	99
138	AL033520	Homo sapiens	dJ349A12.1 (similar to KIAA0701 protein)	424	39
139	AF020261	Santalum album	proline rich protein	119	30
140	X70394	Homo sapiens	zinc finger protein	1634	100
141	Y06439	Homo sapiens	Human protease HUPM-8.	936	100
142	Z68493	Caenorhabdit is elegans	predicted using Genefinder	365	42
143	AB018107	Arabidopsis thaliana	ADP-ribosylation factor-like protein	596	65
144	AF161483	Homo sapiens	HSPC134	580	51
145	Y84902	Homo sapiens	A human proliferation and apoptosis related protein.	480	100
146	AB004906	Ipomoea purpurea	transposase	146	20
147	AC007357	Arabidopsis thaliana	F3F19.18	647	31
148	W75155	Homo sapiens	encoded by gene 41 clone HNTME13.	1494	98
149	AF056490	Homo sapiens	cAMP-specific phosphodiesterase 8A	3710	99
150	Y58171	Homo sapiens	Human hydrolase homologue	785	99
151	U10397	Saccharomyce s cerevisiae	Yhr148wp	515	53
152	X73478	Homo sapiens	.1	1719	99
153	AL049697	Homo sapiens	dJ382I10.5.1 (novel protein	2034	99

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
			similar to arginyl-tRNA)		
154	AF169802	Homo sapiens	cytochrome b5 reductase b5R.2	1455	99
155	X94703	Homo sapiens	rab28	1126	99
156	Y25716	Homo sapiens	Human secreted protein encoded from gene 6.	1471	100
158	W77404	Homo sapiens	Secreted salivary polypeptide zsig32.	937	100
159	Y17248	Homo sapiens	Human protein kinase inhibitor-2 (PKI-2).	383	100
160	J04970	Homo sapiens	carboxypeptidase M precursor	2395	100
161	W54040	Homo sapiens	Human interferon-inducible protein, HIFI.	484	98
162	AL022724	Homo sapiens	dJ413H6.1.1 (hamster Androgen-dependent Expressed Protein LIKE PUTATIVE protein) (isoform 1)	1357	100
163	AF125535	Homo sapiens	pp21 homolog	193	45
164	G03632	Homo sapiens	Human secreted protein, SEQ ID NO: 7713.	463	97
165	AJ250839	Homo sapiens	serine/threonine protein kinase	1442	71
166	L09649	Zymomonas mobilis	zm2	173	37
167	Y73337	Homo sapiens	HTRM clone 1944530 protein sequence.	1204	100
168	W88645	Homo sapiens	Secreted protein encoded by gene 112 clone HUKFC71.	1084	100
169	AF214731	Homo sapiens	ATP-dependent RNA helicase	4402	100
170	AE000871	Methanobacte rium thermoautotr ophicum	conserved protein	166	27
171	Y27684	Homo sapiens	Human secreted protein encoded by gene No. 118.	821	100
172	AF226044	Homo sapiens	HSNFRK	2904	100
173	AJ245946	Homo sapiens	neuroglobin	779 3202	100
174	D43949	Homo sapiens	This gene is novel.	1205	100
175 176	¥07923 ₩90338	Homo sapiens	GTP-binding protein Human DP1 homologue protein.	966	100
177	Y41675	Homo sapiens	Human channel-related molecule HCRM-3.	1122	100
178	Y41674	Homo sapiens	Human channel-related molecule HCRM-2.	936	99
179	AF220492	Homo sapiens	krueppel-like zinc finger protein HZF2	4100	99
180	X03084	Homo sapiens	Clq B-chain precursor	1240	100
181	U57344	Mus musculus	Meis3	1813	89
183	U57344	Mus musculus	Meis3	1743	86
184	U57344	Mus musculus	Meis3	1070	86
185	AF033120	Homo sapiens	p53 regulated PA26-T2 nuclear protein	1389	58
186	AF200357	Mus musculus	pantothenate kinase 1 beta	1605	82
187	W75058	Homo sapiens	Human secreted protein encoded by gene 2 clone HLDBG33.	1188	99
188	AJ292529	Homo sapiens	suppressor of sterile four 1	2424	100
190	X54134	Homo sapiens	protein-tyrosine phosphatase	3705	100
191	Y22203	Homo sapiens	Human calcium-binding phosphoprotein, CBPP-1, protein sequence.	1083	99
192	W63692	Homo sapiens	Human secreted protein 12.	1975	100
193	W87772	Homo sapiens	Human serum glucocorticoid- regulated kinase (H-SGK2) polypeptide.	2605	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	1 042 001	· · · · · · · · · · · · · · · · · · ·
ĮD	NUMBER	DIBCIDS	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:)		SCORE	IDENTITI
194	AF084259	Mus musculus	bromodomain-containing protein BP75	693	54
195	Y00752	Rattus norvegicus	serine dehydratase (AA 1 - 327)	994	61
196	W95349	Homo sapiens	Human foetal brain secreted protein fh170 7.	2596	100
197	AB028859	Homo sapiens	hD19	1890	100
198	W95633	Homo sapiens	Homo sapiens secreted protein	1614	100
199	Y44277	Homo	gene clone hm236_1. Human nucleic acid methylase-	2096	99
		sapiens	2.	2036	99
200	AB030039	Homo sapiens	hPACPL1	2258	100
201	X54162	Homo sapiens	64 Kd autoantigen	2918	99
202	G02061	Homo sapiens	Human secreted protein, SEQ ID NO: 6142.	558	99
203	X13885	Nicotiana tabacum	extensin (AA 1-620)	185	33
204	J04204	Bos taurus	32 kd accessory protein	1837	100
205	J04204	Bos taurus	32 kd accessory protein	1101	100
207	¥87283	Homo sapiens	Human signal peptide containing protein HSPP-60 SEQ ID NO:60.	1318	100
208	Y02860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	936	98
209	AL121889	Homo sapiens	dJ1076E17.1 (KIAA0823 protein (continues in AL023803))	694	54
210	AF226732	Homo sapiens	NPD007	1345	76
211	X66295	Mus musculus	Clq C chain	970	73
212	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	966	100
213	Z29328	Homo sapiens	Ubiquitin-conjugating enzyme UbcH2	542	98
214	AJ002030	Homo sapiens	progresterone binding protein	1163	100
215	X70649	Homo sapiens	member of DEAD box protein family	3933	100
216	AF250558	Homo sapiens	claudin-2	1169	99
217	AL021453	Homo sapiens	dJ821D11.1 (PUTATIVE protein)	259	100
218	Y08565	Homo sapiens	UDP-GalNAc:polypeptide N- acetylgalactosaminyltransfera se	3331	99
219	Y94452	Homo sapiens	Human inflammation associated protein	2067	100
220	AL035521	Arabidopsis thaliana	putative protein	315	42
221	AL031786	Schizosaccha romyces pombe	putative proline-trna synthetase	811	41
222	AL109736	Schizosaccha romyces pombe	WD repeat protein	626	40
223	X52493	Glycine max	DNA-directed RNA polymerase	136	23
224	AL035659	Homo sapiens	dJ979N1.1 (dJ979N1.1)	5199	98
225	AB032401	Mus musculus	mmDj4	1761	92
226	AB032401	Mus musculus	mmDj4	1988	92
227	X83502	Saccharomyce s cerevisiae	J1007	112	26
228	X83502	Saccharomyce s cerevisiae	J1007	79	25
229	AF143723	Homo sapiens	heat shock protein HSP60	2557	99
230	Y66677	Homo sapiens	Membrane-bound protein PRO828.	982	100
231	AB027466	Homo sapiens	spondin 2	1756	99
232	W95634	Homo sapiens	Homo sapiens secreted protein.	1391	100
233	W00365	Homo sapiens	Human cyclin B1.	2218	99
233					

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
	L	<u> </u>	designated RAQ.		
235	Z50749	Homo sapiens	yeast sds22 homolog	1800	100
236	Z50749	Homo sapiens	yeast sds22 homolog	1754	98
237	AB026491	Homo sapiens	PICK1	2137	100
238	AJ270205	Entodinium	putative	114	37
		caudatum	phosphatidylinositol-4-	Į	Ì
			phosphate 5-kinase		<u> </u>
239	AB030189	Mus musculus	contains transmembrane (TM) region and ATP binding region	710	93
240	W56538	Homo sapiens	Human hedgehog interacting protein (HIP).	3785	99
241	W56538	Homo sapiens	Human hedgehog interacting protein (HIP).	3436	99
242	AF155107	Homo sapiens	NY-REN-37 antigen	996	99
243	AF155107	Homo sapiens	NY-REN-37 antigen	1005	100
244	AL031320	Homo sapiens	dJ20N2.1 (novel protein	763	99
			similar to yeast and bacterial cytosine deaminase)		
245	U37026	Rattus norvegicus	sodium channel beta 2 subunit	162	30
246	AL078599	Homo sapiens	dJ991C6.1 (novel protein similar to C. elegans	2391	98
	1		F55A12.9 (Tr:P91086))		}
247	U32274	Saccharomyce s cerevisiae	Ydr386wp; CAI: 0.12	191	37
248	Y41719	Homo sapiens	Human PRO864 protein sequence.	1879	100
249	AB029434	Homo sapiens	ghrelin precursor	611	100
250	X97831	Rattus norvegicus	carnitine/acylcarnitine carrier protein	246	38
251	W80993	Homo sapiens	Human RIP-interacting factor RIF.	1724	100
252	Y94873	Homo sapiens	Human protein clone HP02632.	1876	100
253	W59878	Homo sapiens	Amino acid sequence of the cDNA clone AIF-2 (HEBGM49).	765	100
254	AL354533	Leishmania major	possible adenylate kinase	265	34
255	AF233322	Mus musculus	zinc transporter like 2	1916	95
256	Y78113	Homo sapiens	Human cytokine signal regulator CKSR-1 SEQ ID NO:1.	2247	99
257	AL035539	Arabidopsis thaliana	putative amino acid transport protein	390	27
258	W74787	Homo sapiens	Human secreted protein encoded by gene 58 clone HHFHN61.	1171	100
259	AL035689	Homo sapiens	dJ187J11.1 (novel protein similar to protein kinase C inhibitors)	974	100
260	AE000909	Methanobacte rium thermoautotr ophicum	serine/threonine protein kinase related protein	363	30
261	AL050131	Homo sapiens	hypothetical protein	626	100
262	AF019661	Mus musculus	zeta proteasome chain; PSMA5	1214	100
263	AL035593	Homo sapiens	dJ310J6.1 (novel protein)	821	100
264	AL022318	Homo sapiens	bK150C2.3 (PUTATIVE novel protein similar to APOBEC1)	1072	100
265	AF205940	Homo sapiens	endomucin	1289	100
266	AL023583	Homo sapiens	dJ500L14.1 (novel protein)	789	100
267	AL034548	Homo sapiens	dJ1103G7.3 (novel protein kinase domains containing protein similar to phosphoprotein C8FW)	1888	99

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:	AF161470	772	HSPC121	SCORE	
268	1.	Homo sapiens	HSPC121	1884	98
269	AF161470	Homo sapiens		1232	96
270	X90763	sapiens	HHa5 hair keratin type I intermediate filament	2190	99
271	AF207600	Homo sapiens	ethanolamine kinase	1952	100
272	M32334	Homo sapiens	intercellular adhesion molecule 2	1436	100
273	AF161483	Homo sapiens	HSPC134	663	61
274	Y53C52	Homo sapiens	Human secreted protein clone df202 3 protein sequence SEQ ID NO:110.	587	100
276	Y77576	Homo sapiens	Human cytoskeletal protein (HCYT) (clone 2195418).	762	100
277	AF077042	Homo sapiens	30S ribosomal protein S7 homolog	1269	100
278	Y94907	Homo sapiens	Human secreted protein clone cal06_19x protein sequence SEQ ID NO:20.	1619	98
279	Y68788	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-20.	2801	·99
280	Z75134	Canis familiaris	rod transducin	1816	100
281	275134	Canis familiaris	rod transducin	1718	96
282	AF249873	Homo sapiens	muscle-specific protein	1395	100
283	AL050007	Homo sapiens	hypothetical protein	405	98
284	AF201931	Homo sapiens	DCi	1859	99
285	AF156102	Homo sapiens	ELL complex EAP30 subunit	1318	99
286	Y35897	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 146.	1250	99
287	U88964	Homo sapiens	HEM45	923	100
288	AL050143	Homo sapiens	hypothetical protein	598	100
289	AJ011098	Homo sapiens	telethonin	574	100
290	Y66724	Homo sapiens	Membrane-bound protein PRO836.	2321	100
291	AF034801	Homo sapiens	liprin-alpha4	2565	98
292	AF034801	Homo sapiens	liprin-alpha4	2590	100
293	AL049851	Homo sapiens	dJ889J22B.1 (novel protein (isoform 1))	1738	100
294	Y73348	Homo sapiens	HTRM clone 839651 protein	1245	99
295	L11672	Homo sapiens	zinc finger protein	1694	44
296	AL035423	Homo sapiens	dJ2013.1 (brain mitochondrial carrier protein-1 (BMCP1))	1024	79
297	AF198532	Homo sapiens	lymphoid enhancer binding factor-1	2173	100
298	AF161417	Homo sapiens	HSPC299	1147	85
299	AF159141	Homo sapiens	breast cancer metastasis- suppressor 1	1236	99
300	U26397	Rattus norvegicus	inositol polyphosphate 4- phosphatase	160	30
301	AF036145	Homo sapiens	meningioma-expressed antigen	3458	100
302	Z82022	Homo sapiens	GlcNac-1-P transferase	2067	99
303	AF269232	Mus musculus	butyrophilin-like protein BUTR-1	271	50
304	AJ222644	Arabidopsis thaliana	asparaginyl-tRNA synthetase	659	50
305	AF054180	Homo sapiens	hematopoietic cell derived zinc finger protein	351	79
	 	Homo sapiens	APOBEC-1 stimulating protein	3056	100
306	םניתנינינית ו				
306 308	AJ272079 Y44486	Homo sapiens	Human GPRW receptor polypeptide.	1721	100

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SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
310	AF293335	Homo sapiens	p30 DBC	1248	92
311	AF176525	Mus musculus	F-box protein FBL12	1501	93
312	X57802	Homo sapiens	immunoglobulin lambda light chain	959 .	81
313	Z36715	Homo sapiens	Net	2048	98
314	AF161532	Homo sapiens	HSPC047	727	100
315	AF208068	Homo sapiens	kelch-like protein KLHL3a	3046	100
316	Y66666	Homo sapiens	Membrane-bound protein PRO1013.	1166	100
317	Y29666	Homo sapiens	Human Ras protein RAPR-1.	1253	98
318	AJ387747	Homo sapiens	sialin	2614	99
319	AF161362	Homo sapiens	HSPC099	224	40
320	Y68773	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-5.	2243	99
321	AJ238379	Homo sapiens	putative TH1 protein	3013	100
322	AB040812	Homo sapiens	protein kinase PAK5	3792	99
323	Y95013	Homo sapiens	Human secreted protein vc48 1, SEQ ID NO:66.	913	100
324	Y13381	Homo sapiens	Amino acid sequence of protein PRO271.	1976	100
325	Y94944	Homo sapiens	Human secreted protein clone bf157_16 protein sequence SEQ ID NO:94.	2305	98
326	Y76884	Homo sapiens	Retinoblastoma binding protein-7sequence.	6728	99
327	AF198532	Homo sapiens	lymphoid enhancer binding factor-1	2173	100
328	Z78013	Caenorhabdit is elegans	Similarity to Drosophila Cadherin-related tumor suppressor	569	33
329	AF212921	Mus musculus	MMTV receptor variant 1	484	94
330	275330	Homo sapiens] >R65207 R65207 02- MAR-1995 27- AUG-1993 Human stromalin-1. [Homo sapiens	nuclear protein SA-1	6492	99
331	AL008583	Homo sapiens	dJ327J16.3 (supported by GENSCAN, FGENES and GENEWISE)	2133	99
332	Y36104	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 489.	310	41
333		Homo sapiens	putative sialoglycoprotease	1747	100
334	AF156598	Mus musculus	p53-regulated DDA3	997	64
335	M99058	Eimeria maxima	em100 gene is homologous the Bimeria tenella gene et100	154	26
336	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3386	97
337	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	2602	94
338	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3447	98
339	266561	Caenorhabdit is elegans	Similarity to Human rabl3 protein (PIR Acc. No. A49647).	716	34
		ŀ			
340	AB021643	Homo sapiens	gonadotropin inducible transcription repressor-3	2761	99
341	AB021643 G01946	1		2761 465	99
		sapiens	transcription repressor-3 Human secreted protein, SEQ	· .	

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
	 		VDJ region	- SCORE	+
344	U10281	Sus scrofa	gastric mucin	279	24
345	AK000404	Homo sapiens	unnamed protein product	1177	99
346	L22557	Rattus norvegicus	calmodulin-binding protein	1949	84
347	L22557	Rattus norvegicus	calmodulin-binding protein	2363	91
348	AL049481	Arabidopsis thaliana	AIG1-like protein	316	30
350	AJ251516	Mus musculus	cysteine and histidine-rich protein	1460	99
351	AK024477	Homo sapiens	FLJ00070 protein	1773	100
352	U50133	Homo sapiens	ankyrin	502	33
353	AK000625	Homo sapiens	unnamed protein product	721	100
354	AF161420	Homo sapiens	HSPC302	2623	97
355	AJ010014	Homo sapiens	M96A protein	1269	47
356	AF151029	Homo sapiens	HSPC195	941	91
357 358	AL022327 W78128	Homo sapiens	dJ355C18.1 (KIAA0027)	1911	100
358	W/8128	Homo sapiens	Human secreted protein encoded by gene 3 clone HOSBI96.	1117	100
359	X03414	Drosophila melanogaster	Kr polypeptide	316	45
360	AF151079	Homo sapiens	HSPC245	643	100
361	Y53886	Homo sapiens	A suppressor of cytokine signalling protein designated HSCOP-6.	530	41
362	AF254741	Drosophila melanogaster	Centaurin Gamma 1A	681	46
363	AF213465	Homo sapiens	dual oxidase	2016	100
364	AF181562	Homo sapiens	proSAAS	1319	100
365	AF181562	Homo sapiens	proSAAS	1024	99
366	U73200	Mus musculus	p116Rip	884	82
367	AF263744	Homo sapiens	erbb2-interacting protein ERBIN	4973	99
368	U37501	Mus musculus	laminin alpha 5 chain	5867	72
369	AF043695	Caenorhabdit is elegans	similar to the protein phosphates 2c family	549	36
370	Y73440	Homo sapiens	Human secreted protein clone yj23_1 protein sequence SEQ ID NO:102.	1484	99
371	AF272833	Homo sapiens	misato	2869	97
372	AF198454	Homo sapiens	epithelial protein lost in neoplasm beta	3927	100
373	Y73345	Homo sapiens	HTRM clone 438283 protein sequence.	273	80
374	AF169017	Homo sapiens	formiminotransferase cyclodeaminase	2717	98
375	A95106	unidentified	RED ALPHA	1202	99
376	W74828	Homo sapiens	Human secreted protein encoded by gene 100 clone HLQAB52.	1012	99
377	Y32131	Homo sapiens	Human LYST-2 protein.	3556	99
378	M14912	Homo sapiens	pol	132	86
379	AF090934	Homo sapiens	PRO0518	382	100
380	X66363	Homo sapiens	serine/threonine protein kinase	2499	100
381	Y41699	Homo sapiens	Human PRO703 protein sequence.	2362	100
382	AF174498	Homo sapiens	GR AF-1 specific protein phosphatase	7008	98
383	U64608	Caenorhabdit is elegans	coded for by C. elegans cDNA yk173c12.5	246	36
384	U50133	Homo sapiens	ankyrin	502	33
385	AJ238520	Homo sapiens	putative transcription	4123	97
	<u> </u>	L	factor-like nuclear regulator	L	

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
387	AF208845	Homo sapiens	BM-003	SCORE	-
389	X57821	Homo sapiens	immunoqlobulin lambda light	1375 797	99
390	AF182404	Homo sapiens	chain		76
]	mitochondrial uncoupling protein 1	1670	99
391	Y85564	Homo sapiens	Human homologue of UNC-53 (Hs-UNC-53/1) sequence.	3386	97
393	AF178432	Homo sapiens	SH3 protein	3700	100
394	AF229928	Drosophila melanogaster	cytoplasmic protein 89BC	1616	62
395	AF181721	Homo sapiens	RU2S	2254	100
396	Y69197	Homo sapiens	Amino acid sequence of a human betaIV-spectrin protein.	1626	98
397	U48238	Mus musculus	zinc finger protein neuro-d4	749	60
398	AL390137	Homo sapiens	hypothetical protein	263	51
399	AF217525	Homo sapiens	Down syndrome cell adhesion molecule	5337	60
400	AL022599	Schizosaccha romyces pombe	WD repeat protein	447	27
401	AC004B59	Homo sapiens	similar to 2-oxoglutarate dehydrogenase ; similar to Q02218 (PID:g1352618)	4176	78
402	AB010266	Mus musculus	tenascin-X	10246	62
403	AL133288	Homo sapiens	dJ671D7.1 (similar to	761	100
		nome suprem	D.melanogaster CG5986 protein)	761	100
404	268753	Caenorhabdit is elegans	ZC518.3b	888	48
405	Z78013	Caenorhabdit is elegans	Similarity to Drosophila Cadherin-related tumor suppressor	569	33
406	AB031230	Homo sapiens	protein containing CXXC domain 2	1196	97
407	AF155106	Homo sapiens	NY-REN-36 antigen	1168	100
408	Y57945	Homo sapiens	Human transmembrane protein HTMPN-69.	1538	99
409	Z18361	Ovis aries	trichohyalin	184	30
410	AF249744	Homo sapiens	RhoGEF	2733	100
411	AF176529	Mus musculus	F-box protein FBX13	2072	94
412	AF210842	Homo sapiens	HARP	4880	100
413	AL031658	Homo sapiens	dJ310013.7 (novel protein similar to H. roretzi HRPET- 3)	776	98
414	X57398	Homo sapiens	pm5 protein	6131	99
415	AB029826	Homo sapiens	3-methylcrotonyl-CoA carboxylase biotin-containing subunit	2961	99
416	U43503	Saccharomyce s cerevisiae	Lph1p	115	42
417	AL160493	Leishmania major	possible t26f17.21	239	35
418	Y08100	Homo sapiens	Human PRO331 protein.	330	29
419	U15131	Homo sapiens	p126	2228	54
420	AF117946	Homo sapiens	Link guanine nucleotide exchange factor II	2363	100
421	AF190635	Drosophila melanogaster	ankyrin 2	755	30
422	AF302150	Homo sapiens	phosphoinositol 3-phosphate- binding protein-2	1962	100
423	AL137530	Homo sapiens	hypothetical protein	433	94
424	X63753	Homo sapiens	son-a	7269	100
425	AB027249	Homo sapiens	MAPKK like protein kinase	1693	100
426	AF279144	Homo sapiens	tumor endothelial marker 7	1084	55
			precursor		

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
NO:	NUMBER			WATERMAN SCORE	IDENTITY
427	AF279144	Homo sapiens	tumor endothelial marker 7 precursor	1259	56
428	AE003683	Drosophila melanogaster	CG8312 gene product	149	29
429	Y07829	Homo sapiens	RING finger protein	2201	99
430	AF096897	Drosophila melanogaster	pushover	4442	47
431	U41387	Homo sapiens	Gu protein	4021	99
432	AF023674	Homo sapiens	nephrocystin	3783	100
433	AF146760	Homo sapiens	septin 2-like cell division control protein	2284	100
434	AB006697	Arabidopsis thaliana	cleft lip and palate associated transmembrane protein-like	886	42
437	Y94247	Homo sapiens	Human calcium binding protein hCBP.	1704	100
438	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N- acetylgalactosaminyltransfera se	1075	63
439	AF105228	Bos taurus	tuftelin .	285	33
440	R06463	Homo sapiens	Derived protein of clone ICA13 (ATCC 40553).	3073	99
441	X14971	Mus musculus	alpha-adaptin (A) (AA 1-977)	4897	98
442	X53773	Rattus norvegicus	alpha-c large chain (AA 1- 938)	3979	81
443	Y66689	Homo sapiens	Membrane-bound protein PRO1136.	3299	99
444	AC067754	Arabidopsis thaliana	unknown protein; 20348-23707	114	33
445	AF229032	Mus musculus	piL	2077	93
446	AF056035	Rattus norvegicus	s-nexilin	2662	85
447	AF132484	Mus musculus	unknown	478	51
448	W89024	Homo sapiens	Polypeptide fragment encoded by gene 156.	528	45
449	AF161445	Homo sapiens	HSPC327	1606	100
450	Z68753	Caenorhabdit is elegans	ZC518.3b	951	49
451	W39160	Homo sapiens	Human partial complement factor H protein fragment 3.	155	32
452	W85727	Homo sapiens	Novel protein (Clone BM46_10).	2799	99
453	Y53629	Homo sapiens	A bone marrow secreted protein designated BMS115.	2810	100
454	D87438	Homo sapiens	Similar to a C.elegans protein in cosmid C14H10	4069	100
455	AF240468	Homo sapiens	nicastrin	3687	100
456	Z15005	Homo sapiens	CENP-E	13305	99
457	M59216	sapiens	gamma-aminobutyric acid receptor beta-1 subunit	2477	100
458	Y73467	Homo sapiens	Human secreted protein clone yd61_1 protein sequence SEQ ID NO:156.	966	100
459	W67824	Homo sapiens	Human secreted protein encoded by gene 18 clone HSLFM29.	535	100
460	AF163151	Homo sapiens	dentin sialophosphoprotein precursor	279	19
461	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	9196	99
462	G04044	Homo sapiens	Human secreted protein, SEQ ID NO: 8125.	486	93
463	AC002398	Homo sapiens	F25965_1	1018	100
464	AF064856	Rattus sp.	7acomp protein	1845	84
465	AF223408	Homo sapiens	B99	3686	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
466	AF223408	Homo sapiens	B99	2878	87
467	AF104415	Mus musculus	gene trap locus-13	6336	91
468	U53450	Rattus	Jun dimerization protein 1	196	49
		norvegicus	JDP-1		
469	AL031297	Homo sapiens	dJ97220.1 (novel gene)	3564	99
470	AF257077	Homo sapiens	eukaryotic translation initiation factor EIF2B subunit 3	1274	95
471	L28125	Podospora anserina	beta transducin-like protein	284	38
472	Y84903	Homo sapiens	A human proliferation and apoptosis related protein.	2337	100
473	AF144237	Homo sapiens	LOMP protein	252	44
474	Y71213	Homo sapiens	Human irritable bowel disease related polypeptide IMX39.	838	100 .
475	Y95006	Homo sapiens	Human secreted protein vel3 1, SEQ ID NO:52.	3411	100
476	D38549	Homo sapiens	hal025 is new	6533	99
477	AF241230	Homo sapiens	TAK1-binding protein 2	3656	100
478	AL031534	Schizosaccha romyces pombe	putative asparagine synthase	482	40
479	L28125	Podospora anserina	beta transducin-like protein	233	26
480	AF161544	Homo sapiens	HSPC059	434	77
481	AJ238248	Homo sapiens	centaurin beta2	3986	99
482	Z38061	Saccharomyce s cerevisiae	mal5, stal, len: 1367, CAI: 0.3, AMYH_YEAST P08640 GLUCOAMYLASE S1 (EC 3.2.1.3)	295	23
483	AF161381	Homo sapiens	HSPC263	1404	100
484	AF223468	Homo sapiens	AD021 protein	1314	100
486	X57527	Homo sapiens	alpha 1(VIII) collagen	4166	99
487	Y19062	Homo sapiens	39k3 protein	2475	100
488	Y73373	Homo sapiens	HTRM clone 921803 protein sequence.	555	56
489	AL021918	Homo sapiens	b3418.1 (Kruppel related Zinc Finger protein 184)	4184	100
490	X53773	Rattus norvegicus	alpha-c large chain (AA 1- 938)	4675	97
491	U52426	Homo sapiens	GOK	1459	59
492	AL359773	Leishmania major	possible threonine synthase	702	45
493	AF226614	Homo sapiens	ferroportin1	2929	100
494	Z93241	Homo sapiens	dJ222Ei3.1 (novel protein with some similarity to Drosophila KRAKEN)	513	96
495	AF036977	Homo sapiens	unknown	1812	100
496	U93564	Homo sapiens	p40	133	45
497	Y91405	Homo sapiens	Human secreted protein sequence encoded by gene 2 SEQ ID NO:126.	357	100
498	AF069781	Drosophila melanogaster	Bem46-like protein	653	43
499	Y16601	Homo sapiens	Human cell-cycle phosphoprotein CECYP-2.	1658	98
500	X70944	Homo sapiens	PTB-associated splicing factor	3883	100
501	AF027503	Mus musculus	putative membrane-associated guanylate kinase 1	205	36
502	AF282874	Homo sapiens	nectin 3; PRR3	2856	99
503	AJ249732	Homo sapiens	G8 protein	669	100
504	AF208861	Homo sapiens	BM-019	1629	100
505	L09708	Homo sapiens	complement component C2	4022	100
507	X66285	Mus musculus	HC1 ORF	115	43
207					

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	1DENTITY
509	Y94971	Homo sapiens	Human secreted protein clone fal71_1 protein sequence SEQ	SCORE 2176	100
			ID NO:148.		
510	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	781	77
511	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1347	100
512	AB019038	Homo sapiens	beta-1,4 mannosyltransferase	1520	99
513 514	X84908 X52851	Homo sapiens	phosphorylase kinase	5729	99
515	AF186084	Homo	peptidylprolyl isomerase epidermal growth factor	650 3046	76 99
516	G03602	sapiens Homo sapiens	repeat containing protein Human secreted protein, SEQ		
		nomo sapiens	ID NO: 7683.	505	99
517	U04706	Bos taurus	50 kDa protein	1749	77
518	G00653	Homo sapiens	Human secreted protein, SEQ ID NO: 4734.	530	100
519	AF161475	Homo sapiens	HSPC126	1368	100
520	Y99366	Homo sapiens	Human PRO1475 (UNQ746) amino acid sequence SEQ ID NO:88.	3394	97
521	AF266852	Homo sapiens	PTPLA	1295	100
522	AE000995	Archaeoglobu	chromosome segregation	153	20
	l Bosso	s fulgidus	protein (smc1)		<u> </u>
523	AF062249	Homo sapiens	immunoglobulin heavy chain variable region	605	97
524	AJ223830	Rattus norvegicus	AREI	2950	98
525	W01535	Homo sapiens	Cellular homologue of the SV40 large T antigen.	1276	83
526	AF145658	Drosophila melanogaster	BcDNA.GH10229	320	33
527	AF112213	Homo sapiens	putative Rab5-interacting protein	524	79
528	D49387	Homo	NADP dependent leukotriene b4	1616	100
529	Y30819	sapiens Homo sapiens	12-hydroxydehydrogenase Human secreted protein		
			encoded from gene 9.	328	32
530	AL079335	Homo sapiens	dJ132F21.3 (72.1 KDa protein (DKFZP564A032, SBB188) similar to mouse IFN-gamma induce MG11.)	1059	99
531	Y91506	Homo sapiens	Human secreted protein sequence encoded by gene 56 SEQ ID NO:179.	1159	98
532	X76116	Caenorhabdit	carrier protein (c2)	576	50
533	X76116	is elegans Caenorhabdit	carrier protein (c2)		
		is elegans		506	50
534	X12966	Homo sapiens	3-oxoacyl-CoA thiolase propeptide (424 AA)	1972	100
535	Y09267	Homo sapiens	flavin-containing monooxygenase 2	2486	100
536	Z11773	Homo sapiens	SRE-ZBP	2201	99
537	D84224	Homo sapiens	methionyl tRNA synthetase	4741	99
538	D84224	Homo sapiens	methionyl tRNA synthetase	3887	99
539 540	D84224 D84224	Homo sapiens	methionyl tRNA synthetase	2933	96
541	J03244	Homo sapiens Bos taurus	methionyl tRNA synthetase H+ ATPase 31kDa subunit (EC	4529 848	99 77
542	Y92514	Vene content	3.6.1.3)	-	
543	AF221712	Homo sapiens	Human OXRE-11. Smad- and Olf-interacting	2301	99
		sapiens	zinc finger protein	2151	61
544	AE000919	Methanobacte rium thermoautotr	conserved protein	207	38
		ophicum			1
545	A06669	synthetic construct	preTGF-betal	2070	99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	† IDENTITY
546	Y02698	Homo sapiens	Human secreted protein encoded by gene 49 clone HTPCS60.	854	98
547	AF112205	Homo sapiens	WSB-1 protein	2275	100
548	X60271	Mus musculus	c-rel	2264	74
549	AC016827	Arabidopsis thaliana	putative GTPase	810	42
550	Y70400	Homo sapiens	Human cell-signalling protein-2.	429	68
551	AB048365	Homo sapiens	NEDD4-like ubiquitin ligase 1	8290	99
552	Y57880	Homo sapiens	Human transmembrane protein HTMPN-4.	1112	95
553	AF119855	Homo sapiens	PRO1847	265	67
554	M17236	Homo sapiens	MHC HLA-DQ alpha precursor	1332	100
555	AL078468	Arabidopsis thaliana	putative protein	540	40
556	AC006963	Homo sapiens	similar to Kelch proteins; similar to BAA77027 (PID:g4650844)	515	44
557	AK024487	Homo sapiens	FLJ00086 protein	1623	98
558	M12140	Homo sapiens	pol gene protein; Xxx	117	48
559	W74825	Homo sapiens	Human secreted protein encoded by gene 97 clone HAQBF73.	225	56
560	X56681	Homo sapiens	junD protein	373	88
561	AF003136	Caenorhabdit is elegans	contains weak similarity to an AMP-binding motif	2926	54
562	AL109839	Homo sapiens	dJ1069P2.3.1 (novel PABPC1 (poly(A)-binding protein)	877	100
563	AF181640	Drosophila melanogaster	BcDNA.GH09817	289	42
564	AF052723	Feline leukemia virus	gag-pol precursor polyprotein gPr80	1547	43
565	AF161472	Homo sapiens	HSPC123	439	44
566	Y28817	Homo sapiens	pt326_4 secreted protein.	3338	100
567	U09848	Homo sapiens	zinc finger protein	1738	100
569	AF155113	Homo sapiens	NY-REN-55 antigen	3603	93
570	AF155113	Homo sapiens	NY-REN-55 antigen	3951	99
571 572	AL032821 M69181	Homo sapiens	dJ55C23.1 (vanin 1)	1821	98
572		Homo sapiens	non-muscle myosin B	7350	99
574	M69181 Y59678	Homo sapiens	non-muscle myosin B Secreted protein 108-008-5-0-	7311	98
575		Home sapiens	E6-FL.	772	100
	AL365234	Arabidopsis thaliana	putative protein	788	40
576	AL365234	Arabidopsis thaliana	putative protein	788	40
577	X06745	Homo sapiens	DNA polymerase alpha-subunit (AA 1 - 1462)	7619	99
578	AB041642	Homo sapiens	PAR-6	1342	100
579	D86984	Homo sapiens	similar to yeast adenylate cyclase (S56776)	2446	100
580	AF165124	Homo sapiens	gamma-aminobutyric acid A receptor gamma 2	2499	99
581	W88812	Homo sapiens	Polypeptide fragment encoded by gene 58.	2339	99
582	U82319	Homo sapiens	novel ORF	342	100
583	P92219	Homo sapiens (human)	CR1 protein.	11425	99
584	AJ223948	Homo sapiens	RNA helicase	6608	99
585	Y08612	Homo sapiens	88kDa nuclear pore complex protein	3874	99
586	Y42384	Homo sapiens	Amino acid sequence of lv310 7.	1007	37
587	AF129756	Homo sapiens	BAT4	1873	98

ID	ACCESSION	SPECIES	DESCRIPTION	SMITH-	1
NO:	NUMBER			WATERMAN SCORE	IDENTITY
588	AF131775	Homo sapiens	Unknown	1929	99
589	AJ250865	Homo sapiens	TESS 2	2348	100
591	298885	Homo sapiens	dJ522J7.2 (bromodomain-	4167	100
		·	containing 1 (similar to	1	
		İ	peregrin, BR140))	1	
592	L76571	Homo sapiens	nuclear hormone receptor	1355	100
593	AF091622	Homo sapiens	PHD finger protein 3	9054	100
594	X56807	Homo sapiens	desmocollin type 2a	4443	100
595	AL137802	Homo sapiens	dJ798A10.1 (novel protein)	212	55
596	AL022329	Homo	bK407F11.2 (adrenergic, beta,	3653	100
		sapiens	receptor kinase 2)	1	
597	AF226048	Homo sapiens	GL003	2009	99
598	AJ278112	Homo	putative cell cycle control	335	23
		sapiens]	protein]
		>Y49635		ļ	
		Y49635 21-	1	l	
		OCT-1999 15-			
	1	APR-1998			1
		Human sdp3.5			j
		protein.			
		[Homo			
		sapiens			L
599	Y59741	Homo sapiens	Human normal ovarian tissue	1574	99
			derived protein 18.		
600	L36531	Homo sapiens	integrin alpha 8 subunit	5386	99
601	Y38458	Homo sapiens	Human secreted protein	895	100
			encoded by gene No. 20.		
602	AF218584	Homo sapiens	GGA1	3265	100
603	Y13115	Homo sapiens	serine/threonine protein	5071	99
			kinase		
604	AL132776	Homo sapiens	dJ393D12.1 (KIAA0776)	2413	99
605	AL034452	Homo sapiens	dJ682J15.1 (novel Collagen	1979	100
			triple helix repeat	•	
	- 		containing protein)		
606	Y14494	Homo sapiens	aralari	3465	99
608	AJ001981	Homo sapiens	OXA1L	2603	100
608	X86098	Homo	binds directly to adenovirus	3069	100
610	AF163572	Homo sapiens	type 5 ElA protein Forssman glycolipid	1865	L
910	Ar 1632/2	Homo sabrens		1 1865	
		_			99
<u> </u>	NE1 (1 E02		synthetase		
611	AF161503	Homo sapiens	HSPC154	1261	97
612	L41834	Homo sapiens Ensis minor	HSPC154 nuclear protein	1261 345	97
	1	Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated	1261	97
612 613	L41834 Y91954	Homo sapiens Ensis minor Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9).	1261 345 3668	97 30 100
612 613	L41834 Y91954 AL022327	Homo sapiens Ensis minor Homo sapiens Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027)	1261 345 3668	97 30 100
612 613 614 615	L41834 Y91954 AL022327 X85786	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor	1261 345 3668 361 3203	97 30 100 94
612 613 614 615 616	L41834 Y91954 AL022327 X85786 Y08319	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2	1261 345 3668 361 3203 3487	97 30 100 94 100 99
612 613 614 615 616 617	L41834 Y91954 AL022327 X85786 Y08319 D12644	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein	1261 345 3668 361 3203 3487 3609	97 30 100 94 100 99 97
612 613 614 615 616 617 618	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT	1261 345 3668 361 3203 3487 3609 5936	97 30 100 94 100 99 97 89
612 613 614 615 616 617	L41834 Y91954 AL022327 X85786 Y08319 D12644	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted	1261 345 3668 361 3203 3487 3609	97 30 100 94 100 99 97
612 613 614 615 616 617 618	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO.	1261 345 3668 361 3203 3487 3609 5936	97 30 100 94 100 99 97 89
612 613 614 615 616 617 618 619	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163.	1261 345 3668 361 3203 3487 3609 5936 1684	97 30 100 94 100 99 97 89
612 613 614 615 616 617 618	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger	1261 345 3668 361 3203 3487 3609 5936	97 30 100 94 100 99 97 89
612 613 614 615 616 617 618 619	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein	1261 345 3668 361 3203 3487 3609 5936 1684	97 30 100 94 100 99 97 89 99
612 613 614 615 616 617 618 619	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23	1261 345 3668 361 3203 3487 3609 5936 1684	97 30 100 94 100 99 97 89
612 613 614 615 616 617 618 619	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120)	1261 345 3668 361 3203 3487 3609 5936 1684	97 30 100 94 100 99 97 89 99
612 613 614 615 616 617 618 619 620 621	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P	1261 345 3668 361 3203 3487 3609 5936 1684	97 30 100 94 100 99 97 89 99 23
612 613 614 615 616 617 618 619 620 621	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortflin	1261 345 3668 361 3203 3487 3609 5936 1684 199 3440 861 4436	97 30 100 94 100 99 97 89 99 23 99
612 613 614 615 616 617 618 619 620 621	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH	1261 345 3668 361 3203 3487 3609 5936 1684	97 30 100 94 100 99 97 89 99 23
612 613 614 615 616 617 618 619 620 621 622 623 624	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248 X61100	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH dehydrogenase precursor	1261 345 3668 361 3203 3487 3609 5936 1684 199 3440 861 4436 3734	97 30 100 94 100 99 97 89 99 23 99
612 613 614 615 616 617 618 619 620 621	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH dehydrogenase precursor 75 kda infertility-related	1261 345 3668 361 3203 3487 3609 5936 1684 199 3440 861 4436	97 30 100 94 100 99 97 89 99 23 99
612 613 614 615 616 617 618 619 620 621 622 623 624	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248 X61100	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortflin 75 kDa subunit NADH dehydrogenase precursor 75 kda infertility-related sperm protein	1261 345 3668 361 3203 3487 3609 5936 1684 199 3440 861 4436 3734 2125	97 30 100 94 100 99 97 89 99 23 99 100 99
612 613 614 615 616 617 618 619 620 621 622 623 624 625	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248 X61100 S58544 AF151027	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortilin 75 kDa subunit NADH dehydrogenase precursor 75 kda infertility-related sperm protein HSPC193	1261 345 3668 361 3203 3487 3609 5936 1684 199 3440 861 4436 3734 2125	97 30 100 94 100 99 97 89 99 23 99 100 99 99
612 613 614 615 616 617 618 619 620 621 622 623 624	L41834 Y91954 AL022327 X85786 Y08319 D12644 U28789 Y35914 AB046382 Y00062 AF068286 X98248 X61100	Homo sapiens Ensis minor Homo sapiens Homo sapiens Homo sapiens Homo sapiens Mus musculus Mus musculus Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	HSPC154 nuclear protein Human cytoskeleton associated protein 9 (CYSKP-9). dJ355C18.1 (KIAA0027) binding regulatory factor kinesin-2 KIF2 protein PACT Extended human secreted protein sequence, SEQ ID NO. 163. testis-abundant finger protein precursor polypeptide (AA -23 to 1120) HDCMD38P sortflin 75 kDa subunit NADH dehydrogenase precursor 75 kda infertility-related sperm protein	1261 345 3668 361 3203 3487 3609 5936 1684 199 3440 861 4436 3734 2125	97 30 100 94 100 99 97 89 99 23 99 100 99 99

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
629	Y50911	Homo sapiens	Human fetal brain cDNA clone vb7 1 derived protein	1694	100
630	AF098786	Homo sapiens	17 beta-hydroxysteroid dehydrogenase type VII	1754	100
631	AL034555	Homo sapiens	dJ134019.3 (zinc finger protein 151 (pHZ-67))	4273	100
632	W74826	Homo sapiens	Human secreted protein encoded by gene 98 clone HAQBT94.	794	96
633	AF288288	Homo sapiens	HPT protein	2236	. 100
634	AF041429	Homo sapiens	pRGR1	823	99
635	X66357	Homo sapiens	serine/threonine protein kinase	1589	100
636	Y11284	Homo sapiens	AFX1	2571	98
637	AB004884	Homo sapiens	PKU-alpha	3718	99
638	AJ002303	Homo sapiens	synaptogyrin 1c	1020	100
639 640	AJ002304 AJ002303	Homo sapiens	synaptogyrin 1c	933	94
641	D87682	Homo sapiens	similar to a C.elegans protein encoded in cosmid T26A5.	2676	100
642	M14660	Homo sapiens	ISG-K54	2473	99
643	X06661	Homo sapiens	calbindin (AA 1-261)	1358	100
644	AF119900	Homo sapiens	PRO2822	185	76
645	AB031048	Drosophila melanogaster	microtubule associated- protein orbit	738	27
646	AF250842	Drosophila melanogaster	multiple asters	834	29
647	X86691	Homo sapiens	Mi-2 protein	10110	99
648	U67934	Homo sapiens	44.9 kDa protein C18B11 homolog	827	96
649	AF236061	Oryctolagus cuniculus	RING-finger binding protein	3830	91
650	AL034553	Homo sapiens	dJ914F20.2 (KIAA0784 protein similar to Mus musculus activity-dependent neuroprotective protein (Adnp))	5708	100
653	X14766	Homo sapiens	GABA-A receptor alpha 1 subunit	2388	99
654	AC004614	Homo sapiens	similar to f-spondin proteins AB006086 (PID:g2529225)	3026	99
655	Y57908	Homo sapiens	Human transmembrane protein HTMPN-32.	608	99
656	Z34975	Homo sapiens	ldlCp	3733	100
658	AL050306	Homo sapiens	dJ475B7.2 (novel protein)	1942	99
659	W76734	Homo sapiens	Human mDia Rho targeting protein.	781	34
660	AF202724	Homo sapiens	Sad1 unc-84 domain protein 1	2172	100
661	Z21966	Homo sapiens	mPOU homeobox protein	1529 4752	100 59
662 663	AJ242954 AF182316	Mus musculus Homo sapiens	dysferlin myoferlin	6232	99
665	AL161516	Arabidopsis thaliana	hypothetical protein	209	30
667	X59303	Homo sapiens	valyl-tRNA synthetase	3393	99
668	Y13355	Homo sapiens	Amino acid sequence of protein PRO220.	3692	100
669	AB010692	Arabidopsis thaliana	contains similarity to endo- beta-N-acetylglucosaminidase gene	611	52
671	X56123	Mus musculus	talin	4474	76
672	AB039371	Homo sapiens	mitochondrial ABC transporter	2902	99
673	AF269223	Homo sapiens	TCP11	806	42
674	AF229633	Mus musculus	groucho-related protein 4	4053	99
675	L14463	Rattus	'transducin	3619	92

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		norvegicus			
676	AC005757	Homo sapiens	R32611_1	2779	100
677	S61069	Homo sapiens	reverse transcriptase homolog=pol {retroviral element}	252	65
678	AF271388	Homo sapiens	CMP-N-acetylneuraminic acid synthase	2273	100
679	X79066	Homo sapiens	ERF-1	1783	100
680	AF118566	Mus musculus	hematopoietic zinc finger protein	769	50
681	Y51415	Homo sapiens	Human wild type pKe83 , protein.	2621	99
682	AL133545	Homo sapiens	bA386N14.1 (novel protein similar to a dual specificity phosphatase)	700	68
683	Y86214	Homo sapiens	Nuclear transport protein clone hfb341 protein sequence.	5888	99
684	¥94952	Homo sapiens	Human secreted protein clone fh116_11 protein sequence SEQ ID NO:110.	354	98
685	AL021878	Homo sapiens	dJ257120.4 (transcription factor 20 (AR1) (KIAA0292) (isoform 2))	154	67
686	AE000198	Escherichia coli	orf, hypothetical protein	628	100
687	M58378	Homo sapiens	synapsin I	3730	99
688	AF039697	Homo sapiens	antigen NY-CO-31	508	98
689	U09355	Oryctolagus cuniculus	protein phosphatase 2A1 B gamma subunit	2356	99
690	AF155106	Homo sapiens	NY-REN-36 antigen	265	50
691	AC004774	Homo sapiens	Dlx-5	1542	100
692	X90530	Homo sapiens	ragB	1926	99
693 694	X90530	Homo sapiens	ragB	1405	99
695	X90530 G01563	Homo sapiens Homo sapiens	ragB Human secreted protein, SEQ ID NO: 5644.	1590 330	100
696	AC011810	Arabidopsis thaliana	Putative methionine aminopeptidase	669	52
697	AJ250425	Rattus norvegicus	Collybistin I	2455	98
698	AB037901	Homo sapiens	gene amplified in squamous cell carcinoma-1	5364	99
699	Y99401	Homo sapiens	Human PRO1327 (UNQ687) amino acid sequence SEQ ID NO:218.	1386	100
701	AF221712	Homo sapiens	Smad- and Olf-interacting zinc finger protein	6705	100
702	X83573	Homo sapiens	ARSE	3184	99
703	АJ243274	Homo sapiens	AP-2rep protein	2078	99
704	Y71262	Homo sapiens	Human chondromodulin-like protein, Zchml.	1697	94
705	¥71262	Homo sapiens	Human chondromodulin-like protein, Zchml.	1736	99
706	¥41257	Homo sapiens	Amino acid sequence of long human FAIM.	1060	100
707	AL022237	Homo sapiens	bK1191B2.3 (PUTATIVE novel Acyl Transferase similar to C. elegans C50D2.7) (isoform 1))	2030	100
708	AJ006266	Homo sapiens	AND-1 protein	5942	100
709	G01571	Homo sapiens	Human secreted protein, SEQ ID NO: 5652.	777	99
710	Y08698	Homo sapiens	ranbp3	2849	98
711	Y68770	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-2.	754	99

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	1
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
712	U93574	Homo sapiens	putative p150	799	59
713	AC004531	Homo sapiens	Gene with similaity to DEAD	2715	99
			box helicases		
714	D89016	Homo sapiens	Neuroblastoma	538	48
715	Y92175	Homo sapiens	Human cardiovascular system	734	98
		į	associated protein tyrosine		i
***			phosphatase 2.		<u> </u>
716	AL137013	Homo sapiens	bA311P8.3 (probable uracil	862	100
	30025453		phosphoribosyltranferase)		
717	AB035123	Mus musculus	GD1 alpha/GT1a alpha/GQ1b alpha synthase	1696	93
718	Y96290	Homo >P40254	Human IGFAM-2 immunoglobulin.	2345	85
110	136230	P40254 25-	Adman 1GFAM-2 1mmunog1obulin.	2345	85
*		OCT-1984 09-			
		APR-1983			
	1	Human IgD.			
		[Homo		1	:
		sapiens			ļ
719	X07979	Homo sapiens	integrin beta 1 subunit	4347	99
		•	precursor		"
720	AJ224819	Homo sapiens	tumor suppressor	2149	99
721	Y07595	Homo sapiens	transcription factor TFIIH	2373	100
722	W41565	Homo	Human calpain.	1591	99
		sapiens]	.		""
		>W41564		1	1
		W41564 08-		1	J
		OCT-1997 05-			
		APR-1996			
		Human		ļ	
		calpain.		i	!
		[Homo			
		sapiens			
723	AF161341	Homo sapiens	HSPC078	1097	98
724	AF187318	Homo sapiens	F-box protein Fbx2	1607	100
725	AC006708	Caenorhabdit	contains simlarity to	1143	46
		is elegans	Saccharomyces cerevisiae pre-		i
	1		mRNA splicing protein PRP31		
506	20000		(GB: Z72876)	<u> </u>	
726	AC006708	Caenorhabdit	contains similarity to	988	46
	1	is elegans	Saccharomyces cerevisiae pre-		1
	1		mRNA splicing protein PRP31 (GB:Z72876)	į	ł
727	AC024818	Caenorhabdit	contains similarity to Pfam	950	ļ
121	AC024010	is elegans	family PF00400 (WD domain,	950	44
	ļ	is elegans	G-beta repeat), score=81.8,		
	1		E=1.4e-20, N=3		
728					4.2
	1 AJOO5897		I JMS	1 2 3 1	
729	AJ005897 Y45377	Homo sapiens	JMS Human secreted protein	831	47
729	AJ005897 Y45377	Homo sapiens	Human secreted protein	908	97
729			Human secreted protein fragment encoded from gene		1
729		Homo sapiens	Human secreted protein fragment encoded from gene 27.	908	97
	Y45377		Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ		1
	Y45377	Homo sapiens	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012.	908 578	100
730	Y45377 G03931	Homo sapiens	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ	908	97
730	Y45377 G03931	Homo sapiens Homo sapiens Oncorhynchus	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein	908 578 3865	97 100 76
730 731	Y45377 G03931 AB012720	Homo sapiens Homo sapiens Oncorhynchus masou	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein	908 578	100
730 731	Y45377 G03931 AB012720	Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8.	908 578 3865 862	97 100 76 97
730 731 732	Y45377 G03931 AB012720 W73404	Homo sapiens Homo sapiens Oncorhynchus masou	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein	908 578 3865	97 100 76
730 731 732	Y45377 G03931 AB012720 W73404	Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731.	908 578 3865 862 644	97 100 76 97
730 731 732 733	Y45377 G03931 AB012720 W73404 G02650	Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ	908 578 3865 862	97 100 76 97
730 731 732 733	Y45377 G03931 AB012720 W73404 G02650	Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit is elegans	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a	908 578 3865 862 644	97 100 76 97 97
730 731 732 733 734	Y45377 G03931 AB012720 W73404 G02650 AC024813	Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein Y54F10AL.a dJ967N21.6 (novel CDP-alcohol	908 578 3865 862 644	97 100 76 97
730 731 732 733 734	Y45377 G03931 AB012720 W73404 G02650 AC024813	Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit is elegans	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase	908 578 3865 862 644	97 100 76 97 97
730 731 732 733 734	Y45377 G03931 AB012720 W73404 G02650 AC024813	Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit is elegans	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein)	908 578 3865 862 644 152	97 100 76 97 97 24
730 731 732 733 734 735	Y45377 G03931 AB012720 W73404 G02650 AC024813 AL035461	Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase	908 578 3865 862 644	97 100 76 97 97
730 731 732 733 734 735	Y45377 G03931 AB012720 W73404 G02650 AC024813 AL035461	Homo sapiens Homo sapiens Oncorhynchus masou Homo sapiens Homo sapiens Caenorhabdit is elegans Homo sapiens	Human secreted protein fragment encoded from gene 27. Human secreted protein, SEQ ID NO: 8012. GTP-binding protein Human secreted protein encoded by Gene No. 8. Human secreted protein, SEQ ID NO: 6731. Hypothetical protein y54F10AL.a dJ967N21.6 (novel CDP-alcohol phosphatidyltransferase family member protein) similar to S. cerevisiae YJU2	908 578 3865 862 644 152	97 100 76 97 97 24

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	identity
738	AJ131712	Homo sapiens	nucleolar RNA-helicase	2793	100
739	AJ133115	Homo sapiens	TSC-22-like protein	2054	99
740	X98258	Homo sapiens	M-phase phosphoprotein 9	953	100
741	X98258	Homo sapiens	M-phase phosphoprotein 9	564	74
	1			960	85
742	U97191	Caenorhabdit is elegans	strong similarity to the YPT1 sub-family of RAS proteins	960	85
743	X76057	Homo sapiens	phosphomannose isomerase	2191	100
744	G03209	Homo sapiens	Human secreted protein, SEQ	496	98
			ID NO: 7290.	4034	99
745	X97064	Homo sapiens	Sec23 protein		1
746	W93946	Homo sapiens	Human regulatory molecule HRM-2 protein.	994	100
747	Y73388	Homo sapiens	HTRM clone 3376404 protein sequence.	1565	99
748	M19529	Sus scrofa	follistatin A	1906	98
	1	Trichomonas	centrin, putative	183	28
749	AJ249457	vaginalis	centrin, putative		
750	AC004410	Homo sapiens	fos39554_1	2094	100
751	AF074968	Homo sapiens	p47ING3 protein	2167	100
752	AF252284	Homo sapiens	transcription specificity factor Sp1	4005	100
753	AB049629	Homo sapiens	phospholysine	1375	99
153	AB049629	HOMO Saprens	phosphohistidine inorganic	1373	"
		· ·	pyrophosphate phosphatase		
754	D79205	Homo sapiens	ribosomal protein L39	160	77
755	AB008430	Homo sapiens	CDEP	142	29
758	L32162	Homo sapiens	transcription factor	574	80
759	AF037204	Homo sapiens	RING zinc finger protein	295	54
760	Y44250	Homo sapiens	Human cell signalling protein-13.	625	100
			Cide-b	1136	100
761	AF218586	Homo sapiens			1
762	U38934	Gallus gallus	histone H2A	625	97
763	AF226053	Homo sapiens	HSKM-B	606	32
764	X13403	Homo sapiens	Oct-1 protein (AA 1 - 743)	3626	100
765	D87446	Homo sapiens	Similar to a C.elegans protein encoded in cosmid C27F2 (U40419)	568	38
766	AL023828	Caenorhabdit is elegans	Y17G7B.14	200	27
767	Y82777	Homo sapiens	Human chordin related protein (Clone dw665 4).	2551	99
768	X92475	Homo sapiens	ITBA1	1429	100
769	Y42752	Homo sapiens	Human calcium binding protein 3 (CaBP-3).	1426	100
770	X51416	Homo sapiens	hormone receptor hERR1 (AA 1-	2641	97
	1 7005555	11		1793	100
771	AJ006591	Homo sapiens	cysteine-rich protein		100
772 773	A08695 Z12173	Homo sapiens Homo sapiens	rap2 N-acetylglucosamine-6-	935 2970	100
774	Y91950	Homo sapiens	sulphatase Human cytoskeleton associated	565	43
776	1 022700	Vomo con les	protein 5 (CYSKP-5). dJ322P7.1 (zinc finger)	855	56
776	AL023799	Homo sapiens		855	56
777	AL023799	Homo sapiens	dJ322P7.1 (zinc finger)		.1
778	G01880	Homo sapiens	Human secreted protein, SEQ ID NO: 5961.	849	98
779	AJ012590	Homo sapiens	glucose 1-dehydrogenase	4155	99
780	AL078582	Homo sapiens	dJ130E4.2 (KIAA0796)	1321	68
781	275955	Caenorhabdit	similar to mitochondrial	384	34
782	AL109965	is elegans	dJ1121G12.2 (SCAN domain-	900	100
783	AF061262	sapiens Mus	containing 1 protein) semaF cytoplasmic domain	1316	83
	G03873	musculus	associated protein 2		95
784		Homo sapiens	Human secreted protein, SEQ	649	

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
	1		ID NO: 7954.		<u> </u>
785	Y84441	Homo sapiens	Amino acid sequence of a human RNA-associated protein.	2074	100
786	Y00918	Homo sapiens	Human Rab protein, RABP-1, protein sequence.	1048	99
787	Z97029	Homo sapiens	ribonuclease HI large subunit	1548	99 .
788	AB035384	Homo sapiens	SRp25 nuclear protein	962	94
789	AF024631	Homo sapiens	ANG2	2644	100
790	AJ006710	Rattus norvegicus	phosphatidylinositol 3-kinase	4508	97
792	V00638	bacteriophag e lambda	reading frame eal0	600	100
793	AF049103	Homo sapiens	Huntingtin interacting protein	819	100
795	226317	Homo sapiens	desmoglein 2	4810	99
796	Y76884	Homo sapiens	Retinoblastoma binding protein-7sequence.	5080	99
797	U15155	Gallus gallus	trypsinogen	372	37
798	U97189	Caenorhabdit is elegans	strong similarity to thw P13/P14 family of kinases	227	28
799	AF112201	Homo sapiens	neuronal protein NP25	1053	100
800	AF234765	Rattus norvegicus	serine-arginine-rich splicing regulatory protein SRRP86	958	63
801	AF267852	Homo sapiens	placental protein 13-like protein	743	99
802	AF208851	Homo sapiens	BM-009 Similarity to Human	152	27
803	Z81097	is elegans	retinoblastoma-binding protein RBAP46 yk662d12.5 comes from this gene Human secreted protein, SEQ	496	98
804	G02113	Homo sapiens	ID NO: 6194.	1160	100
805	AL121673	Homo sapiens	bA305P22.1 (novel protein) putative GTPase activator	264	30
806	AC013483	Arabidopsis thaliana Arabidopsis	protein putative GTPase activator	264	30
807	AC013483	thaliana	protein beta-ureidopropionase	1494	100
808	AB013885 AF078842	Homo sapiens	HOTTL protein	1581	99
809	AF161421	Homo sapiens	HSPC303	2134	96
810 811	AF261689	Homo sapiens	DNA polymerase epsilon p17 subunit	734	100
812	274029	Caenorhabdit is elegans	Similarity to C.elegans alcohol dehydrogenase comes from this gene	610	71
813	Z73497	Homo sapiens	cU240C2.2 (Core histone H2A/H2B/H3/H4)	324	100
814	W87689	Homo sapiens	Human HTXFT19 polypeptide.	1484	99
815	X16282	Homo sapiens	zinc finger protein (217 AA) (1 is 2nd base in codon)	1109	99
816	292539	Mycobacteriu m tuberculosis	pth	300	36
818	AB030483	Mus musculus	В9	197	27
819	AL117555	Homo sapiens	hypothetical protein	321	94
820 821	AC005328 G03951	Homo sapiens	R26660_2, partial CDS Human secreted protein, SEQ	865 700	97
			ID NO: 8032.	174	20
822	L34807	Musca	uzunzponar.	1	
822	L34807 G02928	domestica Homo sapiens	Human secreted protein, SEQ	558	78

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		romyces	protein 1		
225	27005500	pombe			ļ
825	AJ006692	Homo sapiens	ultra high sulfer keratin	693	68
826	U23037	Oryctolagus cuniculus	eIF-2Bepsilon	3406	90
827	G03412	Homo sapiens	Human secreted protein, SEQ ID NO: 7493.	464	100
828	Y30827	Homo sapiens	Human secreted protein encoded from gene 17.	113	44
829	Y32199	Homo sapiens	Human receptor molecule (REC) encoded by Incyte clone 2022379.	1012	100
830	W78279	Homo sapiens	Fragment of human secreted protein encoded by gene 33.	1264	99
832	AB011542	Homo sapiens	MEGF9	2097	100
833	G02639	Homo sapiens	Human secreted protein, SEQ ID NO: 6720.	223	70
834	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1574	100
835	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1144	89
836	AF119664	Homo sapiens	transcriptional regulator protein HCNGP	1448	94
837	X12517	Homo sapiens	C protein (AA 1-159)	918	100
838	U32865	Drosophila melanogaster	linotte protein	164	24
839	AF067730	Homo sapiens	TLS-associated protein TASR-2	631	56
840	U27831	Homo sapiens	striatum-enriched phosphatase	2840	98
841	AF286366	Homo sapiens	CamKI-like protein kinase	1796	100
842	G02309	Homo sapiens	Human secreted protein, SEQ ID NO: 6390.	278	98
843	AE003615	Drosophila melanogaster	ade3 gene product	113	48
844	G01350	Homo sapiens	Human secreted protein, SEQ ID NO: 5431.	629	100
845	U27838	Mus musculus	glycosyl-phosphatidyl- inositol-anchored protein homolog	3305	96
847	Y87788	Homo sapiens	Human RBP-26 protein.	2026	100
848	AF164794	Homo sapiens	Diff33 protein homolog	2398	100
849	U41315	Homo sapiens	ZNF127-Xp	2458	93
850	AF192784	Homo sapiens	makorin 1	2062	97
851	Y58628	Homo sapiens	Protein regulating gene expression PRGE-21.	1548	100
852	Z22968	Homo sapiens	M130 antigen	6205	100
853	Z22971	Homo sapiens	M130 antigen extracellular variant	6380	100
854	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	330	96
855	G03362	Homo sapiens	Human secreted protein, SEQ ID NO: 7443.	203	100
856	AF285118	Homo sapiens	CGI-203	452	100
857	AC006069	Arabidopsis thaliana	putative cleavage and polyadenylation specifity factor	1383	55
858	AL021546	Homo sapiens	Cytochrome C Oxidase Polypeptide VIa-liver precursor (EC 1.9.3.1)	593	100
859	L02956	Xenopus laevis	ribonucleoprotein	1664	85
860	AF201947	Homo sapiens	MEK binding partner 1	616	100
861	L31783	Mus musculus	uridine kinase	1266	92
862	AF161472	Homo sapiens	HSPC123	602	73
863	Z49068	Caenorhabdit is elegans	mitochondrial carrier protein	370	43
864	AF154108	Homo sapiens	tumor necrosis factor type 1	3559	99

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
ID	NUMBER	}		SCORE	1
NO:			receptor associated protein		
365	AE001530	Helicobacter	putative	230	32
	ABOULDSO	pylori J99	ļ •		
366	X57807	Homo sapiens	immunoglobulin lambda light chain	699	91
367	AL031673	Homo sapiens	dJ694B14.1 (PUTATIVE novel KRAB box protein with 18 C2H2 type Zinc finger domains)	4066	99
			phosphate cyclase	238	100
368	Y11652	Homo sapiens	high-qlucose-regulated	3041	99
369	AF192968	Homo sapiens	protein 8	3012	_
870	AB020648	Homo sapiens	KIAA0841 protein	3237	99
371	AL031427	Homo sapiens	dJ167A19.1 (novel protein)	1608	100
872	AF151534	Homo sapiens	core histone macroH2A2.2	1866	100
873	AL021331	Homo sapiens	dJ366N23.1 (putative C. elegans UNC-93 (protein 1, C46F:1.1) LIKE protein)	1129	100
874	X14608	Homo sapiens	propionyl-CoA carboxylase	3579	100
875	AL117334	Homo sapiens	dJ687F11.1 (novel protein (part of translation of cDNA DKFZp434N061, Em:AL110249))	306	100
876	X79489	Saccharomyce	E-925 protein	446	35
877	Y53001	B cerevisiae Homo sapiens	Human secreted protein clone	811	100
077	133001		dn834_1 protein sequence SEQ ID NO:8.		
878	AF281064	Homo sapiens	CHMP1.5	957	100
879	X79417	Sus scrofa	40S ribosomal protein S12	687	100
880	AF001317	Saccharomyce s cerevisiae	Soilp	478	28
881	Y87275	Homo sapiens	Human signal peptide containing protein HSPP-52 SEQ ID NO:52.	2547	100
882	M14036	Homo sapiens	C1-inhibitor	598	77
883	AB041261	Homo sapiens	calcium-independent phospholipase A2	2903	100
		Mus musculus	proline-rich protein 48	999	84
884	AF020313	1	hypothetical protein	1104	99
885 886	Y10936 AF073997	Homo sapiens Mus musculus	myotubularin related protein	866	36
887	¥57893	Homo sapiens	Human transmembrane protein	1099	94
			HTMPN-17.	929	99
888	AL117635	Homo sapiens	hypothetical protein facilitative glucose	2046	99
889	AF210317	Homo sapiens	transporter family member GLUT9	2046	39
890	Y36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 416.	583	100
891	Y36031	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO.	192	57
892	AF237631	Homo sapiens	416. ubiquitous tropomodulin U- Tmod	1798	100
893	AF090929	Homo sapiens		653	99
894	AL031228	Homo sapiens	dJ1033B10.2 (WD40 protein BING4 (similar to S.	3196	100
			cerevisiae YER082C, M. sexta MNG10 and C. elegans F28D1.1)		
895	AL031228	Homo sapiens		2825	96
	1,	\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\		1302	95
896	AF171102	Homo sapiens			
897	AE003551	Drosophila	CG18176 gene product	633	33

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	* IDENTITY
898	AJ237946	Homo sapiens	DEAD Box Protein 5	2443	100
B99	Z97184	Homo sapiens	HKE2	624	100
900	Z97184	Homo sapiens	HKE2	409	98
901	AJ245587	Homo sapiens	Kruppel-type zinc finger	1942	100
902	AF091034	Homo sapiens	GTP-binding protein RAB22A	1011	100
903	R95953	Homo sapiens	Eukaryotic cell growth	414	96
		· · · · ·	inhibiting factor.	""	1
904	L04733	Homo sapiens	kinesin light chain	1936	72
905	AE003540	Drosophila	CG10984 gene product	446	33
906		melanogaster			
	M55542	Homo sapiens	guanylate binding protein isoform I	2993	98
907	M55542	Homo sapiens	guanylate binding protein isoform I	2901	96
908	W84085	Homo sapiens	Human membrane fusion protein WDProl.	1889	100
909	AF168676	Homo	TNF intracellular domain-	647	100
		sapiens	interacting protein	""	100
910	AB029150	Homo sapiens	KRAB zinc finger protein	2196	100
		-	HFB101L		
911	G02871	Homo sapiens	Human secreted protein, SEQ ID NO: 6952.	521	100
912	G03162	Homo sapiens	Human secreted protein, SEQ ID NO: 7243.	387	87
913	AJ243721	Homo	dTDP-4-keto-6-deoxy-D-glucose	1710	100
		sapiens)	4-reductase		
	ļ	>Y92508			
		Y92508 13-		1	
		APR-2000 06-			
		OCT-1998		ļ	
	1	Human OXRE-		ł	ļ
		5. [Homo		ļ	i
		sapiens		1	ł
914	U24189	Caenorhabdit	humahhari and makede 1997 1	1244	l-,
714	024109		hypothetical protein 1207-1;	244	41
		is elegans	Method: conceptual		
	ļ	Ì	translation supplied by	1	1
			authors	L	
915	Y02591	Homo sapiens	A human progesterone receptor	843	99
			complex p23-like protein.		
916	AE000984	Archaeoglobu	dinitrogenase reductase	171	26
		s fulgidus	activating glycohydrolase (draG)		
918	M23159	Cricetus	DHFR-coamplified protein	163	30
720	1.00235	cricetus	Diffit Coumpailined processis	1 203	30
919	L12018	Caenorhabdit	putative	1232	41
717	112015	is elegans	pucative	1232	4.1
920	AF102177	Homo sapiens	tumor antigen SLP-8p	1260	97
921		 -			
241	AL096712	Homo sapiens	dJ744124.2 (similar to a	1017	78
			novel human gene mapping to		
	<u> </u>		Activator)		
922	AL161495	Arabidopsis	putative WD-repeat protein	866	42
		thaliana		<u></u>	
923	AL161495	Arabidopsis	putative WD-repeat protein	442	36
	1	thaliana			
				1 685	51
	U97001	Caenorhabdit	similar to	605	
	U97001			605	
924	U97001 X71978	Caenorhabdit is elegans Mus musculus	Schizosaccharomyces pombe	l	
92 4 925	X71978	is elegans Mus musculus	Schizosaccharomyces pombe Fif	1503	95
924 925 926		is elegans Mus musculus Drosophila	Schizosaccharomyces pombe	l	
924 925 926	X71978 M92288	is elegans Mus musculus Drosophila melanogaster	Schizosaccharomyces pombe Fif beta-spectrin	1503 290	95 51
924 925 926	X71978	is elegans Mus musculus Drosophila	Schizosaccharomyces pombe Fif beta-spectrin Human secreted protein	1503	95
924 925 926 927	X71978 M92288 Y27575	is elegans Mus musculus Drosophila melanogaster Homo sapiens	Schizosaccharomyces pombe Fif beta-spectrin Human secreted protein encoded by gene No. 9.	1503 290 1392	95 51 100
924 925 926 927	X71978 M92288	is elegans Mus musculus Drosophila melanogaster	Schizosaccharomyces pombe Fif beta-spectrin Human secreted protein encoded by gene No. 9. Human secreted protein	1503 290	95 51
924 925 926 927 928	X71978 M92288 Y27575 Y22499	is elegans Mus musculus Drosophila melanogaster Homo sapiens	Schizosaccharomyces pombe Fif beta-spectrin Human secreted protein encoded by gene No. 9. Human secreted protein sequence clone mh703_1.	1503 290 1392	95 51 100
924 925 926 927	X71978 M92288 Y27575	is elegans Mus musculus Drosophila melanogaster Homo sapiens	Schizosaccharomyces pombe Fif beta-spectrin Human secreted protein encoded by gene No. 9. Human secreted protein	1503 290 1392	95 51 100
924 925 926 927	X71978 M92288 Y27575 Y22499	is elegans Mus musculus Drosophila melanogaster Homo sapiens Homo sapiens	Schizosaccharomyces pombe Fif beta-spectrin Human secreted protein encoded by gene No. 9. Human secreted protein sequence clone mh703_1.	1503 290 1392 2249	95 51 100

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:	 	is elegans	cm21c7		
932	AL080065	Homo sapiens	hypothetical protein	210	25
933	G01884	Homo sapiens	Human secreted protein, SEQ	767	98
		_	ID NO: 5965. integral membrane transporter	1200	100
934	AJ276485	Homo sapiens	protein		
935	AL035681	Homo sapiens	dJ756G23.3 (novel protein similar to drosophila transcriptional repressor)	1142	80
936	AB026808	Mus musculus	synaptotagmin XI	2142	95
937	AB020000	Homo sapiens	HRIHFB2216	2601	99
938	X65724	Homo sapiens	ORF2	498	100
939	W89024	Homo sapiens	Polypeptide fragment encoded	1487	100
			by gene 156.	117	100
940	G04047	Homo sapiens	Human secreted protein, SEQ ID NO: 8128.		
941	AF094583	Homo sapiens	putative HIV-1 infection related protein	452	100
942	AC024200	Caenorhabdit	contains similarity to	350	69
		is elegans	several zinc finger proteins but not to the zinc finger		
		Warra Garage	domains GSc	273	100
943	AF129756	Homo sapiens	alpha-tropomyosin	133	96
944	M23765	Rattus norvegicus			47
945	AC009917	Arabidopsis thaliana	Contains similarity to	583	
946	AF223468	Homo sapiens	AD021 protein	551	44
947	AF055473	Homo sapiens	GAGE-8	273	51
948	X75756	Homo sapiens	protein kinase C mu	2019	68
949	AF143956	Mus musculus	coronin-2	2300	93
950	Y36729	Homo sapiens	Human PG1 protein sequence.	1861	99
951	W49041	Homo sapiens	Human low density lipoprotein binding protein LBP-2.	282	67
952	AB016881	Arabidopsis thaliana	gene_id:MXC17.7~	203	46
953	Y01785	Homo sapiens	Human ubiquitin-conjugating enzyme >Y25341 Y25341 01-JUL- 1999 12-AUG-1998 Human NCE-2 protein.	365	100
954	AF145615	Drosophila melanogaster	BcDNA.GH03377	823	46
955	U09410	Homo sapiens	zinc finger protein ZNF131	2483	99
956	U09410	Homo sapiens	zinc finger protein ZNF131	1853	99
957	AF195623	Homo sapiens	cholinephosphotransferase 1 alpha	2126	99
958	X94917	Drosophila melanogaster	head-elevated expression in 0.9 kb	155	32
959	U54807	Rattus	GTP-binding protein	1167	97
960	AF058807	Bos taurus	GTP-binding protein rah	606	97
961	G03244	Homo sapiens	Human secreted protein, SEQ ID NO: 7325.	471	100
962	AF078850	Homo sapiens	steroid dehydrogenase homolog	583	40
963	AP001754	Homo sapiens	transient receptor potential- related channel 7, a novel	317	30
964	AL035419	Homo sapiens	putative Ca2+ channel protein dJ1100H13.1 (putative novel protein)	1129	100
965	X61381	Rattus	interferon-induced protein	202	46
966	D38169	rattus Homo	inositol 1,4,5-trisphosphate	3278	100
		sapiens	3-kinase isoenzyme dJ465N24.2.1 (PUTATIVE novel	893	100
967	AL031432	Homo sapiens	protein) (isoform 1)	093	100

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
968	U79275	Homo sapiens	unknown	611	100
969	AJ011306	Homo sapiens	guanine nucleotide exchange factor (long isoform)	2752	99
970	AF281134	Homo sapiens	exosome component Rrp46	1186	100
971	Ú53336	Caenorhabdit is elegans	weak similarity over a short region to myosin heavy chain	536	23
972	AC018749	Leishmania major	L8840.12	589	53
973	AF188504	Mus musculus	LNV	544	85
974	U25801	Homo sapiens	Taxl binding protein	852	98
975	AP049523	Homo sapiens	huntingtin-interacting protein HYPA/FBP11	1390	97
976	AF161530	Homo sapiens	HSPC182	1040	100
977	G04020	Homo sapiens	Human secreted protein, SEQ ID NO: 8101.	626	100
978	AF164797	Homo sapiens	ribosomal protein L17 isolog	908	100
979	U94991	Xenopus laevis	transcription factor XLMO1	795	97
980	\$73775	Homo sapiens	calmitine; calsequestrine	2029	100
981	Y94888	Homo sapiens	Human protein clone HP01462.	2501	100
982	AJ243191	Homo sapiens	heat shock protein	827	96
983	X65020	Bos taurus	PSST subunit of the NADH: ubiquinone oxidoreductase complex	964	85
984	AJ249207	Rhodococcus sp. AD45	putative racemase	351	43
985	Z30093	Homo sapiens	basic transcription factor 2, 35 kD subunit	1576	99
986	AB030835	Homo sapiens	contains two glutamine rich domains, three zinc-finger domains, and matrin 3 homologous domain 3 (MH3)	4697	99
987	AF227258	Bos taurus	RPGR-interacting protein-1	1262	38
988	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	4048	99
989	AL022238	Homo sapiens	dJ1042K10.2 (supported by GENSCAN, FGENES and GENEWISE)	2321	99
990	AF161426	Homo sapiens	HSPC308	448	92
991	AF161426	Homo sapiens	HSPC308	448	92
992	AF161426	Homo sapiens	HSPC308	453	92
993	AL023859	Schizosaccha romyces pombe	trna-splicing endonuclease subunit	172	42
994	AL049631	Homo sapiens	dJ513M9.1 (novel Homeobox domain protein)	241	47
995	AC005253	Homo sapiens	R26445_1	902	100
996	AF265206	Homo sapiens	MOG1 isoform A .	974	100
997	AJ248285	Pyrococcus abyssi	sarcosine oxidase, subunit beta (soxB)	195	28
998	AE003641	Drosophila melanogaster	BG:DS00941.3 gene product	218	58
999	W69343	Homo sapiens	Secreted protein of clone CR930_1.	1340	98
1000	AY007135	Homo sapiens	similar to bovine ADP/ATP translocase T1 mRNA with GenBank Accession Number M24102.1	1543	100
1001	Y73381	Homo sapiens	HTRM clone 1877278 protein sequence.	1668	100
1002	AF208844	Homo sapiens	BM-002	428	100
1003	AE004944	Pseudomonas aeruginosa	hypothetical protein	134	35
1004	AL031431	Homo sapiens	dJ462023.2 (novel protein)	2058	100
1005	S45367	Canis familiaris	centractin	1949	100
				l	

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:				SCORE	
1006	\$45367	Canis familiaris	centractin	1315	98
1007	AB022158	Mus musculus	chaperonin containing TCP-1 epsilon subunit	2649	96
1008	Y76332	Homo sapiens	Fragment of human secreted protein encoded by gene 38.	1282	97
1009	AB011414	Homo sapiens	Kruppel-type zinc finger protein	1671	58
1010	Z68218	Caenorhabdit is elegans	K01H12.1	269	67
1011	AB011414	Homo sapiens	Kruppel-type zinc finger protein	1671	58
1012	Z14000	Homo sapiens	RING1	2017	100
1013	G02841	Homo sapiens	Human secreted protein, SEQ ID NO: 6922.	332	93
1014	AF145659	Drosophila melanogaster	BcDNA.GH10333	1244	52
1015	X05860	Homo sapiens	Fragment of human secreted protein encoded by gene 65.	664	67
1016	Y02591	Homo sapiens	A human progesterone receptor complex p23-like protein.	772	97
1017	Y99448	Homo sapiens	Human PRO1759 (UNQ832) amino acid sequence SEQ ID NO:374.	2323	100
1018	X67250	Rattus norvegicus	n-chimaerin	1710	97
1019	AF183417	Homo sapiens	microtubule-associated proteins 1A/1B light chain 3	631	100
1020	AF164795	Homo sapiens	sex-regulated protein janus-a	674	100
1021	AF190625	Coturnix coturnix	qdgl-1	638	96
1022	AL133363	Arabidopsis thaliana	putative protein	155	37
1023	AB034912	Homo sapiens	WD-repeat like sequence	2483	100
1024	AY007091	Homo sapiens	similar to Homo sapiens mammalian inositol hexakisphosphate kinase 2 (IP6K2) mRNA with Ge	2243	100
1025	X69910	Homo sapiens	P63 protein	2958	99
1026	U80736	Homo sapiens	CAGF9	1657	100
1027	AB029333	Halocynthia roretzi	HrPET-1	1048	54
1028	AB032931	Homo sapiens	ubiquitin-conjugating enzyme isolog	1045	100
1029	G01797	Homo sapiens	Human secreted protein, SEQ ID NO: 5878.	749	98
1030	G01797	Homo sapiens	Human secreted protein, SEQ ID NO: 5878.	749	98
1031	AF193795	Homo sapiens	vacuolar sorting protein VPS29/PEP11	960	100
1032	AJ222968	Mus musculus	L-periaxin	120	30
1033	281317	Schizosaccha romyces pombe	DNA2-NAM7 helicase family protein	685	31
1034	Y41519	Homo sapiens	Fragment of human secreted protein encoded by gene 75.	1321	99
1035	AJ276004	Mus musculus	Paxneb protein	1709	77
1036	AF025459	Caenorhabdit is elegans	H14A12.3 gene product	190	30
1037	U37251	Homo sapiens	Description: KRAB zinc finger protein; this is a splicing supplied by author	196	43
1038	W74580	Homo sapiens	Human membrane protein BA0306.	1921	97
1039	U88173	Caenorhabdit is elegans	weak similarity to Arabidopsis thaliana ubiquitin-like protein 8	331	80

TABLE 2

1040	AF290204			SCORE	
1041	l .	Homo sapiens	blood group carrier molecule DOK1	1637	99
	Y96730	Homo sapiens	PR0539, a Costal-2 homologue.	162	22
1042	AF140683	Mus musculus	F-box protein FWD2	2397	98
1043	AF151023	Homo sapiens	HSPC189	1104	100
1044	AF181631	Drosophila melanogaster	BcDNA.GH04929	204	37
1045	Y77985	Homo sapiens	Human collectin amino acid sequence.	1940	100
1046	AJ243972	Homo sapiens	6-phosphogluconolactonase	1317	100
1047	AB035863	Homo sapiens	ATP specific succinyl CoA synthetase beta subunit precursor	2324	99
1048	AL034550	Homo sapiens	dJ1184F4.2 (novel protein similar to nucleolar protein 4 (NOL4) (NOLP))	981	92
1049	AF163825	Homo sapiens	pre-B lymphocyte protein 3	634	100
1050	AF201949	Homo sapiens	60S ribosomal protein L30 isolog	868	100
1051	AF190624	Mus musculus	mdgl-1	236	85
1052	AE003529	Drosophila melanogaster	CG6151 gene product	160	44
1053	G01191	Homo sapiens	Human secreted protein, SEQ ID NO: 5272.	646	98
1054	AL162756	Neisseria meningitidis	Glu-tRNA(Gln) amidotransferase subunit A	682	44
1055	AF181856	Rattus norvegicus	tRNA selenocysteine associated protein	1525	99
1056	U89649	Chlamydomona s reinhardtii	Mr19,000 outer arm dynein light chain	244	34
1057	AF159141	Homo sapiens	breast cancer metastasis- suppressor 1	663	53
1058	AF230929	Homo sapiens	keratinocyte annexin-like protein pemphaxin	1710	99
1059	AJ270952	Homo sapiens	putative membrane protein	1363	100
1060	AF224263	Heterodontus francisci	HoxD8	742	83
1061	X63417	Homo sapiens	IRLB	1037	100
1062	AL079345	Streptomydes coelicolor A3(2)	hypothetical protein	143	27
1063	Y71112	Homo sapiens	Human Hydrolase protein-10 (HYDRL-10).	2547	100
1064	AF263614	Homo sapiens	acetyl-CoA synthetase	3493	99
1065	Y13356	Homo sapiens	Amino acid sequence of protein PRO221.	1363	100
1066	AC006153	Homo sapiens	similar to Aquifex aeolicus GTP-binding protein; similar to AE000771 (PID:g2984292)	662	98
1067	Y18930	Sulfolobus solfataricus	hypothetical protein	162	29
1068	R65969	Homo sapiens T98G	Glioblastoma-derived polypeptide.	887	100
1069	Y07964	Homo sapiens	Human secreted protein fragment	863	96
1070	AF177476	Rattus norvegicus	CDK5 activator-binding protein	1995	86
1071	AF245505	Homo sapiens	adlican	3109	99
1072	U92794	Mus musculus	alpha glucosidase II, beta subunit	147	36
1073	G03889	Homo sapiens	Human secreted protein, SEQ ID NO: 7970.	698	98
1074	U15779	Homo sapiens	p70	380	28
1075	Y13392	Homo sapiens	Amino acid sequence of	1271	91

SEQ	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	* IDENTITY
NO:		Į		SCORE	ļ
			protein PRO328.		
1076	AF161457	Homo sapiens	HSPC339	571	100
1077	Y79509	Homo sapiens	Human carbohydrate-associated	2151	98
	1		protein CRBAP-5.	Ì	
1078	AF223466	Homo sapiens	HT015 protein	831	66
1079	AL132965	Arabidopsis	putative WD-40 repeat-protein	286	29
		thaliana	Francisco de defens (* esse		1
1080	AB024937	Homo sapiens	LUNX	1284	100
1081	Y14768	Homo sapiens	V-ATPase G-subunit like	579	100
1001	1 1 1 7 0 0	nomo Bapieno	protein	1 3,73	
1082	AF016416	Caenorhabdit	F29A7.4 gene product	141	31
1002	MOTOTIO	is elegans	resince gone product		
1083	L13291	Homo sapiens	ADP-ribosylarginine hydrolase	802	45
1084	AB041541	Mus musculus	unnamed protein product	151	44
1085	G01922	Homo sapiens	Human secreted protein, SEQ	202	97
1085	G01922	HOMO Sapiens	ID NO: 6003.	202) "
		<u> </u>	H-REV107 protein homolog	833	100
1086	AB030814	Homo sapiens			
1087	AF151638	Homo sapiens	phosphatidylcholine transfer	1142	100
			protein	1000	100
1088	3 Y84432 Homo sapiens Amino acid sequence of a 2783	2783	100		
		1	1	ļ	1
			protein.	 	1.00
1089	Y94867	Homo	Human protein clone HP10563.	613	100
	<u> </u>	sapiens		<u> </u>	
1090	AK023982	Homo sapiens	unnamed protein product	130	49
1091	AB041586	Mus musculus	unnamed protein product	1103	81
1092	¥71277	Homo sapiens	Human Zlipo3 protein.	606	100
1093	U34973	Mus musculus	protein tyrosine phosphatase-	1131	95
	İ		like		j
1094	Y66677	Homo	Membrane-bound protein	522	56
		sapiens	PRO828.		
1095	Y87276	Homo sapiens	Human signal peptide	1029	99
			containing protein HSPP-53		1
	j	1	SEQ ID NO:53.		1
1096	Y87276	Homo sapiens	Human signal peptide	863	98
			containing protein HSPP-53		
			SEQ ID NO:53.	1	
1097	AF161455	Homo sapiens	HSPC337	742	98
1098	U80029	Caenorhabdit	similar to thioredoxin	242	39
		is elegans			
1099	AJ005866	Homo sapiens	Sqv-7-like protein	1321	99
1100	AJ005866	Homo sapiens	Sqv-7-like protein	1118	99
1101	AJ005866	Homo sapiens	Sqv-7-like protein	891	99
1102	AJ005866	Homo sapiens	Sqv-7-like protein	1016	99
1103	AL110244	Homo sapiens	hypothetical protein	299	31
1104	AF242194	Drosophila	brakeless-B	147	52
	13432173	melanogaster			
1105	AL031010	Homo sapiens	dJ422F24.1 (PUTATIVE novel	968	100
1102	MINGIOIO	"Outo sabrens	protein similar to C. elegans	1	1 200
			C02C2.5)		1
1100	1129016	Mus musculus	parathion hydrolase	1624	87
1106	U28016	mus musculus		1024	1 0 '
	1		(phosphotriesterase) - related		
110=	N TOROLES	11000	protein	1202	00
1107	AJ278150	Homo sapiens	putative lipid kinase	2207	99
1108	G03733	Homo sapiens	Human secreted protein, SEQ	495	98
	L	<u> </u>	ID NO: 7814.	1-2	L
1109	AF217287	Drosophila	G protein RhoBTB	834	54
		melanogaster		<u> </u>	<u> </u>
1110	Y28921	Homo	Human regulatory protein	941	48
	1	sapiens	HRGP-7.	L	L
1111	Y28921	Homo	Human regulatory protein	1331	51
	1	sapiens	HRGP-7.	1	1
1112	AF176704	Homo sapiens	F-box protein FBX9	2027	99
1113	AF182076	Homo	glioma tumor suppressor	2418	100
	1			1	1
	}	sapiens	candidate region protein 2		

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:			ID NO: 8120.		
1115	AF229439	Mus musculus	zinc finger protein 289	1697	91
1116	L40357	Homo sapiens	thyroid receptor interactor	509	100
1117	L40357	Homo sapiens	thyroid receptor interactor	404	85
1118	A12155	Homo sapiens	Human X5L cDNA.	1673	100
1119	AL161542	Arabidopsis	isomerase like protein	607	53
1120	AL023754	thaliana Homo sapiens	dJ272L16.1 (Rat	234)	98
1120			Ca2+/Calmodulin dependent Protein Kinase LIKE protein)		
1121	Y57901	Homo sapiens	Human transmembrane protein HTMPN-25.	321	36
1122	Z14122	Xenopus laevis	XLCL2	455	77
1123	AF225418	Homo sapiens	lipase	1531	97
1124	Y06518	Homo sapiens	Zen GTPase interacting protein ZIP.	3227	100
1125	AL035690	Homo sapiens	dJ202I21.1 (novel protein)	952	100
1126	AJ000217	Homo sapiens	CLIC2	1286	99
1127	AB030505	Mus musculus	UBE-1c2	1069	79
1128	Y73375	Homo sapiens	HTRM clone 1427838 protein sequence.	874	100
1129	Y78941	Homo sapiens	Cyclophilin-type peptidyl prolyl cis/trans isomerase amino acid sequence.	877	100
1130	AL023553	Homo sapiens	dJ347H13.4 (novel protein)	557	100
1131	Y91945	Homo sapiens	Human chaperone protein 6 (HCHP-6).	1408	100
1132	Z68197	Schizosaccha romyces pombe	putative nuclear pore protein	596	39
1133	268197	Schizosaccha romyces pombe	putative nuclear pore protein	389	35
1134	AF180681	Homo sapiens	guanine nucleotide exchange factor	3597	100
1135	AF079765	Mus musculus	enhancer of polycomb	264	41
1136	M62419	Mus musculus	clathrin-associated protein	2189	99
1137	AJ006219	Drosophila melanogaster	clathrin-associated protein	1254	78
1138	Y76218	Homo sapiens	Human secreted protein encoded by gene 95.	440	98
1139	W88104	Homo sapiens	A Rab protein designated HRABS-2.	1065	99
1140	Y13401	Homo sapiens	Amino acid sequence of protein PRO339.	3979	98
1141	W85026	Chimeric - Homo sapiens	Green fluorescent protein- Zap70 fusion product.	3309	100
1142	Y13402	Homo sapiens	Amino acid sequence of protein PRO310.	1694	99
1143	G03875	Homo sapiens	Human secreted protein, SEQ ID NO: 7956.	660	99
1144	Y12917	Homo sapiens	Amino acid sequence of a human secreted peptide.	750	98
1145	Y12917	Homo sapiens	Amino acid sequence of a human secreted peptide.	1096	100
1146	AL022157	Homo sapiens	SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))	1233	100
1147	AL022157	Homo sapiens	SPIN (SPINDLIN HOMOLOG (PROTEIN DXF34))	1233	100
1148	G02548	Homo sapiens	Human secreted protein, SEQ ID NO: 6629.	370	98
1149	Y73338	Homo sapiens	HTRM clone 2019742 protein sequence.	1492	100
1150	W74841	Homo sapiens	Human secreted protein encoded by gene 113 clone	228	55
		<u> </u>			

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	
	<u> </u>		HEAAR60.		
1151	AF044201	Rattus	neural membrane protein 35;	1570	92
		norvegicus	NMP35		
1152	AF156774	Homo	lysophosphatidic acid	1855	99
		sapiens	acyltransferase-gamma1		
1153	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	872	64
			(translation of the cDNA DKFZp566A0946, Em:AL050069))	J	
3354	10.210.50	771	Unknown	473	100
1154	AF131852 Y41705	Homo sapiens	Human PRO352 protein	1381	97
1155	141705	sapiens	sequence.	1361	97
1156	G04036	Homo sapiens	Human secreted protein, SEQ	607	99
1130	904030	nouc sapiens	ID NO: 8117.	307	
1157	AF112444	Lupinus	L-asparaginase	287	43
1137	71112441	luteus	2 4564543	1 -0.	
1158	AF151848	Homo sapiens	CGI-90 protein	232	32
1159	AJ272267	Homo sapiens	choline dehydrogenase	2449	100
1160	AB001773	Ciona	PEM-6	196	33
-	1	savignyi			
1161	¥87330	Homo sapiens	Human signal peptide	746	83
		1 -	containing protein HSPP-107		1
			SEQ ID NO:107.		1
1162	Y87330	Homo sapiens	Human signal peptide	746	83
			containing protein HSPP-107		
			SEQ ID NO:107.		
1163	AF113534	Homo sapiens	HP1-BP74 protein	2723	96
1164	AF232226	Danio rerio	Dedd1	191	41
1165	AL118501	Homo sapiens	dJ1191N16.1 (A novel protein	1051	71
]		(translation of the cDNA		
** * * *	37110503	772	DKFZp566A0946, Em:AL050069)) dJ1191N16.1 (A novel protein	945	76
1166	AL118501	Homo sapiens	(translation of the cDNA	945	/ 6
			DKFZp566A0946, Em:AL050069))		
1167	AF187733	Homo sapiens	syntaphilin	831	42
1168	AB019435	Homo sapiens	phospholipase	951	55
1169	AF064604	Homo sapiens	KE03 protein	324	33
1170	Y01164	Homo sapiens	Polypeptide fragment encoded	1191	100
	1		by gene 6.		
1171	L03188	Saccharomyce	putative	180	22
	l	s cerevisiae	·		
1172	AF113751	Mus musculus	nuclear pore membrane	3941	81
			glycoprotein POM210		
1173	AJ245417	Homo sapiens	G5b protein	794	100
1174	AL022238	Homo sapiens	dJ1042K10.3 (novel protein)	1285	100
1175	U41278	Caenorhabdit	F33G12.3 gene product	332	28
		is elegans			
1176	M35617	Homo sapiens	T-cell receptor V-alpha-J-	284	83
			alpha region	1	1
1177	AC012680	Arabidopsis	putative protein phosphatase	209	37
	1	thaliana	2C; 55455-56414	1.03	100
1178	G01345	Homo sapiens	Human secreted protein, SEQ	692	99
1179	NT 006767	Vomo comione	ID NO: 5426. dJ579N16.3 (novel protein	1342	100
11/2	AL096767	Homo sapiens	similar to worm, Arabidopsis	1346	1 100
			and pine proteins)		1
1180	AF039716	Caenorhabdit	similar to ATP synthase B	496	55
		is elegans	chain	1	
1181	Y11710	Homo sapiens	collagen type XIV	1048	97
1182	X82240	Homo	T cell leukemia/lymphoma 1	617	100
		sapiens]	- July administry a ymphomia a	1	
	1	>R94974			1
	ļ	R94974 09-		1	
	1	1			
	1	MAY-1996 27-	1	I .	
		MAY-1996 27-			
		l .			

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
		[Homo sapiens			
1183	U42841	Caenorhabdit is elegans	short region of weak similarity to collagen	161	33
1185	AJ131613	Homo sapiens	dicarboxylate carrier protein	1470	99
1186	L27645	Danio rerio	growth-associated protein	130	36 100
1187	Y02738	Homo sapiens	Human secreted protein encoded by gene 89 clone HLHFP03.	636	
1188	AF217544	Xenopus laevis	ornithine decarboxylase-2	1459	60
1189	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	182 .	33
1190	X89602	Homo sapiens	rTSbeta	197	100
1191	U32828	Haemophilus influenzae Rd	ribosomal protein S6 modification protein (rimK)	268	31
1192	AF154831	Rattus norvegicus	PV-1	1403	60
1193	Y50926	Homo sapiens	Human fetal brain cDNA clone vc16_1 derived protein.	918	100
1194	AF026530	Rattus norvegicus	stathmin-like-protein splice variant RB3''	1093	97
1195	U35244	Rattus norvegicus	vacuolar protein sorting homolog r-vps33a	2981	96
1196	Y70470	Homo sapiens	Human p53 target molecule, PRG3 protein.	1680	100
1197	AF157318	Homo sapiens	AD-017 protein	912	47
1198	AF125443	Caenorhabdit is elegans	contains similarity to S. pombe phosphatidyl synthase (GB:Z28295)	460	39
1199	AF201934	Homo sapiens	DC12	1649	88
1200	AL031775	Homo sapiens	dJ30M3.3 (novel protein similar to C. elegans Y63D3A.4)	1902	100
1201	M21103	Ovis aries	BIIIB4 high-sulfur keratin	484	82
1202	Z85986	Homo sapiens	dJ108K11.3 (similar to yeast suppressor protein SRP40)	1143	75
1203	U18762	Rattus norvegicus	retinol dehydrogenase type I	890	52
1204	U35730	Mus musculus	jerky	2235	76
1205	AB002327	Homo sapiens	KIAA0329	151	24
1206	AB019233	Arabidopsis thaliana	ubiquinone/menaquinone biosynthesis methyltransferase-like	762	56
1207	AL136307	Homo sapiens	dJ380B8.2 (Neuritin, a protein which promotes neurite outgrowth)	742	100
1208	AF207989	Homo sapiens	orphan G-protein coupled receptor	2326	100
1209	297630	Homo sapiens	dJ466N1.4 (novel protein similar to ANK3 (ankyrin 3, node of Ranvier (ankyrin G)))	181	44
1210	U21549	Mus musculus	Ac39/physophilin	1280	68
1211	Y27700	Homo sapiens	Human secreted protein encoded by gene No. 12.	1267	100
1212	AF117814	Mus musculus	odd-skipped related 1 protein	945	66
1213	AF277233	Naegleria fowleri	calcineurin B	222	39
1214	D14849	Mus musculus	meiosis-specific nuclear structural protein 1	1950	77
1215	G03022	Homo sapiens	Human secreted protein, SEQ ID NO: 7103.	590	100
1216	Z72510	Caenorhabdit	similarity to yeast UTR3	634	49

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	1DENTITY
		is elegans	protein (Swiss Prot accession yk677h11.5 comes from this gene	3900.2	
1217	Z49703	Saccharomyce s cerevisiae	unknown	134	22
1218	AC013430	Arabidopsis thaliana	F3F9.18	199	29
1219	L10910	Homo sapiens	splicing factor	1026	71
1220	270750	Caenorhabdit is elegans	similar to vanadate resistance protein transmembranous comes from this gene	965	58
1221	AL163815	Arabidopsis thaliana	putative protein	653	61
1222	AF155100	Homo sapiens	zinc finger protein NY-REN-21 antigen	2261	100
1223	J05071	Bos taurus	GTP-binding regulatory protein gamma-6 subunit	356	100
1224	Y73364	Homo sapiens	HTRM clone 2765991 protein sequence.	1169	99
1225	AL050170	Homo sapiens	hypothetical protein	714	100
1226	X64002	Homo sapiens	RAP74	2661	99
1227	X04085	Homo sapiens	catalase	2846	100
1228	AJ005620 AF045564	Mus musculus	skeletal muscle-specific gene	1416	90
		Rattus norvegicus	development-related protein	1715	93
1230	X97571	Mus musculus	HCMV-interacting protein	479	96
1231	L0B239	Homo sapiens	located at OATL1	2274	100
1232 1233	AF121863	Homo sapiens	sorting nexin 14	1964	100
1233	AF121863 AC024805	Homo sapiens Caenorhabdit	sorting nexin 14 contains similarity to	1203 744	1
		is elegans	TR:004595		31
1235	AC006634	Caenorhabdit is elegans	contains similarity to Saccharomyces cerevisiae probable membrane protein YLR418c (GB:U20162)	357	33
1236	Y18101	Mus musculus	macrophage actin-associated- tyrosine-phosphorylated protein	1559	87
1237	AB042646	Homo sapiens	TGIF2	1224	100
1238	AB026264	Homo sapiens	IMPACT	1694	100
1239 1240	AB026264 G00429	Homo sapiens	IMPACT Human secreted protein, SEQ	1123 324	100
1241	Y76144	Homo sapiens	ID NO: 4510. • Human secreted protein	1363	53
1242	AL035602	Arabidopsis	encoded by gene 21. putative protein	499	28
1243	X76483	thaliana Gallus gallus	Yes-associated protein	574	4.8
1244	AF220186	Homo sapiens	(65kDa) uncharacterized hypothalamus protein HT012	503	100
1245	AL021453	Homo sapiens	dJ821D11.3 (PUTATIVE protein)	856	100
1246	AJ276003	Homo sapiens	GAR1 protein	1216	100
1247	Y57910	Homo sapiens	Human transmembrane protein HTMPN-34.	1369	98
1248	AC004874	Homo sapiens	similar to N- acetylgalactosaminyltransfera se; similar to Q07537 (PID:q1171989)	957	100
1249	AF199597	Homo sapiens	A-type potassium channel modulatory protein 1	1139	100
1250	Y13148	Rattus norvegicus	PAG608	1350	88
1251	M24852	Rattus norvegicus	neuron-specific protein PEP-	124	46
	.1			L	L

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1252	AF146738	Rattus norvegicus	testis specific protein	771	83
1253	G02725	Homo sapiens	Human secreted protein, SEQ ID NO: 6806.	419	97
1254	W44375	Homo sapiens	Human ubiquitin-conjugating enzyme polypeptide.	1045	99
1255	AC006538	Homo sapiens	BC41195_1	831	78
1256	AB004316	Bos taurus	mitochondrial methionyl-tRNA transformylase	1556	88
1257	235094	Homo sapiens	SURF-2	1354	97
1258	Y13362	Homo sapiens	Amino acid sequence of protein PRO214.	2383	100
1259	AC006014	Homo sapiens	similar to RFP transforming protein; similar to P14373 (PID:g132517)	1299	100
1260	AC005099	Homo sapiens	match to AI222572 (NID:g3804775)	469	100
1261	V00507	Homo sapiens	coding sequence of DHFR (1 is let base in codon) (561 is 3rd base in codon)	984	100
1262	X15443	Rattus sp.	gamma-glutamyltranspeptidase (AA 1-568)	697	32
1263	AF173871	Mus musculus	neuronal PAS3	977	94
1264	AF178983	Homo sapiens	Ras-associated protein Rapl	433	97
1265	Y70473	Homo sapiens	Human cyclic nucleotide- associated protein-1 (CNAP- 1).	2785	99
1266	Y41738	Homo sapiens	Human PRO541 protein sequence.	1622	100
1267	AF061346	Mus musculus	Edpl protein	1077	64
1268	U97006	Caenorhabdit is elegans	C13F10.4 gene product	154	23
1269	AF233582	Mus musculus	GTPase Rab37	942	95
1270	AF195951	Homo sapiens	signal recognition particle	3127	98
1271	AL031177	Homo sapiens	dJ889M15.3 (novel protein)	1150	55
1272	AF201933	Homo sapiens	DC11	650 346	100
1273	AF201933	Homo sapiens	DC11 putative protein	348	49
1274	AL021710	Arabidopsis thaliana	R33683 3	556	100
1275	AC004449 Y86295	Homo sapiens	Human secreted protein	1920	100
1276	Y71111	Homo sapiens	HL2AG87, SEQ ID NO:210. Human Hydrolase protein-9	1576	99
	S94421	Homo sapiens	(HYDRL-9). T cell receptor eta-exon	478	100
1278	Y66695	Homo sapiens	Membrane-bound protein	1909	100
4613	100033	sapiens	PRO1344.		1
1280	AF161380	Homo sapiens	HSPC262	772	100
1281	Y48610	Homo sapiens	Human breast tumour- associated protein 71.	779	100
1282	AC015446	Arabidopsis thaliana	Similar to AIG1 protein	406	35
1283	AK024432	Homo sapiens	FLJ00022 protein	403	35
1284	W96153	Homo sapiens	Human FADD-interacting protein (FIP).	1825	81
1285	AJ001019	Homo sapiens	ring finger protein	1301	100
1286	AE003823	Drosophila melanogaster	CG13178 gene product	195	29
1287	AF178632	Homo sapiens	FEM-1-like death receptor binding protein	3261	100
1288	AC006033	Homo sapiens	similar to MLN 64; similar to 138027 (PID:g2135214)	1195	100
1289	AC006033	Homo sapiens	similar to MLN 64; similar to 138027 (PID:g2135214)	668	93
1290	AB023811	Homo sapiens	TU3A	351	54

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	† IDENTITY
1291	273424	Caenorhabdit is elegans	C44B9.1	235	36
1292	Y94871	Homo sapiens	Human protein clone HP02551.	1222	100
1293	AF180425	Homo sapiens	retinoblastoma-associated protein RAP140	489	29
1294	G03856	Homo sapiens	Human secreted protein, SEQ ID NO: 7937.	538	99
1295	AF133670	Mus musculus	ARL-6 interacting protein-2	367	51
1296	AJ249735	Homo sapiens	claudin-6	1142	100
1297	X57560	Escherichia coli	pspE protein	535	100
1298	AF169284	Homo sapiens	LIM and cysteine-rich domains protein 1	1997	100
1299	U41023	Caenorhabdit is elegans	coded for by C. elegans cDNA yk61f1.3; coded for by C. yk109h8.5	324	29
1300	AB024523	Homo sapiens	basic kruppel like factor	1206	100
1301	X55989	Homo sapiens	eosinophil cationic-related protein	737	99
1302	AF007151	Homo sapiens	unknown	1481	100
1303	X52904	Escherichia coli	open reading frame (AA 1-65)	359	100
1304	U19577	Escherichia coli	galactonate dehydratase	242	93
1305	AF266508	Mus musculus	NELF protein	1409	97
1306	Y57901	Homo sapiens	Human transmembrane protein HTMPN-25.	932	100
1307	U58750	Caenorhabdit is elegans	similar to the mitochondrial carrier family	365	54
1308	AF044774	Homo sapiens	breakpoint cluster region protein 2	2681	99
1309	AL078593	Homo sapiens	dJ210B1.1 (KIAA0680)	267	34
1310	X82693	Homo sapiens	E48 antigen	620	96
1311	Z82263	Caenorhabdit is elegans	C47A4.1	283	35
1312	AF131218	Homo sapiens	chromosome 16 open reading frame 5	1493	100
1313	Y41763	Homo sapiens	Human PRO938 protein sequence.	1636	100
1314	AF196972	Homo sapiens	JM24 protein	2239	100
1315	AF053356	Homo sapiens	insulin receptor substrate like protein	228	97
1316	Y66695 AF153127	Homo sapiens Gallus	Membrane-bound protein PRO1344.	1909	100
1317		gallus	SAPK interacting protein	2442	89
1319	AF153127 AF153127	Gallus gallus Gallus	SAPK interacting protein	1477	83
1320	X56932	gallus	SAPK interacting protein	1651	86
1321	AF174605	Homo sapiens	23 kD highly basic protein	1044	100
1321	AP1/4605	Sapiens] >Y83086 Y83086 09- MAR-2000 28- AUG-1998 F- box protein FBP-18. [Homo	F-box protein Fbx25	467	70
1322	M61732	Trypanosoma cruzi	neuraminidase	214	24
1323	Y17013	porcine endogenous	pol	304	64

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
NO:	NUMBER			WATERMAN SCORE	IDENTITY
1324	AL138655	retrovirus Arabidopsis	putative protein	1174	37
1347	ABLIGOSS	thaliana	patative protein		1
1325	AL138655	Arabidopsis thaliana	putative protein	946	35
1326	AL133215	Homo sapiens	bA108L7.2 (novel protein	1322	99 3
	:	_	similar to rat tricarboxylate carrier)	:	
1327	AF161541	Homo sapiens	HSPC056	1357	99
1328	Y73346	Homo sapiens	HTRM clone 619699 protein sequence.	785	96
1329	L10910	Homo sapiens	splicing factor	912	82
1330	AF146568	Homo sapiens	MIL1 protein	1936	100
1331	W87772	Homo sapiens	Human serum glucocorticoid- regulated kinase (H-SGK2) polypeptide.	232	39
1332	Y41741	Homo sapiens	Human PR0704 protein sequence.	1860	100
1333	AF295096	Homo sapiens	zinc-finger protein ZBRK1	411	91
1334	Z82271	Caenorhabdit is elegans	Similarity to Mouse kinensin- like protein KIF4 comes from this gene	578	44
1335	AE000810	Methanobacte rium thermoautotr ophicum	conserved protein	290	43
1336	Y68779	Homo sapiens	Amino acid sequence of a human phosphorylation effector PHSP-11.	1019	91
1337	AB027003	Mus musculus	protein phosphatase	378	84
1338	U64856	Caenorhabdit is elegans	weak similarity to TPR domains	215	40
1339	AE001394	Plasmodium falciparum	protein of the YMR7 family	170	29
1340	X76717	Homo sapiens	MT-11 protein	204	89
1341	AC011914	Arabidopsis thaliana	putative mutT protein; 68398-67881	289	45
1342	AJ276171	Homo sapiens	ASPIC myosin regulatory light chain	2122	100
1343	AF187016	Homo sapiens	interacting protein MIR similar to Kelch proteins;	894	99 35
1344	AC006963	Homo sapiens	similar to BAA77027 (PID:g4650844)		
1345	AF257466	Homo sapiens	N-acetylneuraminic acid phosphate synthase	1880	99
1346	Y25896	Homo sapiens	Human secreted protein fragment encoded from gene 64.	1148	100
1347	AJ272073	Torpedo marmorata	male sterility protein 2-like protein	1664	58
1348	AF161548	Homo sapiens	HSPC063	1018	98
1349	W78128	Homo sapiens	Human secreted protein encoded by gene 3 clone HOSB196.	1117	100
1351	G02144	Homo sapiens	Human secreted protein, SEQ ID NO: 6225.	418	100
1352	D90869	Escherichia coli	similar to	2047	100
1353	A12029	Homo sapiens	MRP-14	613	100
1354	AC005328	Homo sapiens	R26660_1, partial CDS	870	74
1355	AC024876	Caenorhabdit is elegans	contains similarity to SW:RPB1_CRIGR	829	61
1356	AF077226	Homo sapiens	copine III	1876	64
1359	AF217188	Mus musculus	YIPIB	801	63
1360	AC074331	Homo sapiens	ZNF234	3869	100
1361	AL163279	Homo sapiens	homolog to cAMP response	5035	99

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:			element binding and beta	BCCKE	
	,		transducin family proteins		
362	248475	Homo sapiens	glucokinase regulator	3160	99
363	Z48475	Homo sapiens	glucokinase regulator	2682	97
364	AF195764	Homo sapiens	megakaryocyte-enhanced gene	2055	99 .
.304	AP155704	110.110	transcript 1 protein; MEGT1 protein		į.
1365	AF116609	Homo sapiens	PR00915	581	100
366	AF116609	Homo sapiens	PR00915	581	100
367	AL117352	Homo sapiens	dJ876B10.3 (novel protein similar to C. elegans	2581	99
1368	Y34124	Homo	T19B10.6 (Tr:Q22557)) Human potassium channel	1342	100
.500	13122	sapiens	K+Hnov15.		J
369	AJ245621	Homo sapiens	CTL2 protein	3728	99
1370	AF008220	Bacillus	YtaG	429	45
		subtilis			ļ.,
1371	X05562	Homo sapiens	alpha-2 chain precursor (AA - 25 to 1018) (3416 is 2nd base in codon)	5908	99
1372	Z98048	Homo sapiens	dJ408N23.4 (novel DnaJ domain protein)	1296	99
1373	AF154415	Homo sapiens	FLASH	10253	100
1374	U20286	Rattus	lamina associated polypeptide	1567	69
13/4	020238	norvegicus	1C		
1375	U53445	Homo sapiens	DOC1	1645	46
1376	AL117337	Homo	bA393J16.1 (zinc finger	250	60
		sapiens	protein 33a (KOX 31))		1
1377	AC005328	Homo sapiens	R26660 1, partial CDS	1126	100
1378	U35113	Homo sapiens	metastasis-associated gene	1823	69
1379	L15313	Caenorhabdit is elegans	putative	858	58
1380	Y25756	Homo sapiens	Human secreted protein encoded from gene 46.	1508	100
1381	AB037360	Homo sapiens	ANKHZN	5734	95
1382	AB037360	Homo sapiens	ANKHZN	959	97
1383	AF237676	Mus musculus	G beta-like protein GBL	1721	96
1384	AF237676	Mus musculus	G beta-like protein GBL	1043	70
1385	Y58793	Homo sapiens	Human calcium regulatory protein CaREG-1.	715	100
1386	AF212162	Homo sapiens	ninein	10369	99
1387	AL031685	Homo sapiens	dJ963K23.2 (novel protein)	337	33
1388	AC004890	Homo sapiens	similar to zinc finger proteins; similar to BAA24380 >W06316 W06316 03-OCT-1996 27-APR-1995 TRP-1 protein.	542	86
1389	AF187989	Homo sapiens	zinc finger protein ZNF223	2665	99
1390	AC035150	Homo sapiens	Zinc finger protein ZNF221	3459	100
1391	AF287894	Homo sapiens	PIST	1410	97
1392	AF282265	Homo sapiens	inner centromere protein INCENP	1794	99
1393	X90840	Homo sapiens	axonal transporter of synaptic vesicles	4584	99
1394	AF076249	Homo sapiens	zinc finger protein SBBIZ1	3208	99
1395	G02224	Homo sapiens	Human secreted protein, SEQ ID NO: 6305.	299	75
1396	AC004809	Arabidopsis thaliana	Similar to	130	34
1398	AF242519	Homo sapiens	zinc finger protein SBZF3	181	66
1399	AL133396	Homo sapiens	dJ1068H6.4 (prion protein like protein doppel)	962	100
1400	Y48611	Homo sapiens	Human breast tumour- associated protein 72.	817	99
1401	AC004472	Homo sapiens	P1.11659 5	280	54
1401	X91489	Saccharomyce	putative HMG box	164	27
7405	L AJIAOJ	s cerevisiae		1	1

TABLE 2

NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1403	Y79222	Homo sapiens	Human transferase TRNSFS-14.	2842	100
1404	X81058	Mus musculus	tex261	1010	99
1405	AB012084	Mus musculus	ITM	194	29
1406	AB012084 AB030251	Homo sapiens	GTPase activating protein	3233	99
		Rattus	PTB-like protein	2684	99
1407	AJ010585	rattus			
1408	X75760	Drosophila melanogaster	LRR47	364	29
1409	U76618	Mus musculus	N-RAP	804	48
1410	AC005578	Homo sapiens	P20887_1, partial CDS	835	63
1411	AE000284	Escherichia coli	orf, hypothetical protein	360	100
1412	X01563	Escherichia coli	L5 (rplE) (aa 1-179)	911	100
1413	W78279	Homo sapiens	Fragment of human secreted protein encoded by gene 33.	1264	99
1414	AB031051	Homo sapiens	organic anion transporter OATP-E	3832	100
1415	M17466	Homo sapiens	coagulation factor XII	3455	100
1416	AF097994	Homo sapiens	L-kynurenine/alpha- aminoadipate aminotransferase	2202	99
1417	AF151077	Homo sapiens	HSPC243	1262	99
1418	Y09945	Rattus	putative integral membrane transport protein	1098	61
1419	U13152	Mesocricetus	guanine nucleotide-binding protein beta 5	2179	76
1420	AL162458	Homo sapiens	bA465L10.5 (KIAA1176 (novel	5696	100
1420	ABIO2430	Alone Department	protein, presumed ortholog of mouse K-Cl cotransporter KCC2))		
1421	Y99426	Homo sapiens	Human PR01604 (UNQ785) amino acid sequence SEQ ID NO:308.	152	29
1422	Y94923	Homo sapiens	Human secreted protein clone qs14_3 protein sequence SEQ ID NO:52.	4039	99
1423	AF177388	Homo sapiens	cancer-amplified transcriptional coactivator ASC-2	10748	99
1424	Y48517	Homo sapiens	Human breast tumour-	1851	99
	1	1	associated protein 62.		}
1425	AF208848		associated protein 62.	1454	89
		Homo sapiens	BM-006	1454	89 79
1426	AF208848 AF208848 AF112886			1	
1426 1427	AF208848 AF112886	Homo sapiens Homo sapiens	BM-006 BM-006 differentiation enhancing	853	79
1426 1427 1428	AF208848 AF112886 U41387	Homo sapiens Homo sapiens Bos taurus	BM-006 BM-006 differentiation enhancing factor 1	853 4693	79 95
1426 1427 1428 1429	AF208848 AF112886 U41387 AF161534	Homo sapiens Homo sapiens Bos taurus Homo sapiens Homo sapiens	BM-006 BM-006 differentiation enhancing factor 1 Gu protein HSPC049	853 4693 1372 2853	79 95 63
1425 1426 1427 1428 1429 1430 1431	AF208848 AF112886 U41387	Homo sapiens Homo sapiens Bos taurus Homo sapiens Homo sapiens Mus musculus Homo	BM-006 BM-006 differentiation enhancing factor 1 Gu protein	853 4693	79 95 63 78
1426 1427 1428 1429 1430	AF208848 AF112886 U41387 AF161534 AF125043	Homo sapiens Homo sapiens Bos taurus Homo sapiens Homo sapiens Mus musculus	BM-006 BM-006 differentiation enhancing factor 1 Gu protein HSPC049 bisphosphate 3'-nucleotidase Membrane-bound protein	853 4693 1372 2853 275	79 95 63 78 30
1426 1427 1428 1429 1430 1431	AF208848 AF112886 U41387 AF161534 AF125043 Y66718 AF193613	Homo sapiens Homo sapiens Bos taurus Homo sapiens Homo sapiens Mus musculus Homo sapiens Homo sapiens	BM-006 BM-006 differentiation enhancing factor 1 Gu protein HSPC049 bisphosphate 3'-nucleotidase Membrane-bound protein PR01106. cell recognition molecule Caspr2	853 4693 1372 2853 275 1886	79 95 63 78 30 100
1426 1427 1428 1429 1430 1431	AF208848 AF112886 U41387 AF161534 AF125043 Y66718	Homo sapiens Homo sapiens Bos taurus Homo sapiens Homo sapiens Mus musculus Homo sapiens	BM-006 BM-006 differentiation enhancing factor 1 Gu protein HSPC049 bisphosphate 3'-nucleotidase Membrane-bound protein PR01106. cell recognition molecule	853 4693 1372 2853 275 1886	79 95 63 78 30 100
1426 1427 1428 1429 1430 1431 1432	AF208848 AF112886 U41387 AF161534 AF125043 Y66718 AF193613	Homo sapiens Homo sapiens Bos taurus Homo sapiens Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens	BM-006 BM-006 differentiation enhancing factor 1 Gu protein HSPC049 bisphosphate 3'-nucleotidase Membrane-bound protein PRO1105. cell recognition molecule Caspr2 Gliacolin NTII-1 nerve protein,	853 4693 1372 2853 275 1886 568	79 95 63 78 30 100
1426 1427 1428 1429 1430 1431 1432	AF208848 AF112886 U41387 AF161534 AF125043 Y66718 AF193613 AB044560 R99800	Homo sapiens Homo sapiens Bos taurus Homo sapiens Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens	BM-006 BM-006 differentiation enhancing factor 1 Gu protein HSPC049 bisphosphate 3'-nucleotidase Membrane-bound protein PR01106. cell recognition molecule Caspr2 Gliacolin NTII-1 nerve protein, facilitates regeneration of nerve cells.	853 4693 1372 2853 275 1886 568	79 95 63 78 30 100 100
1426 1427 1428 1429 1430 1431 1432 1433 1434	AF208848 AF112886 U41387 AF161534 AF125043 Y66718 AF193613 AB044560 R99900 AF220530 X70944	Homo sapiens Homo sapiens Bos taurus Homo sapiens Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens	BM-006 BM-006 differentiation enhancing factor 1 Gu protein HSPC049 bisphosphate 3'-nucleotidase Membrane-bound protein PRO1106. cell recognition molecule Caspr2 Gliacolin NTII-1 nerve protein, facilitates regeneration of nerve cells. myo-inositol 1-phosphate synthase A1	853 4693 1372 2853 275 1886 568 192 707	79 95 63 78 30 100 100 34 51
1426 1427 1428 1429 1430 1431 1432 1433 1434 1435	AF208848 AF112886 U41387 AF161534 AF125043 Y66718 AF193613 AB044560 R99900 AF220530 X70944 AF271732	Homo sapiens Homo sapiens Bos taurus Homo sapiens Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	BM-006 BM-006 differentiation enhancing factor 1 Gu protein HSPC049 bisphosphate 3'-nucleotidase Membrane-bound protein PR01106. cell recognition molecule Caspr2 Gliacolin NTII-1 nerve protein, facilitates regeneration of nerve cells. myo-inositol 1-phosphate synthase Al PTB-associated splicing factor bridging integrator-3	853 4693 1372 2853 275 1886 568 192 707	79 95 63 78 30 100 100 34 51
1426 1427 1428 1429 1430 1431 1432 1433 1434 1435 1436 1437 1438	AF208848 AF112886 U41387 AF161534 AF125043 Y66718 AF193613 AB044560 R99900 AF220530 X70944 AF271732 Y30811	Homo sapiens Homo sapiens Bos taurus Homo sapiens Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	BM-006 BM-006 differentiation enhancing factor 1 Gu protein HSPC049 bisphosphate 3'-nucleotidase Membrane-bound protein PR01106. cell recognition molecule Caspr2 Gliacolin NTII-1 nerve protein, facilitates regeneration of nerve cells. myo-inositol 1-phosphate synthase A1 PTB-associated splicing factor bridging integrator-3 Human secreted protein encoded from gene 1.	853 4693 1372 2853 275 1886 568 192 707 2904 1261	79 95 63 78 30 100 100 34 51
1426 1427 1428 1429 1430 1431 1432 1433 1434 1435	AF208848 AF112886 U41387 AF161534 AF125043 Y66718 AF193613 AB044560 R99900 AF220530 X70944 AF271732	Homo sapiens Homo sapiens Bos taurus Homo sapiens Homo sapiens Mus musculus Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens Homo sapiens	BM-006 BM-006 differentiation enhancing factor 1 Gu protein HSPC049 bisphosphate 3'-nucleotidase Membrane-bound protein PRO1105. cell recognition molecule Caspr2 Gliacolin NTII-1 nerve protein, facilitates regeneration of nerve cells. myo-inositol 1-phosphate synthase Al PTB-associated splicing factor bridging integrator-3 Human secreted protein	853 4693 1372 2853 275 1886 568 192 707	79 95 63 78 30 100 100 34 51

TABLE 2

			DESCRIPTION	SMITH-	8
SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	WATERMAN SCORE	IDENTITY
NO:			ALEX3	1944	100
1442	AB039669	Homo sapiens	Diablo	191	27
1443	AF237711	Drosophila melanogaster			
1444	AJ011896	Homo sapiens	Nafl beta protein	439	39
1445	X73874	Homo sapiens	phosphorylase kinase	6233	98
1446	AF214114	Homo sapiens	breast carcinoma-associated antigen BCAA	3999	99
1447	AF003924	Homo sapiens	ANC 2H01	2645	99
1448	AF003136	Caenorhabdit	contains weak similarity to	2843	52
1449	AF155112	is elegans	an AMP-binding motif NY-REN-50 antigen	1184	89
1449	Y95004	Homo sapiens	Human secreted protein	985	100
	1	<u> </u>	vc54_1, SEQ ID NO:48.		
1451	AF107203	Homo sapiens	ataxin 2-binding protein	688	57
1452	AF107203	Homo sapiens	ataxin 2-binding protein	456	78
1453	Z38011	Mus musculus	DMR-N9	882	56
1454	X90568	Homo sapiens	Protein sequence and annotation available soon via LABEIT@EMBL-Heidelberg.DE	510	28
1455	AL035409	Homo sapiens	dJ564M11.3 (similar to sialyltranferase)	1356	100
1456	D44480	Mus musculus	MATH-2 protein	272	100
1458	AF141326	Homo sapiens	RNA helicase HDB/DICE1	478	45
1459	AF242552	Gallus gallus	retinovin	945	34
1460	U11036	Homo sapiens	Ibdl	724	84
1461	AB025258	Mus musculus	granuphilin-a	545	39
1462	Y08134	Homo sapiens	acid sphingomyelinase-like	2428	99
		-	phosphodiesterase		1
1463	AC004997	Homo sapiens	match to ESTs 243979 (NID:g573097), R19699 (NID:g774333)	869	98
1464	AC004997	Homo sapiens	match to ESTs 243979 (NID:g573097), R19699 (NID:g774333)	869	98
1465	U32743	Haemophilus influenzae Rd	fucose operon protein (fucU)	315	50
1466	Y09022	Homo sapiens	Not56-like protein	2342	100
1467	AC003034	Homo sapiens	Homolog of rat kidney- specific (KS) gene	1072	99
1468	AF071544	Spinacia oleracea	ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I	333	26
1469	Y57930	Homo sapiens	Human transmembrane protein HTMPN-54.	1053	100
1470	AF032666	Rattus norvegicus	rsec5	4504	93
1471	¥70467	Homo sapiens	Human membrane channel protein-17 (MECHP-17).	452	74
1472	AL031033	Homo sapiens	C321D2.1 (Ribosomal Large Subunit Pseudouridine Synthase protein)	1694	100
1473	AF177292	Homo sapiens	genethonin 3	4026	98
1474	\$45936	Homo sapiens	HTS1	1101	50
1475	Y86241	Homo sapiens	Human secreted protein	1879	98
			HOABR60, SEQ ID NO:156.		68
1476	AJ010317	Fugu rubripes	Sand	1278	
1477	U42831	Caenorhabdit is elegans	coded for by C. elegans cDNA yk99b4.3; similar to human transforming protein (PIR:S22157)	846	44
1478	X62447	Homo sapiens	PR 264	543	61
1479	X82209	Homo sapiens	MN1	7116	100
1480	U10536	Pan paniscus	MHC class I A	675	84

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1481	AL078599	Homo sapiens	dJ991C6.1 (novel protein similar to C. elegans	1274	65
		1	F55A12.9 (Tr:P91086))		
1482	Z98977	Schizosaccha romyces	putative vacuolar protein	256	29
1483	AB005662	pombe Mus musculus	JNK/SAPK-associated protein-1	4968	92
1484	AL050120	Homo sapiens	hypothetical protein	716	100
1485	M27878	Homo sapiens	DNA binding protein	1006	53
1486	Y69161	Homo sapiens	Amino acid sequence of a partial protein kinase.	575	99
1487	X84156	Saccharomyce s cerevisiae	ATH1	341	29
1488	AF038963	Homo sapiens	RNA helicase	446	34
1489	U56966	Caenorhabdit is elegans	coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3	620	42
1490	AE000989	Archaeoglobu s fulgidus	enoyl-CoA hydratase (fad-4)	533	46
1491	M80633	Rattus norvegicus	adenylyl cyclase type IV	707	95
1492	Y73342	Homo sapiens	HTRM clone 2709055 protein sequence.	3513	99
1493	Y17220	Homo sapiens	Human secreted protein (clone fj283-11).	462	37
1494	AF133670	Mus musculus	ARL-6 interacting protein-2	701	97
1495	Y94897	Homo sapiens	Human protein clone HP10574.	1371	100
1496	AL049699	Homo sapiens	dJ747H23.2 (novel protein)	1550	100
1497	AF037447	Homo sapiens	ribosomal S6 protein kinase	2427	100
1498	AL445067	Thermoplasma acidophilum	putative target YPL207w of the HAP2 transcriptional complex related protein	269	35
1499	AB039947	Homo sapiens	X11L-binding protein 51	227	36
1500	AJ277750	Homo sapiens	UBASH3A protein	3509	100
1501	AL050333	Homo sapiens	dJ93K22.1 (novel protein (contains DKFZP564B116))	2439	100
1502	AF179896	Homo sapiens	TALE homeobox protein Meis2b	1140	100
1503	AF178948	Homo sapiens	TALE homeobox protein Meis2a	1177	100
1504	¥53005	Homo sapiens	Human secreted protein clone pm749_8 protein sequence SEQ ID NO:16.	1442	99
1505	X82494	Homo sapiens	fibulin-2	3580	99
1506	X98296	Homo sapiens	ubiquitin hydrolase	783	42
1507	AL034548	Homo sapiens	dJ1103G7.6 (novel protein)	1098	100
1508	Y76144	Homo sapiens	Human secreted protein encoded by gene 21.	1736	100
1509	AF220182	Homo sapiens	uncharacterized hypothalamus protein HT008	1181	98
1510	U64601	Caenorhabdit is elegans	Gene probably begins in the next cosmid	415	58
1511	AL356192	Neurospora crassa	related to MDM1 protein	196	29
1512	D17629	Homo sapiens	N-acetylgalactosamine 6- sulfate sulfatase (GALNS)	1829	100
1513	AF168717	Homo sapiens	x 009 protein	694	99
1514 1515	AJ243531 AC003672	Homo sapiens Arabidopsis	nM15 protein putative C3HC4-type RING zinc	735	30
1516	AF115435	Rattus	finger protein syntaxin 17	1374	90
1517	AF003140	norvegicus Caenorhabdit is elegans	C44E4.5 gene product	274	31
1518	AB002584	Rattus norvegicus	beta-alamine-pyruvate aminotransferase	2238	82
	AL121764	Schizosaccha	yeast atp12 protein precursor	270	30

TABLE 2

650	T 3 ggrag Tax	SPECIES	PROGREDATON	C C C C C C C C C C C C C C C C C C C	
SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH-	*
NO:	NUMBER			WATERMAN SCORE	IDENTITY
NO:	 	romyces	homolog	SCORE	ļ
		pombe	nomorog		
1520	AF255910	Homo	vascular endothelial	547	100
	1	sapiens	junction-associated molecule		
1521	D31764	Homo sapiens	KIAA0064	170	27
1522	Y66634	Homo	Membrane-bound protein	985	100
		sapiens	PRO190.		l
1523	Y94450	Homo sapiens	Human inflammation associated	250	43
1524	AC000107	Arabidopsis	protein		
1524	AC000107	thaliana	F1/F8.22	277	37
1525	AF109377	Mus musculus	ldlBp	1277	83
1526	AL031427	Homo sapiens	dJ167A19.4 (novel protein)	1432	99
1527	Y08135	Mus musculus	acid sphingomyelinase-like	1496	79
			phosphodiesterase		"
1528	AK024423	Homo sapiens	FLJ00012 protein	611	100
1529	AF154502	Homo sapiens	quiescent cell proline	679	100
			dipeptidase		
1530	AF205598	Homo sapiens	transposase-like protein	1368	100
1531	AF251039	Homo sapiens	putative zinc finger protein	1420	50
1532	W74805	Homo sapiens	Human secreted protein	493	57
	1		encoded by gene 77 clone HOEAS24.		
1533	AF039023	Homo sapiens	Ran-GTP binding protein;	5707	99
1233	AF039023	HOMO Saptens	RanBP6	5707	99
1534	AC007190	Arabidopsis	F23N19.9	374	37
150.		thaliana	1231123.3	3,74] 3 '
1535	AB027564	Homo sapiens	DINB1	4482	100
1536	Y36178	Homo sapiens	Human secreted protein	377	87
1537	Y50907	Homo sapiens	Human fetal brain cDNA clone	3693	99
			vb3_1 derived protein.		
1538	AF017368	Mus musculus	faciogenital dysplasia	177	47
1539	AF266756	Homo sapiens	protein 2 sphingosine kinase	2011	
1540	Z48804	Homo sapiens	OA1	2238	99 100
1541	AF000195	Caenorhabdit	Contains similarity to Pfam	379	42
	1	is elegans	domain: PF00169 (PH),	373	12
			Score=20.6, E-value=1.9e-05,		
		ļ	N=1		
1542	Y71159	Homo sapiens	Human phosphodiesterase	9415	99
	Ì		interacting protein,		
			myomegalin.		
1543	X76092 AB015330	Homo sapiens	DNA binding protein RFX3 HRIHFB2007	3327	100
1544 1545	AF198487	Homo sapiens		631	50
1546	AF016417	Caenorhabdit	transcription factor LBP-1b Similar to BZIP transcription	2822 518	100
~770	1 201011	is elegans	factor	310	**
1547	X55885	Homo sapiens	KDEL receptor	1106	100
1548	AB035495	Carassius	ubiquitin-activating enzyme	836	42
		auratus	B1		
1549	AL021707	Homo sapiens	dJ508I15.4 (KIAA0668)	3688	100
1550	AJ223978	Bacillus	YvqK protein	292	42
		subtilis			
1551	AF145615	Drosophila	BcDNA.GH03377	822	44
1552	AL157734	melanogaster Schizosaccha	mitables manual description	425	
1004	m12//3#	romyces	putative mannosyltransferase involved in N-glycosylation	435	37
		pombe		!	
1553	AF079527	Mus musculus	IER5	691	63
1554	AB026291	Rattus	acetoacetyl-CoA synthetase	1099	88
	1	norvegicus			
1555	Y44722	Homo sapiens	Human immune system molecule,	1780	99
			ISMO-3.	<u> </u>	
1556	AF116553	Drosophila	antennal-specific short-chain	277	32
1555	V71067	melanogaster	dehydrogenase/reductase		
1557	Y71056	Homo sapiens	Human membrane transport	1975	99

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN	IDENTITY
NO:				SCORE	
	V73 056	Uses sanions	protein, MTRP-1. Human membrane transport	1975	99
1558	Y71056	Homo sapiens	protein, MTRP-1.	13/3	"
1559	Y71056	Homo sapiens	Human membrane transport	1894	97
			protein, MTRP-1.		
1560	AF092050	Mus musculus	beta-1,3-N- acetylglucosaminyltransferase	262	44
1561	AL109827	Homo sapiens	dJ309K20.2 (acrosomal protein ACR55 (similar to rat sperm	1607	97
			antigen 4 (SPAG4)))		
1562	AJ131890	Homo sapiens	DNA polymerase lambda	3002	100
1563	AL035424	Homo sapiens	dA22D12.1 (novel protein similar to Drosophila Kelch proteins)	3015	100
1564	AC002400	Homo sapiens	Gene product with similarity to Ubiquitin binding enzyme	2790	100
1565	AC005306	Homo sapiens	R27216 1	919	82
1566	AF000195	Caenorhabdit	Contains similarity to Pfam	550	45
2500	111111111111111111111111111111111111111	is elegans	domain: PF00169 (PH), Score=20.6, E-value=1.9e-05,		
			N=1	1	
1567	AB033281	Homo	F-box and WD-repeats protein beta-TRCP2 isoform C	2879	100
1568	D49473	sapiens Mus musculus	truncated form of Sox17	1047	78
1569	AK025270	Homo sapiens	unnamed protein product	210	91
1570	X75756	Homo sapiens	protein kinase C mu	4797	99
1571	AF145713	Homo sapiens	SCHIP-1	2388 .	100
1572	AE003831	Drosophila melanogaster	CG18445 gene product	180	31
1573	AF074603	Streptomyces	NonF	205	38
13,3		griseus subsp.			
1574	U28993	griseus Caenorhabdit is elegans	F22D3.3 gene product	144	27
1575	AF129507	Homo sapiens	transcription factor ICBP90	287	68
1576	X64878	Homo sapiens	oxytocin receptor	2002	100
1577	AF237711	Drosophila melanogaster	Diablo	421	54
1578	G00975	Homo sapiens	Human secreted protein, SEQ ID NO: 5056.	480	100
1579	AF248744	Cryptosporid ium parvum	thrombospondin-related adhesive protein	123	33
1580	AL121782	Homo sapiens	dJ585114.2 (novel protein (translation of cDNA Em:AK000219))	663	100
1581	AF041853	Homo sapiens	kinesin family member protein KIF3A	345	33
1582	AF025441	Homo sapiens	Opa-interacting protein OIP5	1198	100
1583	AE001803	Thermotoga maritima	glycerate kinase, putative	349	34
1584	AF252283	Homo sapiens	Kelch-like 1 protein	3973	100
1585	AF169675	Homo sapiens	leucine-rich repeat transmembrane protein FLRT1	3494	99
1586	AF118274	Homo sapiens	DNb-5	2628	97
1587	X79440	Homo sapiens	NADP+-dependent malic enzyme	3167	99
1588	X99802	Homo sapiens	ZYG homologue	3966	99
1589	AF169803	Homo sapiens	flavohemoprotein b5+b5R	2563	100
1590	Y29861	Homo sapiens	Human secreted protein clone cb98 4.	181	47
1591	Z2 5535	Homo sapiens	nuclear pore complex protein hnup153	7567	99
1592	X13293	Homo sapiens	B-myb protein (AA 1-700)	3678	99
1593	M74027	Homo sapiens	mucin	242	27
1594	AL139314	Schizosaccha	hypothetical protein	235	54
	1	romyces		<u> </u>	<u> </u>

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIËS	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
110.		pombe			
.595	W78324	Homo sapiens	Fragment of human secreted protein encoded by gene 81.	1318	98
.596	Y94906	Homo sapiens	Human secreted protein clone rb649_3 protein sequence SEQ ID NO:18.	2236	98
597	AF174605	Homo sapiens	F-box protein Fbx25	1408	99
.598	AB032254	Homo	bromodomain adjacent to zinc finger domain 2A	9676	98
		sapiens	slow MVBP-C	5568	95
599	X73114	Homo sapiens	gpStaf50	2305	100
600	X82200	Homo sapiens	Human LAPH-1 protein	1149	98
601	Y00876	Homo sapiens	sequence.	2821	99
1602	AJ223351	Homo sapiens	HIRA-interacting protein 3		99
1603	AJ222801	Homo sapiens	neutral sphingomyelinase	2268 1601	99
1604	AJ222801	Homo sapiers	neutral sphingomyelinase		99
1605	AF185576	Mus musculus	POZ/zinc finger transcription factor ODA-8	3435	_
1606	AF093744	Homo sapiens	unknown	131	100
1607	A12142	synthetic construct	IFN-pseudo-omega 2	800	98
1608	Y57949	Homo sapiens	Human transmembrane protein HTMPN-73.	1868	100
1609	AF151044	Homo sapiens	HSPC210	681	97
1610	X15218	Homo sapiens	ski protein (AA 1 - 728)	3765	100
1611	Y08200	Homo sapiens	rab geranylgeranyl transferase	2976	100
1612	AF220560	Homo sapiens	B/K protein	2486	99
1613	AC004481	Arabidopsis	nodulin-like protein	371	26
1614	Y09501	Homo sapiens	NADH-cytochrome-b5 reductase	1607	100
1615	Y15521	Homo sapiens	start position 1	3150	97
1616	AJ010750	Rattus norvegicus	Castration induced prostatic apoptosis related protein-1, (CIPAR-1)	890	62
1617	X58079	Homo sapiens	S100 alpha protein	481	100
1618	Y66678	Homo	Membrane-bound protein	967	100
	AJ242973	sapiens Homo sapiens	PRO1009. peptide methionine sulfoxide	929	100
1619		·	reductase AD-014 protein	288	100
1620	AF150733	Homo sapiens	E1B-55kDa-associated protein	4646	98
1621	AJ007509	Homo sapiens	metallothionein	380	100
1622	X64177	Homo sapiens Archaeoglobu	A. fulgidus predicted coding	240	36
1623	AE001045	s fulgidus	region AF0859	403	34
1624	AL355013	Schizosaccha romyces pombe			
1625	Y66746	Homo sapiens	Membrane-bound protein PRO1198.	1184	100
1626	D90053	Sus scrofa	destrin	863	100
1627	Y35954	Homo sapiens	protein sequence, SEQ ID NO. 203.	756	100
1628	AL031775	Homo sapiens	dJ30M3.2 (novel protein)	470	100
1629	AF132484	Mus musculus	unknown	286	68
1630	AF017096	Drosophila melanogaster	similar to C. elegans R10H10.6 and S. cerevisiae YD8419.03c	493	61
1631	X03077	Homo sapiens		1704	100
1631		Homo sapiens		763	100
1632	AF151084			255	97
1633 1634	AJ001874 AC012187	Homo sapiens Arabidopsis thaliana	Contains weak similarity to GATA-6 DNA-binding protein gb H36135, gb Z26200 come	143	38

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
1635	AF026246	Homo sapiens	HERV-E integrase	411	90
1636	Y50943	Homo sapiens	Human adult brain cDNA clone ve8_1 derived protein.	1126	95
1637	AF134593	Homo sapiens	L-pipecolic acid oxidase	2068	99
1638	AJ238247	Mus musculus	putative phosphatase subunit	1948	96
1639	Y94942	Homo sapiens	Human secreted protein clone yk251_1 protein sequence SEQ ID NO:90.	1320	100
1640	AF235030	Homo sapiens	BM88 antigen	766	99
1641	AF233288	Drosophila melanogaster	WDS	358	26
1642	M19351	Mus musculus	immunoglobulin heavy chain binding protein	145	34
1643	Y70452	Homo sapiens	Human membrane channel protein-2 (MECHP-2).	1352	100
1644	AF176520	Mus musculus	WD repeat-containing F-box protein FBW5	2676	88
1645	W67816	Homo sapiens	Human secreted protein encoded by gene 10 clone HCEMU42.	1156	100
1646	X67155	Homo sapiens	mitotic kinase-like protein-1	4456	99
1647	M63180	Homo sapiens	threonyl-tRNA synthetase	1040	61
1648	Y87342	Homo sapiens	Human signal peptide containing protein HSPP-119 SEQ ID NO:119.	1566	93
1649	R95332	Homo sapiens	Tumor necrosis factor receptor 1 death domain ligand (clone 3TW).	4137	100
1650	AC007136	Homo sapiens	Putative map kinase interacting kinase	856	99
1651	AB015346	Homo sapiens	Eps15R	4464	99
1652	AL161576	Arabidopsis thaliana	putative protein	1341	48
1653	AC005313	Arabidopsis thaliana	putative calmodulin	288	28
1654	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1655	AL031428	Homo sapiens	dJ184J9.1 (KIAA0601 protein)	3526	100
1656	AB017910	Dictyosteliu m discoideum	myoM	297	32
1657	Y28919	Homo sapiens	Human regulatory protein HRGP-5.	2251	99
1658	AF056191	Homo sapiens	TPA inducible protein	2744	98
1659	U76846	Arabidopsis thaliana	ubiquitin-specific protease	137	35
1660	AL078627	Schizosaccha romyces pombe	actin-like protein; (2 actin domains)	320	34
1662	X52022	Homo sapiens	collagen type VI, alpha 3 chain	16274	99
1663	AF300648	Homo sapiens	guanine nucleotide binding protein beta subunit 4	1811	100
1664	AF214736	Homo sapiens	EH domain containing protein 2	2774	100
1665	Z48613	Saccharomyce s cerevisiae	unknown	138	26
1666	AF177385	Homo sapiens	cytochrome c oxidase assembly protein isoform 2	1395	99
1667	AC007842	Homo sapiens	BC331191_1	1581	47
1668	S67513	Borna disease virus BDV, WT-1, Halle B1/91, horse brain, field isolate,	p40	397	43
	<u></u>	Peptide, 370	<u> </u>		l

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID	NUMBER			WATERMAN	IDENTITY
NO:				SCORE	l
		aa			
1669	299753	Schizosaccha	putative NOL1-NOP2-sun family	569	47
		romyces	nucleolar protein		
		pombe			
1670	G03130	Homo sapiens	Human secreted protein, SEQ	427	97
			ID NO: 7211.		
1671	M96625	Gallus	cardiac muscle tensin	1185	54
		gallus			L
1672	AF174482	Homo sapiens	polycomb 3	2005	99
1673	Y51846 .	Homo sapiens	Human 18.1 homolog protein	233	29
			fragment.	152	29
1674	AF255334	Homo sapiens	EXP35	109	30
1675	Y94867	Homo	Human protein clone HP10563.	109	1 30
		sapiens	The state of the s	3043	99
1676	Y25712	Homo sapiens	Human secreted protein encoded from gene 2.	3043	33
			Human secreted protein	1580	91
1677	Y25712	Homo sapiens	encoded from gene 2.	1300	31
	10.63.6		dentin sialophosphoprotein	170	17
1678	AF163151	Homo sapiens	precursor	1,0	1 * '
1679	AF163151	Homo sapiens	dentin sialophosphoprotein	170	17
1679	AF163151	Homo sapiens	precursor	1 - 7 - 7	1 -
1680	AK024453	Homo sapiens	FLJ00045 protein	1349	100
1681	AF019236	Dictyosteliu	TipD	613	34
1081	AF019236	m discoideum	1195		
1682	AJ243459	Leishmania	proteophosphoglycan	153	26
1002	AU243433	major	proceophicophical and		
1683	Z69369	Schizosaccha	putative GTP-binding protein	560	46
1003	209309	romyces	pacacite oil samany parties		
	1	pombe		1	
1684	X94910	Homo sapiens	ERp28	1334	100
1685	AF286475	Takifugu	retinitis pigmentosa GTPase	196	19
1003	AI ZOUT/S	rubripes	regulator-like protein		
1686	AF191298	Homo sapiens	vacuolar sorting protein 35	4087	100
1687	AJ275986	Homo sapiens	transcription factor	2958	100
1688	AJ275986	Homo sapiens	transcription factor	1886	88
1689	X07311	Drosophila	heat shock protein	138	43
		melanogaster			-
1690	AF240463	Rattus	LIS1-interacting protein	1383	83
		norvegicus	NUDE1	1	
1691	AJ272078	Homo sapiens	APOBEC-1 stimulating protein	1256	68
1692	AJ272079	Homo sapiens	APOBEC-1 stimulating protein	1336	60
1693	AF177942	Xenopus	katanin p60	1664	66
		laevis			
1694	AF263539	Homo sapiens	arginine N-methyltransferase	1774	100
1695	AF222689	Homo	protein arginine N-	1182	81
		sapiens	methyltransferase 1-variant 2	1	<u> </u>
1696	AK000193	Homo sapiens	unnamed protein product	1060	100
1697	AB041035	Homo sapiens	kidney superoxide-producing	3122	100
			NADPH oxidase	2101	
1698	AB041035	Homo sapiens	kidney superoxide-producing	2181	100
			NADPH oxidase	1	
1699	AF025772	Homo sapiens	C2H2 zinc finger protein	488	54
1700	Y44676	Homo sapiens	Human ARF-Related Protein-1	938	97
			(HARP-1).	1215	+
1701	AKC22407	Homo sapiens	unnamed protein product	315	98
1702	AB024574	Homo sapiens	GTP-binding like protein 2	1172	100
1703	AF055078	Homo sapiens	zinc finger protein 42	421	52
1704	AF198092	Mus musculus	RP42	1057	77
1705	AE003573	Drosophila	CG12474 gene product	161	33
L		melanogaster			
1706	AB036345	Drosophila	aquaporin	164	24
		melanogaster		1	1
1707	Y55927	Homo sapiens	Human STLK2 protein.	2146	100
1708	U27121	Danio rerio	G12	212	47
1709	AL391710	Arabidopsis	putative protein	505	50

TABLE 2

SEQ ID NO:	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO.		thaliana			
1710	B01311	Homo sapiens	Human PRO241 polypeptide.	1649	97
711	U40750	Mus musculus	formin binding protein 30	4561	85
1712	AJ011118	Mus musculus	skeletal muscle and cardiac protein	1490	89
1713	AF255303	Homo sapiens	membrane-associated nucleic acid binding protein	4416	99
1714	AF255303	Homo sapiens	membrane-associated nucleic acid binding protein	2960	100
1715	U08227	Rattus norvegicus	Ras-related protein	511	51
1716	AF168795	Rattus norvegicus	schlafen-4	1129	99
1717	AF196304	Homo sapiens	SUMO-1-specific protease	1782	100
1718	AL355737	Homo sapiens	HMG20A	1069	46
1719	AB029333	Halocynthia roretzi	HrPET-1		97
1720	AF071317	Mus musculus	COP9 complex subunit 7b	1297	99
1721	AJ272215	Homo sapiens	HEYL protein	718	100
1722	G01982	Homo sapiens	Human secreted protein, SEQ ID NO: 6063.	1	
1723	AL032643	Caenorhabdit is elegans	similar to Uncharacterized protein family UPF0034,	825	92
1724	G01972	Homo sapiens	Human secreted protein, SEQ ID NO: 6053.	1231	100
1725	Y94441	Homo sapiens	Human Adipose Specific Protein 1.	4397	99
1726	AF255443	Homo sapiens	CGI-201 protein	1810	99
1727	AF183426	Homo sapiens	HT004 protein	1002	99
1728	D10884	Bos taurus	neurocalcin	1411	84
1729	Z18529	Gallus gallus	tensin CDNA EST EMBL:Z14908 comes	233	41
1730	273423	Caenorhabdit is elegans	from this gene~cDNA EST this gene		
1732	AF090891	Homo sapiens	PRO0105	470	30
1733	AJ277724	Homo sapiens	histone deacetylase 8	2015	100
1734	G04050	Homo sapiens	Human secreted protein, SEQ ID NO: 8131.	503	95
1735	D45913	Mus musculus	leucine-rich-repeat protein	3531	94
1736	AF096709	Drosophila virilis	failed axon connections protein	276	32
1737	AF195120	Homo sapiens	dynactin p62 subunit	2417	99
1738	L15314	Caenorhabdit is elegans	contains similarity to Pfam family PF01772 N=1	206	37
1739	X54618	Listeria monocytogene s	phosphadidylinositol specific phospholipase C	134	27
1740	AL031658	Homo sapiens	similar to predicted C. elegans an C. intestinalis proteins)	123	31
1741	Y35924	Homo sapiens	Extended human secreted protein sequence, SEQ ID NO. 173.	1013	99
1742	AC013354	Arabidopsis thaliana	F15H18.15	202	32
1743	W75771	Homo sapiens	Human GTP binding protein APD08.	1932	59
1744	W75771	Homo sapiens	Human GTP binding protein APD08.	1854	61
1745	AF221098	Homo sapiens	Ral guanine nucleotide exchange factor RalGPS1A	1224	70
1746	Y99372	Homo sapiens	acid sequence SEQ ID NO:116.	1332	99
1747	Y94294	Homo sapiens	Human coenzyme A-utilising	842	100

TABLE 2

SEQ	ACCESSION	SPECIES	DESCRIPTION	SMITH-	*
ID	NUMBER			WATERMAN	IDENTITY
NO:			·	SCORE	
			enzyme CoAEN-2.		
1748	AK024436	Homo sapiens	FLJ00026 protein	1619	100
1749	AE000877	Methanobacte	conserved protein	231	36
		rium			
		thermoautotr			1
		ophicum			<u> </u>
1750	AF101361	Drosophila	Abnormal X segregation	193	33
		melanogaster		<u></u>	
1751	Y15067	Homo sapiens	ZNF232	889	100
1752	AF251038	Homo sapiens	GAP-like protein	822	100
1753	AC003093	Homo sapiens	OXYSTEROL-BINDING PROTEIN;	352	57
			45% similarity to P22059	ļ	1
		i	(PID:g129308)	1	
1754	X69089	Homo sapiens	165kD protein	5703	99
1755	AL049795	Homo sapiens	dJ622L5.3 (novel protein)	1039	100
1756	AL031393	Homo sapiens	dJ733D15.1 (Zinc-finger	2765	100
			protein)		
1757	AB040672	Homo sapiens	UDP-GalNAc: polypeptide N-	2020	99
	1		acetylgalactosaminyltransfera		1
			se		
1758	AL022238	Homo sapiens	dJ1042K10.4 (novel protein)	776	43
1759	AF117653	Homo sapiens	double homeobox protein	375	54
1760	Y12065	Homo sapiens	hNop56	2959	99
1761	AL049712	Homo sapiens	dJ686C3.2 (nucleolar protein	2595	99
			hNop56)		
1762	AC002394	Homo	Gene product with similarity	1542	51
		sapiens	to dynein beta subunit	i	<u> </u>
1763	AF169017	Homo sapiens	formiminotransferase	877	100
			cyclodeaminase		<u> </u>
1764	U91541	Homo sapiens	human formiminotransferase	596	100
			cyclodeaminase (ftcd)protein,	•	1
			carboxy-terminal end		
1765	AB013365	Bacillus	YlqF	350	34
		halodurans			
1766	Y38421	Homo sapiens	Human secreted protein	145	71
	Ĺ <u> </u>		encoded by gene No. 36.		-
1767	AC009176	Arabidopsis	putative ribulose-1,5-	216	27
		thaliana	bisphosphate		
			carboxylase/oxygenase small	-	
	1770000		subunit N-methyltransferase I	737	99
1768	AK000647	Homo sapiens	unnamed protein product VNN3 protein		99
1769	AJ238982	Homo sapiens	AMSH	2665 1214	1
1770	U73522	Homo sapiens		829	86
1771	U89435	Mus musculus	unknown		
1772	S70011	Rattus sp.	tricarboxylate carrier	1604	95
1773	AL035086	Homo sapiens	dJ44A20.2 (novel protein) Human PRO1604 (UNO785) amino	2036	100
1774	Y99426	Homo sapiens		1057	99
	1.531222	10	acid sequence SEQ ID NO:308.	3146	100
1775	AF110330	Homo sapiens	glutaminase	3146	100
1776	AJ269529	Homo sapiens	glycerol 3-phosphate permease	2787	100
1777	Z81579	Caenorhabdit	cDNA EST yk76f1.5 comes from	232	31
		is elegans	this gene	1005	
1778	AY007239	Homo sapiens	monooxygenase X	1875	99
1779	AL109608	Schizosaccha	oxysterol-binding protein	644	38
	1	romyces	family		
1700	A BOC4060	pombe Homo sapiens	buffelier 1	1729	100
1780	AF254260	Mus musculus	tuftelin 1	247	50
1781	L07924	Mus musculus	guanine nucleotide	24 /	30
1700	3 7505555	117	dissociation stimulator	142	10
1782	AF295773	Homo	ral guanine nucleotide	142	49
100-	37001155	sapiens	dissociation stimulator	4333	100
1783	AK024475	Homo sapiens	FLJ00068 protein	4333	100
1784	AK024475	Homo sapiens	FLJ00068 protein	3996	93
1785	G03933	Homo sapiens	Human secreted protein, SEQ	570	100
	1		ID NO: 8014.	L	1
1786	\$82637	Homo sapiens	Ig lambda-like gene/beta-	247	100

TABLE 2

SEQ ID	ACCESSION NUMBER	SPECIES	DESCRIPTION	SMITH- WATERMAN SCORE	IDENTITY
NO:			glucuronidase exon 11 homolog		

TRADOCS:1416280.1(%CT401!.DOC)

TABLE 3

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
2	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 8.250e- 12 157-181
3	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109D 17.04 8.085e- 13 358-381
4	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.400e- 10 1129-1146 BL00028 16.07 1.257e-09 820- 837
5	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
6	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
7	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 B.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
8	BL00023	Type II fibronectin collagen-binding domain proteins.	BL00023 24.31 8.920e- 33 413-450 BL00023 24.31 4.545e-27 353- 390
9	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.119e- 09 863-917
10	PR00464	E-CLASS P450 GROUP II SIGNATURE	PR00464D 17.40 6.182e- 12 294-312 PR00464G 12.41 4.231e-11 377- 393
11	PR00734	GLYCOSYL HYDROLASE FAMILY 7 SIGNATURE	PR00734I 11.46 4.296e- 09 502-520
12	PF00023	Ank repeat proteins.	PF00023B 14.20 6.500e- 10 89-99 PF00023B 14.20 2.636e-09 56-66
14	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 3.848e- 09 79-113
15	PR00208	GLIADIN AND LMW GLUTENIN SUPERFAMILY SIGNATURE	PR00208A 12.59 9.868e- 10 517-535 PR00208A 12.59 2.233e-09 520- 538
17	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e- 14 282-295 PD00066 13.92 9.400e-14 477- 490 PD00066 13.92 6.500e-13 505-518 PD00066 13.92 9.500e- 13 254-267 PD00066 13.92 1.429e-12 393- 406 PD00066 13.92 6.571e-12 421-434
18	BL00845	CAP-Gly domain proteins.	BL00845 16.43 2.200e- 25 55-80
20	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e- 26 154-199 BL00487F 18.79 8.984e-22 235- 276 BL00487G 26.82 4.082e-12 287-329
21	BL00487	IMP dehydrogenase / GMP reductase proteins.	BL00487E 16.12 5.737e- 26 154-199 BL00487F 18.79 8.984e-22 235- 276 BL00487G 26.82 4.082e-12 348-390
22	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 3.250e- 26 302-333

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
23	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 3.250e- 26 302-333
25	BL00115	Bukaryotic RNA polymerase II heptapeptide repeat proteins.	BL00115T 8.45 7.273e- 29 1208-1242 BL00115Q 18.08 2.776e-21 953- 983 BL00115Y 11.86 8.000e-17 1604-1650 BL00115M 19.19 8.130e- 16 731-774 BL00115H 14.34 9.392e-16 463- 496 BL00115A 15.44 7.414e-15 43-82 BL00115R 6.50 6.128e- 14 983-1010 BL00115J 16.71 9.289e-14 591- 617 BL00115I 8.33 4.336e-13 535-590 BL00115L 12.25 5.939e- 13 662-694 BL00115G 11.65 6.011e-13 435- 463 BL00115K 15.03 3.417e-10 617-659 BL00115O 16.76 5.805e- 10 863-913 BL00115P 11.54 7.538e-10 913- 953 BL00115S 18.24 7.968e-10 1010-1052 BL00115U 10.34 4.475e-
26	BL00420	Speract receptor repeat proteins domain proteins.	09 1242-1265 BL00420A 20.42 4.109e- 11 81-110 BL00420A 20.42 8.820e-10 84-113
27	BL00050	Ribosomal protein L23 proteins.	BL00050A 23.71 9.250e- 27 94-127 BL00050B 14.81 8.125e-12 133- 147
28	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925B 3.73 3.089e- 10 41-54
29	PF00756	Putative esterase.	PF00756C 14.12 1.108e-
32	BL00557	FMN-dependent alpha- hydroxy acid dehydrogenases proteins.	BL00557D 17.76 5.065e- 37 274-316 BL00557A 35.08 8.909e-29 24-73 BL00557C 15.59 1.000e- 28 227-257 BL00557B 21.27 8.898e-22 130- 169
34	PR00629	SHC PHOSPHOTYROSINE INTERACTION DOMAIN SIGNATURE	PR00629E 9.90 5.886e- 35 299-328 PR00629F 10.95 8.364e-32 334- 361 PR00629B 13.66 3.786e-27 224-247 PR00629A 13.45 8.364e- 21 206-222 PR00629C 3.80 4.000e-12 249-261 PR00629D 12.45 3.739e- 11 276-286
35	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270A 17.22 1.000e- 40 39-79 PD01270B 22.18 2.875e-38 94-131 PD01270D 24.66 3.700e- 34 171-207 PD01270C 19.54 3.455e-30 137- 166
36	PD01270	RECEPTOR FC IMMUNOGLOBULIN AFFIN.	PD01270A 17.22 1.000e- 40 39-79 PD01270B 22.18 2.875e-38 94-131

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	 .,		PD01270D 24.66 3.700e-
			34 171-207 PD01270C
			19.54 3.455e-30 137-
			166
37	BL00412	Neuromodulin (GAP-43)	BL00412C 10.28 9.241e-
		proteins.	10 264-298 BL00412C 10.28 9.241e-
38	BL00412	Neuromodulin (GAP-43)	10 264-298
		proteins.	BL00412C 10.28 9.241e-
39	BL00412	Neuromodulin (GAP-43)	10 264-298
		proteins. KINESIN HEAVY CHAIN	PR00380B 12.64 7.366e-
40	PR00380	SIGNATURE	14 342-360 PR00380C
	Ì	SIGNATORE	13.18 6.927e-13 375-
	1		394 PR003B0D 9.93
	1	İ	2.180e-12 429-451
			PR00380A 14.18 5.154e-
	İ		12 143-165
44	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e-
			40 239-290 BL00345A
			13.96 2.452e-14 204-
			223
45	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e- 40 215-266 BL00345A
			13.96 2.452e-14 180-
			199
		kw OSTEOINDUCTIVE YOPM	DM01551A 15.63 3.538e-
46	DM01551	MEMBRANE OUTER.	26 172-202 DM01551C
		MEMBRANE COTER:	14.62 3.571e-17 232-
			252 DM01551B 8.84
			4.750e-11 214-226
47	PR00876	NEMATODE METALLOTHIONEIN	PR00876B 7.66 9.328e-
4′	PROOB	SIGNATURE	11 246-260
48	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 4.231e-
] 30		ZINC-FINGER METAL-	33 6-45
		BINDING NU.	
50	BL00972	Ubiquitin carboxyl-	BL00972D 22.55 7.750e-
		terminal hydrolases	19 994-1019 BL00972A
		family 2 proteins.	11.93 7.120e-18 216- 234 BL00972E 20.72
!			9.471e-14 1020-1042
			BL00972C 16.48 7.000e-
ł			13 360-375 BL00972B
ļ	}	•	9.45 8.269e-10 302-312
	51.00072	Ubiquitin carboxyl-	BL00972D 22.55 7.750e-
51	BL00972	terminal hydrolases	19 990-1015 BL00972A
		family 2 proteins.	11.93 7.120e-18 216-
		, ,	234 BL00972E 20.72
			9.471e-14 1016-1038
			BL00972C 16.48 7.000e-
1			13 360-375 BL00972B
Į.			9.45 8.269e-10 302-312 BL01115A 10.22 3.063e-
52	BL01115	GTP-binding nuclear	
		protein ran proteins.	PR00988A 6.39 8.500e-
53	PR00988	URIDINE KINASE SIGNATURE	17 20-38 PR00988F
			17 20-38 PR00980F
			210 PR00988C 13.64
	'		6.108e-14 104-120
			PR00988E 8.27 3.872e-
	· ·		11 174-186 PR00988D
			5.95 6.878e-10 160-171
			PR00988B 11.60 2.915e-
	1		09 57-69
55	PR00762	CHLORIDE CHANNEL	PR00762C 9.29 4.682e-
33		SIGNATURE	21 294-314 PR00762D
1			11.29 4.103e-19 509-
		Ì	530 PR00762A 14.22
l .		1	9.333e-18 199-217

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00762F 15.12 3.100e- 16 563-583 PR00762B
			12.12 6.063e-16 230- 250 PR00762E 12.07
			2.286e-15 545-562
			PR00762G 14.13 6.276e-
	DI 00016		13 601-616
56	BL00216	Sugar transport proteins.	BL00216B 27.64 8.800e- 10 153-203
58	PF00791	Domain present in ZO-1	PF00791B 28.49 2.049e-
		and Unc5-like netrin receptors.	10 1080-1135
59	PF00791	Domain present in ZO-1 and Unc5-like netrin	PF00791B 28.49 2.049e-
		receptors.	10 1062-1117
61	PD01929	KINASE TYPE RESISTANCE	PD01929E 10.76 9.018e-
		ANTIBIOTIC TRANSFERASE AM.	09 206-221
68	PR00360	C2 DOMAIN SIGNATURE	PR00360A 14.59 7.395e-
69	PR00360	C2 DOMAIN SIGNATURE	09 680-693 PR00360A 14.59 7.395e-
			09 670-683
70	PF00651	BTB (also known as BR-	PF00651 15.00 8.714e-
72	DM00179	C/Ttk) domain proteins. w KINASE ALPHA ADHESION	10 51-64 DM00179 13.97 5.304e-
, 2	20173	T-CELL.	09 108-118
73	BL00239	Receptor tyrosine kinase	BL00239B 25.15 7.075e-
74	BL00790	class II proteins. Receptor tyrosine kinase	12 118-166 BL00790N 13.25 6.116e-
/4	ВЕОО / ЭО	class V proteins.	10 93-120
76	DM00471	0 PROKARYOTIC DNA	DM00471A 11.73 9.357e-
		TOPOISOMERASE I.	13 53-66 DM00471B
80	PD02876	DECARBOXYLASE	8.45 4.857e-12 70-81 PD02876C 8.80 2.723e-
	1202011	PHOSPHATIDYLSERINE.	13 223-236 PD02876D
			12.13 2.588e-12 334-
81	PD02876	DECARBOXYLASE	351 PD02876C 8.80 2.723e-
01	1202010	PHOSPHATIDYLSERINE.	13 282-295 PD02876D
			12.13 2.588e-12 393-
83	BL00708	Prolyl endopeptidase	410 BL00708B 24.91 7.197e-
63	ВДООТОВ	family serine proteins.	12 570-601
84	PR00014	FIBRONECTIN TYPE III	PR00014C 15.44 8.043e-
0.5	2000000	REPEAT SIGNATURE	09 985-1004
86	PR00678	PI3 KINASE P85 REGULATORY SUBUNIT	PR00678H 9.13 1.379e-
		SIGNATURE	
89	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 8.200e-
		REPEAT SIGNATURE	09 264-279 PR00320B 12.19 8.650e-09 264-
			279
93	BL00455	Putative AMP-binding	BL00455 13.31 2.588e-
95	BL00107	domain proteins. Protein kinases ATP-	14 316-332 BL00107A 18.39 4.000e-
	1 220020	binding region proteins.	10 123-154
96	BL00107	Protein kinases ATP-	BL00107A 18.39 4.000e-
97	PR00081	binding region proteins. GLUCOSE/RIBITOL	10 212-243
J !	7,00001	DEHYDROGENASE FAMILY	PR00081B 10.38 6.318e-
		SIGNATURE	10.53 2.500e-12 54-72
98	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 5.500e-
	1	SIGNATURE	24 401-423 PR00380D 9.93 7.188e-20 613-635
			PR00380B 12.64 7.517e-
			16 529-547 PR00380C
			13.18 2.756e-13 560-
	1		579

	7.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5.5	DECONTRACON	DECIM MC+
SEQ ID NO	NO.	DESCRIPTION	RESULTS*
102	PR00300	ATP-DEPENDENT CLP	PR00300A 9.56 7.545e-
		PROTEASE ATP-BINDING SUBUNIT SIGNATURE	14 289-308
104	BL00479	Phorbol esters /	BL00479B 12.57 6.786e-
		diacylglycerol binding	18 298-314 BL00479A
		domain proteins.	19.86 4.913e-16 155-
			178 BL00479A 19.86 4.300e-13 272-295
			BL00479B 12.57 6.294e-
			12 181-197
106	BL01019	ADP-ribosylation factors	BL01019A 13.20 8.013e-
		family proteins.	12 43-83
107	DM01970	0 kw 2K632.12 YDR313C	DM01970B 8.60 5.000e-
		ENDOSOMAL III.	16 403-416
108	BL00191	Cytochrome b5 family, heme-binding domain	BL00191K 17.38 4.951e- 27 238-282 BL00191J
		proteins.	11.37 6.447e-17 182-
		process.	204
109	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 4.938e-
		ZINC-FINGER METAL-	37 8-47
		BINDING NU.	
110	BL01138	Scorpion short toxins	BL01138A 10.96 8.297e-
111	- I	proteins. Protein kinases ATP-	10 38-50 BL00107A 18.39 5.800e-
113	BL00107	binding region proteins.	23 156-187 BL00107B
		January region processis.	13.31 9.100e-14 225-
			241
117	BL00214	Cytosolic fatty-acid	BL00214B 26.51 1.000e-
		binding proteins.	17 46-91 BL00214A
	DY 00107	Protein kinases ATP-	21.17 7.052e-11 5-31
118	BL00107	binding region proteins.	BL00107A 18.39 8.560e-
119	PR00529	GONADOTROPHIN RELEASING	PR00529C 11.03 7.506e-
		HORMONE RECEPTOR	10 158-177
		SIGNATURE	1
120	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 9.400e-
	77.7.7.4.4	REPEAT SIGNATURE	09 80-95
121	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 9.400e- 09 80-95
127	BL00215	Mitochondrial energy	BL00215A 15.82 7.158e-
		transfer proteins.	13 216-241
128	BL01032	Protein phosphatase 2C	BL01032C 6.14 3.195e-
		proteins.	12 147-157 BL01032H
			11.25 5.680e-11 318-
			331 BL01032G 8.33 8.932e-11 282-296
			BL01032I 10.42 8.902e-
			09 379-389
129	BL01310	ATP1G1 / PLM / MAT8	BL01310 14.74 6.694e-
		family proteins.	26 28-64
130	PR00990	RIBOKINASE SIGNATURE	PR00990B 12.32 9.534e- 15 47-67 PR00990A
			15 47-67 PR00990A 16.23 5.500e-14 20-42
			PR00990C 12.62 2.412e-
			09 119-133
133	BL00880	Acyl-CoA-binding	BL00880 17.52 5.576e-
		protein.	26 72-122
134	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 9.308e-
135	PR00315	region RNP-1 proteins.	14 18-37 PR00215C 13.98 6.779e-
133	PR00215	HEOROMODOBIN STOUMTORE	10 475-496
136	BL01310	ATPIG1 / PLM / MAT8	BL01310 14.74 2.432e-
		family proteins.	29 71-107
140	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.882e-
		domain proteins.	14 214-231 BL00028
			16.07 9.471e-14 102-
			119 BL00028 16.07
L			2.800e-13 18-35

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		BL00028 16.07 5.500e-
			13 74-91 BL00028
	Į		16.07 9.100e-13 186-
		1	203 BL00028 16.07
			8.043e-12 46-63
			BL00028 16.07 8.435e-
			12 130-147 BL00028
			16.07 9.217e-12 270-
			287 BL00028 16.07
			6.192e-11 242-259
			BL00028 16.07 4.000e-
			10 158-175
	<u> </u>		BL00501D 16.69 9.538e-
141	BL00501	Signal peptidases I	14 113-133 BL00501C
		serine proteins.	9.61 8.688e-10 89-101
	<u> </u>		BL01020C 15.35 7.722e-
143	BL01020	SAR1 family proteins.	20 79-130
_		The state of the s	PD01066 19.43 6.400e-
146	PD01066	PROTEIN ZINC FINGER	25 335-374
		ZINC-FINGER METAL-	25 555-574
		BINDING NU.	BL00126C 22.07 1.450e-
149	BL00126	3'5'-cyclic nucleotide	25 509-550 BL00126E
		phosphodiesterases	35.22 3.951e-16 654-
		proteins.	709 BL00126D 25.50
		1	1.360e-15 565-604
			BL00126B 15.20 8.200e-
	1		11 483-495 BL00126A
			27.56 8.269e-11 442-
			479
			BL00632 23.79 5.271e-
151	BL00632	Ribosomal protein S4	20 106-149
		proteins.	BL00559I 13.63 5.304e-
154	BL00559	Eukaryotic molybdopterin	19 29-58 BL00559K
	Ì	oxidoreductases	13.17 2.957e-18 172-
	1	proteins.	199 BL00559J 19.63
			8.385e-13 99-151
			BL00559L 13.60 5.814e-
	1		12 241-259
	Ì		PR00449A 13.20 1.692e-
155	PR00449	TRANSFORMING PROTEIN P21	13 13-35
		RAS SIGNATURE	BL00406D 12.58 2.547e-
157	BL00406	Actins proteins.	18 275-330 BL00406A
			9.95 5.776e-16 15-50 BL00406B 5.47 7.429e-
			12 69-124 BL00406C
			6.75 9.682e-12 128-183
160	BL00132	Zinc carboxypeptidases,	BL00132A 26.07 7.000e-
	1	zinc-binding region 1	14 22-63 BL00132C
		proteins.	21.35 3.466e-12 104-
			145
165	PR00109	TYROSINE KINASE	PR00109B 12.27 9.043e-
		CATALYTIC DOMAIN	13 139-158
1		SIGNATURE	
168	BL00362	Ribosomal protein S15	BL00362 24.67 9.700e-
1		proteins.	15 129-172
169	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 1.000e-
		dependent helicases	35 640-686 BL00039A
		proteins.	18.44 1.964e-13 212-
			251 BL00039B 19.19
			4.553e-13 378-404
			BL00039C 15.63 8.773e-
!		1	12 465-489
1	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 3.721e-
175		RAS SIGNATURE	12 14-36
175			BL01310 14.74 2.432e-
	BL01310	ATPIG1 / PLM / MAT8	
175	BL01310	ATP1G1 / PLM / MATE family proteins.	29 133-169
	BL01310	ATPIGI / PLM / MATE family proteins. PROTEIN ZINC FINGER	

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		BINDING NU.	
180	PR00007	COMPLEMENT CIQ DOMAIN SIGNATURE	PR00007B 14.16 7.429e- 20 160-180 PR00007A 19.33 4.938e-19 133- 160 PR00007C 15.60 1.225e-15 206-228 PR00007D 9.64 6.885e- 11 238-249
181	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e- 24 280-323
182	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e- 24 263-306
183	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e- 24 280-323
184	BL00027	'Homeobox' domain proteins.	BL00027 26.43 9.526e- 24 263-306
188	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929C 5.26 3.328e- 09 460-471
189	PR00929	AT-HOOK-LIKE DOMAIN SIGNATURE	PR00929C 5.26 3.328e- 09 440-451
191	PR00450 PF00564	Tyrosine specific protein phosphatases proteins. RECOVERIN FAMILY SIGNATURE Octicosapeptide repeat proteins. BROMODOMAIN SIGNATURE	BL00383F 15.51 7.188e- 17 666-682 BL00383A 13.34 8.714e-17 162- 177 BL00383E 10.35 1.000e-14 333-344 BL00383E 10.35 7.300e- 14 628-639 BL00383F 15.51 1.720e-13 371- 387 BL00383C 10.10 3.000e-13 217-228 BL00383D 11.92 7.000e- 13 295-308 BL00383B 7.61 1.692e-11 187-196 BL00383C 10.10 1.750e- 09 509-520 BL00383D 11.92 4.000e-09 589- 602 BL00383B 7.61 8.000e-09 479-488 PR00450C 12.22 7.911e- 15 83-105 PR00450C 12.22 6.286e-13 47-69 PF00564B 24.74 6.164e- 16 227-278 PR00503D 20.81 9.156e-
194	PR00503	BROMODOMAIN SIGNATURE	15 204-224 PR00503B 9.96 9.571e-13 170-187
195	BL00901	Cysteine synthase/cystathionine beta-synthase P- phosphate att.	BL00901C 20.63 3.429e- 18 67-117
197	BF00636	Nt-dnaJ domain proteins.	BL00636A 8.07 6.211e- 17 40-57 BL00636B 15.11 2.000e-13 67-88
198	PR00690	ADHESIN FAMILY SIGNATURE	PR00690A 10.86 9.866e- 09 463-482
199	BL01131	Ribosomal RNA adenine dimethylases proteins.	BL01131A 26.62 2.343e- 12 84-130
201	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.352e- 12 509-522
203	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.286e- 10 39-72
206	PR00261	LOW DENSITY LIPOPROTEIN (LDL) RECEPTOR SIGNATURE	PR00261A 11.02 4.462e- 19 65-87 PR00261C 11.37 9.308e-19 65-87 PR00261D 12.47 2.667e- 18 65-87 PR00261B 14.12 4.000e-18 143- 165 PR00261A 11.02

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			4.833e-18 143-165 PR00261D 12.47 7.500e- 18 143-165 PR00261B 14.12 5.065e-16 65-87 PR00261C 11.37 8.967e- 16 143-165 PR00261F 11.57 4.938e-13 143- 165 PR00261E 11.08 7.188e-13 65-87 PR00261F 11.57 7.188e- 13 65-87 PR00261E 11.08 1.643e-11 143- 165
209	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 6.143e- 13 118-173 PF00791C 20.98 7.680e-10 132- 171
211	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007A 19.33 5.781e- 19 131-158 PR00007B 14.16 4.115e-18 158- 178 PR00007C 15.60 1.675e-15 201-223 PR00007D 9.64 7.231e- 11 233-244
212	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.545e- 30 43-91
213	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.545e- 30 43-91
215	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 1.900e- 29 568-614 BL00039A 18.44 1.871e-23 21-60 BL00039C 15.63 1.720e- 11 364-388 BL00039B 19.19 4.064e-11 277- 303
217	BL00100	Chloramphenicol acetyltransferase proteins.	BL00100D 17.22 8.484e- 09 68-106
219	PR00213	MYELIN PO PROTEIN SIGNATURE	PR00213C 15.94 3.969e- 11 199-227
222	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.947e-09
224	PR00875	MOLLUSC METALLOTHIONEIN SIGNATURE	PR00875A 5.83 1.000e- 09 901-913
225	BL00636	Nt-dnaJ domain proteins.	BL00636B 15.11 8.200e- 19 18-39
226	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 1.000e- 21 21-38 BL00636B 15.11 8.200e-19 45-66
229	PR00301	70 KD HEAT SHOCK PROTEIN SIGNATURE	PR00301F 13.98 7.563e- 13 329-346 PR00301G 13.78 4.300e-12 361- 382
230	BL00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 8.773e- 20 35-70 BL00460B 9.73 7.429e-16 78-96 BL00460C 14.35 2.831e- 12 111-134 BL00460D 16.89 8.773e-11 140- 160
231	PR00647	SENR ORPHAN RECEPTOR SIGNATURE	PR00647B 10.19 8.522e- 09 273-287
233	BL00292	Cyclins proteins.	BL00292B 20.31 7.429e- 27 244-275 BL00292A 22.87 7.750e-27 201- 235
234	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 6.308e- 13 7-29 PR00449C

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			17.27 4.462e-11 47-70 PR00449D 10.79 7.120e- 11 109-123
235	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e- 10 251-265 PR00019B 11.36 5.320e-09 119- 133 PR00019B 11.36 1.000e-08 229-243
236	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 7.300e- 10 245-259 PR00019B 11.36 5.320e-09 113- 127 PR00019B 11.36 1.000e-08 223-237
237	PD00289	PROTEIN SH3 DOMAIN REPEAT PRESYNA.	PD00289 9.97 8.448e-09 67-81
240	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e- 10 616-635
241	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 3.492e- 10 616-635
244	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 8.941e- 12 54-64
245	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 8.043e- 09 124-134
248	BL00246	Wnt-1 family proteins.	BL00246D 23.97 1.000e- 40 186-239 BL00246E 20.32 1.000e-40 305- 351 BL00246B 13.69 4.176e-36 105-140 BL00246A 15.75 2.286e- 24 70-90 BL00246C 15.56 4.857e-22 150- 175
250	PR00927	ADENINE NUCLEOTIDE TRANSLOCATOR 1 SIGNATURE	PR00927E 14.93 5.114e- 10 253-275
254	BL00674	AAA-protein family proteins.	BL00674B 4.46 1.000e- 09 223-245
255	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 6.045e- 09 61-88
256	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002B 15.18 2.800e- 10 421-435
258	PR00094	ADENYLATE KINASE SIGNATURE	PR00094C 12.94 2.200e- 18 87-104 PR00094D 12.52 2.731e-14 161- 177 PR00094A 10.31 5.500e-14 11-25 PR00094B 11.01 4.115e- 13 39-54 PR00094E 11.25 7.333e-13 178- 193
259	BL00892	HIT family proteins.	BL00892A 18.17 5.500e- 13 60-91
262	BL00388	Proteasome A-type subunits proteins.	BL00388A 23.14 1.000e- 40 8-54 BL00388B 31.38 3.864e-33 66-108 BL00388D 20.71 1.000e- 21 153-184 BL00388C 18.79 8.147e-16 126- 148
264	BL00903	Cytidine and deoxycytidylate deaminases zinc-binding region s.	BL00903 12.93 5.821e- 09 91-101
267	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.529e- 09 241-257
270	BL00226	Intermediate filaments proteins.	BL00226D 19.10 1.000e- 37 362-409 BL00226B

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	NU.		23.86 8.043e-35 196- 244 BL00226C 13.23 7.000e-20 261-292 BL00226A 12.77 6.143e- 15 96-111
271	PD02952	KINASE TRANSFERASE CHOLINE PROTEIN MULTIGENE FAMI.	PD02952C 15.76 9.73le- 16 235-265 PD02952B 15.57 5.625e-09 215- 229
272	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 1.000e- 40 106-160 PD02929B 18.36 8.800e-17 179- 199
274	BL01027	Glycosyl hydrolases family 39 proteins.	BL01027B 15.34 3.486e- 09 213-250
275	PR00424	ADENOSINE RECEPTOR SIGNATURE	PR00424D 14.32 6.451e-
277	BL00052	Ribosomal protein S7 proteins.	BL00052A 27.85 6.000e- 13 137-184 BL00052B 15.17 5.143e-12 208- 235
279	BL00790	Receptor tyrosine kinase class V proteins.	BL00790N 13.25 5.659e- 13 267-294
280	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 1.000e-21 89-105 PR00319A 15.27 8.364e- 21 51-68 PR00319B 11.47 8.200e-19 70-85
281	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 94-112 PR00319C 13.41 1.000e-21 76-92 PR00319A 15.27 8.364e- 21 38-55 PR00319B 11.47 8.200e-19 57-72
287	PF00929	Exonuclease.	PF00929D 16.17 7.366e- 09 149-163
291	BL00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
292	B£00326	Tropomyosins proteins.	BL00326A 14.01 2.360e- 09 93-127
294	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.714e- 12 203-216
295	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 5.500e- 15 322-339 BL00028 16.07 9.471e-14 433- 450 BL00028 16.07 4.600e-13 648-665 BL00028 16.07 5.500e- 13 760-777 BL00028 16.07 9.550e-13 788- 805 BL00028 16.07 3.348e-12 704-721 BL00028 16.07 6.478e- 12 461-478 BL00028 16.07 8.435e-12 844- 861 BL00028 16.07 1.692e-11 593-610 BL00028 16.07 2.038e- 11 211-228 BL00028 16.07 5.154e-11 732- 749 BL00028 16.07 5.846e-11 377-394 BL00028 16.07 6.885e- 11 816-833 BL00028 16.07 7.231e-11 676- 693 BL00028 16.07

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			BL00028 16.07 4.086e-
			09 517-534 BL00028
			16.07 7.429e-09 489-
			506
296	BL00215	Mitochondrial energy	BL00215A 15.82 8.333e-
290	DECOLUS	transfer proteins.	16 111-136 BL00215A
		January I.	15.82 2.723e-11 10-35
			BL00215B 10.44 9.526e-
			11 152-165 BL00215B
			10.44 7.375e-10 59-72
	1		BL00215A 15.82 9.824e-
			10 205-230
			PF00953C 19.70 8.773e-
302	PF00953	Glycosyl transferase.	34 236-269 PF00953A
		· •	19.68 5.000e-25 102-
			129 PF00953B 6.17
			1.000e-13 182-194
304	PF00152	tRNA synthetases class	PF00152D 21.30 8.364e-
	Ì	II.	28 422~461 PF00152C
			28.03 9.250e-21 220-
			257 PF00152B 15.67
			2.658e-13 159-184
			PF00152A 19.68 5.714e-
	i		11 44-67
305	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 8.250e-
305	PD07066	ZINC-FINGER METAL-	35 37-76
		BINDING NU.	33 3. 75
			PD02784B 26.46 5.840e-
306	PD02784	PROTEIN NUCLEAR	09 92-135
		RIBONUCLEOPROTEIN.	PR00454C 11.24 7.808e-
307	PR00454	ETS DOMAIN SIGNATURE	
			09 1167-1186
308	PR00237	RHODOPSIN-LIKE GPCR	PR00237E 13.03 5.091e-
		SUPERFAMILY SIGNATURE	13 188-212 PR00237G
			19.63 7.207e-13 268-
			295 PR00237A 11.48
			4.375e-11 24-49
			PR00237C 15.69 3.057e-
			10 101-124 PR00237D
			8.94 4.750e-10 137-159
			PR00237F 13.57 5.364e-
		1	10 230-255 PR00237B
	1		13.50 9.43Be-10 57-79
309	BL00522	DNA polymerase family X	BL00522C 11.90 7.577e-
202	DECORE	proteins.	24 315-339 BL00522F
	1	P-000	14.90 1.310e-15 470-
	}	i	494 BL00522A 25.52
		}	1.265e-14 179-226
	1	1	BL00522E-19.63 8.615e-
			14 430-460 BL00522B
		1	27.30 9.625e-12 267-
		1	
_			313 BL00326D 8.76 5.235e-
310	BL00326	Tropomyosins proteins.	1
			10 856-897
312	BL00290	Immunoglobulins and	BL00290A 20.89 4.706e-
		major histocompatibility	14 151-174 BL00290B
[1	complex proteins.	13.17 9.000e-12 211-
		1 -	229
313	BL00345	Ets-domain proteins.	BL00345B 21.28 1.000e-
"			40 34-85 BL00345A
}			13.96 9.217e-16 1-20
-	DE000E1	BTB (also known as BR-	PF00651 15.00 5.091e-
315	PF00651	C/Ttk) domain proteins.	15 63-76
		C/TCK) domain proteins.	BL01020C 15.35 3.198e-
317	BL01020	SAR1 family proteins.	b .
	1		17 79-130
318	BL00216	Sugar transport	BL00216B 27.64 4.696e-
1		proteins.	11 164-214
1			
320	PR00109	TYROSINE KINASE	PR00109B 12.27 4.814e-

SEQ ID N	1	DESCRIPTION	RESULTS*
	NO.	SIGNATURE	
321	BL00027	'Homeobox' domain	D1 0000 7 04 10 10 10 10 10 10 10 10 10 10 10 10 10
361	5500027	proteins.	BL00027 26.43 5.688e- 10 329-372
322	PR00109	TYROSINE KINASE	PR00109B 12.27 8.765e-
		CATALYTIC DOMAIN SIGNATURE	12 558-577
324	BL01241	Link domain proteins.	BL01241 35.81 8.313e-
			30 183-236 BL01241 35.81 3.222e-13 282- 335
326	BL00412	Neuromodulin (GAP-43)	BL00412D 16.54 4.000e-
		proteins.	12 515-566 BL00412D 16.54 5.705e-11 516- 567 BL00412D 16.54 7.848e-10 518-569 BL00412D 16.54 1.827e- 09 514-565 BL00412D
			16.54 1.918e-09 513-
			564 BL00412D 16.54 2.102e-09 520-571
328	BL00232	Cadherins extracellular	BL00232B 32.79 9.557e-
		repeat proteins domain proteins.	20 151-199 BL00232B 32.79 2.246e-18 41-89 BL00232B 32.79 5.985e- 18 370-418 BL00232B 32.79 5.500e-16 258- 306 BL00232B 32.79
			9.384e-15 475-523 BL00232C 10.65 2.537e- 12 256-274 BL00232C 10.65 4.326e-11 368- 386 BL00232C 10.65 7.261e-11 473-491 BL00232C 10.65 7.457e- 11 39-57
330	PR00454	ETS DOMAIN SIGNATURE	PR00454C 11.24 7.808e-
			09 1167-1186
331	BL00598	Chromo domain proteins.	BL00598 14.45 8.393e- 18 27-49
333	BL01016	Glycoprotease family proteins.	BL01016C 22.84 3.925e-32 70-115 BL01016E 14.88 5.286e-19 149-177 BL01016H 13.71 7.577e-13 291-301 BL01016D 8.86 3.298e-11 127-140 BL01016G 7.14 5.622e-10 261-271 BL01016A 5.65 7.167e-10 4-19 BL01016F 13.34 1.563e-09 200-212 BL01016B 8.93
339	BL01115	GTP-binding nuclear	8.855e-09 38-50
		protein ran proteins.	BL01115A 10.22 5.500e- 11 17-61
340	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL-	PD01066 19.43 1.231e- 33 10-49
341	BL01160	BINDING NU. Kinesin light chain	BL01160B 19.54 5.042e-
242	PD01000	repeat proteins.	09 55-109
342	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.400e- 30 16-55
343	DM00031	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 1.000e-
346	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	40 20-68 PR00109B 12.27 4.764e- 11 135-154
347		SIGNATURE	
347	PR00109	TYROSINE KINASE	PR00109B 12.27 4.764e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
		CATALYTIC DOMAIN SIGNATURE	11 135-154
351	BL01187	Calcium-binding EGF-like domain proteins pattern proteins.	BL01187B 12.04 1.783e- 13 100-116 BL01187B 12.04 8.435e-13 276- 292 BL01187B 12.04 8.800e-11 13-29 BL01187B 12.04 7.429e- 10 54-70 BL01187B 12.04 5.725e-09 231- 247 BL01187A 9.98 7.000e-09 255-267
352	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e- 10 366-379 PD00078B 13.14 4.522e-09 168- 181
354	BL00380	Rhodanese proteins.	BL00380F 9.76 6.694e- 11 542-553
355	PF00628	PHD-finger.	PF00628 15.84 1.000e- 11 116-131
356	PR00587	SOMATOSTATIN RECEPTOR TYPE 1 SIGNATURE	PR00587A 8.06 9.700e- 09 17-37
359	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 4.462e- 15 261-274 PD00066 13.92 6.500e-13 233- 246 PD00066 13.92 4.300e-09 289-302
361	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 9.604e- 13 54-109 PF00791B 28.49 1.095e-12 21-76 PF00791A 27.85 1.432e- 09 71-126 PF00791B 28.49 7.440e-09 184- 239
362	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 2.273e- 11 279-334
363	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 5.080e- 10 73-95 PR00450C 12.22 3.278e-09 109- 131
364	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
365	PF00242	DNA polymerase (viral) N-terminal domain proteins.	PF00242Q 13.51 2.328e- 09 22-68
366	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.644e- 09 1038-1092
367	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e- 09 229-243 PR00019B 11.36 6.040e-09 91-105 PR00019A 11.19 8.667e- 09 370-384
368	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011D 14.03 9.000e- 15 30-49 PR00011A 14.06 9.830e-15 30-49 PR00011B 13.08 4.500e- 14 30-49 PR00011C 24.25 5.143e-09 6-35
369	BL01032	Protein phosphatase 2C proteins.	BL01032H 11.25 4.150e- 09 417-430
372	BL00478	LIM domain proteins.	BL00478B 14.79 7.750e- 12 410-425
373	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.757e- 34 26-65
376	PR00170	SODIUM CHANNEL SIGNATURE	PR00170E 6.48 2.739e-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
	+	 	10 88-118
380	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 1.000e- 23 276-307 BL00107B 13.31 1.692e-12 342- 358
381	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 5.714e- 12 50-66
382	PR00624	HISTONE H5 SIGNATURE	PR00624G 4.08 4.900e- 09 524-544
384	PD00078	REPEAT PROTEIN ANK NUCLEAR ANKYR.	PD00078B 13.14 5.950e- 10 366-379 PD00078B 13.14 4.522e-09 168- 181
385	PR00511	TEKTIN SIGNATURE	PR00511D 7.11 5.371e-
386	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 6.000e- 10 97-130
388	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 5.000e- 13 516-529
389	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290A 20.89 7.667e- 09 151-174
390	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.200e- 15 221-246 BL00215A 15.82 7.618e-14 20-45 BL00215A 15.82 8.851e- 11 123-148 BL00215B 10.44 9.526e-11 69-82 BL00215B 10.44 7.300e- 09 272-285 BL00215B 10.44 8.500e-09 165- 178
394	BL00674	AAA-protein family proteins.	BL00674B 4.46 2.723e- 16 299-321
397	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 8.579e- 11 141-155
398	PR00761	BINDIN PRECURSOR SIGNATURE	PR00761B 9.93 6.764e- 09 55-74
399	BL00240	Receptor tyrosine kinase class III proteins.	BL00240B 24.70 7.907e- 10 118-142
401	PF00676	Dehydrogenase El component.	PF00676B 24.71 8.071e- 18 331-369 PF00676D 14.40 3.854e-15 486- 506 PF00676C 16.88 9.182e-14 454-478
402	BL00514	Fibrinogen beta and gamma chains C-terminal domain proteins.	BL00514C 17.41 4.673e- 28 4432-4469 BL00514G 15.98 6.092e-14 4555- 4585 BL00514D 15.35 2.532e-12 4473-4486 BL00514F 11.65 4.288e- 10 4519-4534 BL00514H 14.95 4.955e-10 4584- 4609
403	PF00992	Troponin.	PF00992A 16.67 5.974e- 09 105-140
404	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.450e- 10 73-87 PR00019A 11.19 8.043e-10 76-90 PR00019B 11.36 1.000e- 09 50-64 PR00019B 11.36 1.000e-09 96-110
405	BL00232	Cadherins extracellular repeat proteins domain proteins.	BL00232B 32.79 9.557e- 20 139-187 BL00232B 32.79 2.246e-18 29-77 BL00232B 32.79 5.985e- 18 358-406 BL00232B 32.79 5.500e-16 246-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		294 BL00232B 32.79
			9.384e-15 463-511
		1	BL00232C 10.65 2.537e-
			12 244-262 BL00232C 10.65 4.326e-11 356-
			374 BL00232C 10.65
			7.261e-11 461-479
			BL00232C 10.65 7.457e-
			11 27-45
407	PF00426	Outer Capsid protein VP4	PF00426S 15.67 5.634e-
409	BL01160	(Hemagglutinin). Kinesin light chain	BL01160B 19.54 9.695e-
409	Prolied	repeat proteins.	09 126-180
410	BL00741	Guanine-nucleotide	BL00741B 14.27 2.731e-
		dissociation stimulators	09 252-275
		CDC24 family sign.	
411	PF00646	F-box domain proteins.	PF00646A 14.37 6.344e-
410	77.00603	Themiding kinggo	09 86-100 BL00603B 11.39 8.500e-
412	BL00603	Thymidine kinase cellular-type proteins.	09 542-557
415	BL00866	Carbamoyl-phosphate	BL00866B 36.29 3.571e-
		synthase subdomain	31 245-291 BL00866C
		proteins.	23.26 9.000e-25 331-
			366
418	PR00239	MOLLUSCAN RHODOPSIN C- TERMINAL TAIL SIGNATURE	PR00239E 1.58 6.114e-
421	PF00791	Domain present in ZO-1	PF00791B 28.49 7.955e-
421	PF00791	and Unc5-like netrin	14 23-78 PF00791B
		receptors.	28.49 3.653e-12 273-
İ			328 PF00791B 28.49
İ			4.273e-11 156-211
I			PF00791B 28.49 7.818e-
į			11 89-144 PF00791B 28.49 1.524e-10 56-111
			PF00791C 20.98 3.559e-
			09 37-76 PF00791C
			20.98 5.235e-09 170-
			209 PF00791C 20.98
			5.235e-09 381-420 PF00791B 28.49 6.202e-
			09 189-244 PF00791B
		1	28.49 7.028e-09 435-
		1	490 PF00791B 28.49
			8.679e-09 367-422
424	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 7.207e-
		TITLE COLLEGE WILLIAM	28 1645-1679 PR00109D 17.04 5.881e-
425	PR00109	TYROSINE KINASE CATALYTIC DOMAIN	10 228-251
		SIGNATURE	
429	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 4.600e-
		(RING finger), proteins.	11 31-40
431	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 1.844e-
1		dependent helicases	34 490-536 BL00039A 18.44 5.615e-19 205-
		proteins.	18.44 5.615e-19 205- 244 BL00039B 19.19
			8.920e-16 251-277
ĺ			BL00039C 15.63 5.781e-
			15 333-357
432	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 7.652e-
			12 169-185
433	PR00828	FORMIN SIGNATURE	PR00828B 5.23 8.218e-
126	PT 00415	Company	10 382-405 BL00415N 4.29 8.643e-
436	BL00415	Synapsins proteins.	11 195-239 BL00415N
	1	1	
		ļ	I I
443	PR00834	HTRA/DEGO PROTEASE	4.29 3.036e-09 809-853 PR00834F 10.91 6.040e-
443	PR00834	HTRA/DEGQ PROTEASE FAMILY SIGNATURE	4.29 3.036e-09 809-853

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		p15.	10 183-218 PF01140D 15.54 3.093e-09 246- 281
449	PR00568	DOPAMINE D3 RECEPTOR SIGNATURE	PR00568G 13.95 5.551e-
451	PF00084	Sushi domain proteins (SCR repeat proteins.	PF00084B 9.45 3.813e- 10 47-59
452	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.821e- 09 618-649
456	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 1.000e- 25 77-99 PR00380D 9.93 1.000e-21 281-303 PR00380C 13.18 8.286e- 17 230-249 PR00380B 12.64 4.724e-16 194- 212
457	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 9.143e- 24 246-267 PR00253B 13.47 2.000e-23 272- 294 PR00253C 13.85 7.000e-23 306-328 PR00253D 16.68 5.950e- 21 452-473
467	PR00849	GLYCOSYL HYDROLASE FAMILY 58 SIGNATURE	PR00849D 9.77 9.236e- 09 910-937
471	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 8.200e-12 33-44
472	BL00226	Intermediate filaments proteins.	BL00226B 23.86 3.721e- 09 282-330
473	BL00344	GATA-type zinc finger domain proteins.	BL00344 17.99 7.000e- 12 814-852
474	BL00481	Thiol-activated cytolysins proteins.	BL00481E 13.07 8.909e- 09 173-199
479	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 2.571e- 09 393-408
480	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 1.900e- 38 8-47
481	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405C 19.41 1.000e- 19 451-473 PR00405B 11.83 4.333e-18 430- 448 PR00405A 17.71 4.971e-18 411-431
482	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 9.286e- 10 959-974 PR00049D 0.00 9.857e-10 958-973 PR00049D 0.00 1.305e- 09 937-952 PR00049D 0.00 8.322e-09 939-954
486	PR00007	COMPLEMENT C1Q DOMAIN SIGNATURE	PR00007B 14.16 8.615e- 23 653-673 PR00007A 19.33 6.192e-22 626- 653 PR00007C 15.60 5.846e-19 698-720 PR00007D 9.64 3.647e- 13 732-743
487	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567B 18.23 2.853e~ 09 200-214
488	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.569e- 12 3-21
489	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.882e- 27 30-69 PD01066 19.43 3.430e-10 71-110
490	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.864e- 09 663-678
492	BL01128	Shikimate kinase proteins.	BL01128A 18.84 6.464e- 17 58-92
497	PF00429	ENV polyprotein (coat	PF00429 31.08 7.171e-

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	10.	polyprotein).	15 21-71
498	BL00120	Lipases, serine proteins.	BL00120B 11.37 7.923e- 09 185-200
500	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 7.353e-
501	DI 01150	region RNP-1 proteins.	11 299-318
	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 8.579e- 12 131-146
505	BL00021	Kringle domain proteins.	BL00021B 13.33 3.739e- 17 492-510
508	PR00120	H+TRANSPORTING ATPASE (PROTON PUMP) SIGNATURE	PR00120C 9.90 5.800e-
509	DM01417	6 kw INDUCING XPMC2	DM01417E 20.62 2.938e-
į		MUSHROOM SPAC22G7.04.	16 362-395 DM01417D 11.08 3.800e-13 322- 338
510	PF00534	Glycosyl transferases group 1.	PF00534B 14.47 6.625e-
511	PF00534	Glycosyl transferases	PF00534B 14.47 6.625e-
		group 1.	09 293-317
512	PF00534	Glycosyl transferases	PF00534B 14.47 6.625e-
		group 1.	09 366-390
513	PD01841	PHOSPHORYLASE KINASE	PD01841A 21.71 1.000e-
		ALPHA MUSCL.	40 110-160 PD01841B
			14.35 1.000e-40 181-
	1		222 PD01841D 17.87 1.000e-40 243-295
			PD01841F 13.36 1.000e-
			40 333-382 PD01841G
•	l		24.26 1.000e-40 386-
			440 PD01841L 18.42
			1.000e-40 968-1010
			PD01841I 23.00 4.545e-
			37 762-804 PD01841E
	ł		18.60 3.750e-36 295-
			333 PD01841J 14.94
			6.023e-35 851-888 PD01841H 21.30 2.909e-
			33 490-527 PD01841K
			14.81 7.088e-33 924-
			954 PD01841C 13.78
			9.386e-23 222-243
			PD01841M 10.82 8.594e-
			21 1054-1073 PD01841I
			23.00 2.667e-13 549-
514	PR00153	CYCLOPHILIN PEPTIDYL-	591 PR00153C 11.01 7.188e-
	1.00155	PROLYL CIS-TRANS	13 95-111 PR00153E
		ISOMERASE SIGNATURE	9.10 4.150e-12 122-138
515	BL00740	MAM domain proteins.	BL00740A 13.87 7.188e-
		_	12 410-423
516	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 6.087e- 12 1018-1052
517	BL00242	Integrins alpha chain	BL00242C 16.86 8.320e-
523	DM00031	proteins. IMMUNOGLOBULIN V REGION.	09 12-42
-23	2000031	Temorogrosopin v REGION.	DM00031A 16.80 3.750e- 39 20-68 DM00031B
			15.41 1.000e-25 84-118
525	BL00319	Amyloidogenic	BL00319C 17.12 8.375e-
		glycoprotein	10 61-95
		extracellular domain	
		proteins.	<u> </u>
526	PF00789	Domain present in	PF00789B 19.70 3.308e-
		ubiquitin-regulatory	12 322-343 PF00789C
		proteins.	20.98 5.269e-09 367-
528	BL01162		392
320	2001105	Quinone oxidoreductase / zeta-crystallin	BL01162C 22.80 1.500e-
		proteins.	16 120-164
		Processes.	l

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529	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 3.893e-
532	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.000e- 17 11-36 BL00215A 15.82 8.660e-11 123-
533	BL00215	Mitochondrial energy transfer proteins.	148 BL00215A 15.82 4.000e- 17 11-36 BL00215A
534	BL0009B	Thiolases acyl-enzyme intermediate proteins.	15.82 8.660e-11 97-122 BL00098C 21.65 2.800e- 38 181-227 BL00098B 32.59 5.345e-38 86-141 BL00098D 26.30 8.364e- 35 245-288 BL00098E 22.12 1.000e-34 314- 352 BL00098F 10.18 4.971e-22 365-386 BL00098A 10.60 6.455e- 11 38-50
535	PR00370	FLAVIN-CONTAINING MONOOXYGENASE (FMO) SIGNATURE	PR00370E 11.96 7.429e- 22 321-340 PR00370D 16.33 6.143e-21 185- 204 PR00370F 17.75 6.559e-21 376-396 PR00370B 10.91 9.591e- 21 27-46 PR00370C 12.72 3.500e-20 140- 157 PR00370A 3.35 6.442e-17 4-20
536	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.429e- 16 285-302 BL00028 16.07 6.294e-14 341- 358 BL00028 16.07 1.346e-11 369-386 BL00028 16.07 1.692e- 11 397-414 BL00028 16.07 4.462e-11 453- 470 BL00028 16.07 7.231e-11 425-442 BL00028 16.07 4.300e- 10 313-330
537	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 844-881
538	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 819-856
539	BL00762	WHEP-TRS domain proteins.	BL00762A 23.43 9.419e- 15 822-859
540	PR00985	LEUCYL-TRNA SYNTHETASE SIGNATURE	PR00985A 12.10 9.000e- 10 357-375
541	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 1.00De- 40 3-47 PD02102B 18.28 4.375e-34 57-100 PD02102D 21.69 1.923e- 30 179-218 PD02102C 26.34 8.929e-26 100- 146
543	BF00058	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.000e- 10 48-65 BL00028 16.07 6.400e-10 193- 210 BL00028 16.07 1.000e-09 343-360 BL00028 16.07 6.914e- 09 78-95
545	BL00250	TGF-beta family proteins.	BL00250A 21.24 8.000e- 31 293-329 BL00250B 27.37 5.286e-24 354- 390
547	PR00319	BETA G-PROTEIN	PR00319B 11.47 2.714e-

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-		(TRANSDUCIN) SIGNATURE	09 186-201 PR00319A 15.27 7.344e-09 210- 227
548	BL01204	NF-kappa-B/Rel/dorsal domain proteins.	BL01204A 17.74 1.000e- 40 8-56 BL01204D 16.42 1.000e-40 177- 221 BL01204E 13.83 7.652e-30 225-250 BL01204C 13.93 8.714e- 22 141-160 BL01204B 15.41 4.333e-16 102- 116
549	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 8.364e-
551	PF00632	HECT-domain (ubiquitin- transferase).	PF00632C 20.66 3.302e- 23 1569-1601 PF00632B 18.45 3.700e-21 1515- 1543
554	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 1.600e- 14 187-205 BL00290A 20.89 2.059e-14 130- 153
557	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.339e- 09 846-879
559	DM01111	4 kw PHOSPHATASE TRANSFORMING 61K PDF1.	DM01111L 11.93 3.762e- 09 7-35
562	PF00658	Poly-adenylate binding protein, unique domain proteins.	PF00658C 16.33 9.455e- 32 118-155
564	BL00141	Bukaryotic and viral aspartyl proteases proteins.	BL00141A 12.10 4.150e- 10 472-488
566	PF00855	PWWP domain proteins.	PF00855 13.75 5.667e- 15 272-289
567	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 4.977e- 13 229-268
569	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183- 199
570	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.000e- 19 118-149 BL00107B 13.31 5.500e-15 183- 199
572	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e- 34 454-483 PR00193C 12.60 2.636e-31 223- 251 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 508- 537
573	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 1.857e- 34 470-499 PR00193C 12.60 2.636e-31 239- 267 PR00193B 11.69 7.750e-29 171-197 PR00193A 15.41 2.588e- 22 115-135 PR00193E 19.47 6.559e-19 524- 553
575	BL00752	XPA protein.	BL00752B 19.17 9.703e- 10 885-929
576	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.000e- 09 276-295
577	BL00116	DNA polymerase family B	BL00116A 12.81 5.737e-

SEQ ID NO	: ACCESSION NO.	DESCRIPTION	RESULTS*
		proteins.	13 864-877 BL00116B 11.82 1.529e-12 952- 965
578	BL00195	Glutaredoxin proteins.	BL00195B 15.31 7.158e- 09 121-141
579	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019B 11.36 9.000e- 11 217-231 PR00019B 11.36 1.360e-09 386- 400 PR00019A 11.19 3.333e-09 389-403 PR00019B 11.36 8.920e- 09 363-377
580	PR00253	GAMMA-AMINOBUTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 2.125e- 25 275-296 PR00253B 13.47 7.923e-24 301- 323 PR00253D 16.68 5.846e-23 444-465 PR00253C 13.85 2.241e- 20 335-357
583	PR00343	SELECTIN SUPERFAMILY COMPLEMENT-BINDING REPEAT SIGNATURE	PR00343C 16.85 2.286e- 11 1233-1252 PR00343C 16.85 5.500e-11 333- 352 PR00343C 16.85 5.500e-11 783-802 PR00343C 16.85 4.246e- 10 1491-1510 PR00343C 16.85 8.230e-10 1686- 1705
584	DM01537	kw SKI2W SKI2 NUCLEOLAR HELICASE.	DM01537B 21.63 1.878e- 37 79-126 DM01537B 21.63 9.491e-30 916- 963 DM01537A 15.14 3.186e-11 784-804
586	PF00013	KH domain proteins family of RNA binding proteins.	PF00013 5.78 1.450e-09 124-136
587	DM00892	3 RETROVIRAL PROTEINASE.	DM00892C 23.55 4.409e- 13 262-296
589	BL00478	LIM domain proteins.	BL00478B 14.79 1.643e- 13 261-276 BL00478B 14.79 7.709e-09 321- 336
590	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 931-948
591	PF00855	PWWP domain proteins.	PF00855 13.75 8.000e- 15 1062-1079
593	PF00628	PHD-finger.	PF00628 15.84 3.455e- 12 424-439
594	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 2.241e- 16 558-576 PR00205A 14.73 9.308e-13 542- 558 PR00205C 13.65 5.304e-12 594-609 PR00205B 11.39 4.273e- 10 336-354
596	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.789e- 18 307-338
598	PD01675	GLYCOPROTEIN MAJOR ENVELOPE PROBABLE U3.	PD01675C 19.89 2.330e- 10 55-89
600	BL00242	Integrins alpha chain proteins.	BL00242E 9.03 9.591e- 27 985-1014 BL00242C 16.86 4.115e-26 286- 316 BL00242D 13.57 4.150e-25 357-385 BL00242B 8.13 7.353e- 12 189-199 BL00242D 13.57 3.455e-11 421- 446 BL00242A 13.80

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			5.000e-11 61-73 BL00242D 13.57 4.986e- 10 291-316
601	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 5.610e- 09 198-213
602	PR00278	PANCREATIC HORMONE SIGNATURE	PR00278A 12.43 4.569e- 10 331-348
603	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479C 12.01 3.250e- 12 170-183
604	BL00315	Dehydrins proteins.	BL00315A 9.35 1.672e- 09 424-452
605	BL00415	Synapsins proteins.	BL00415N 4.29 9.794e- 10 295-339
606	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926F 17.75 1.000e- 13 335-358
608	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e- 15 265-282
609	PF00855	PWWP domain proteins.	PF00855 13.75 5.167e-
612	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 7.411e- 10 877-897 DM01206B 10.69 8.027e-10 861- 881 DM01206B 10.69 9.137e-10 873-893 DM01206B 10:69 1.456e- 09 859-879 DM01206B 10.69 1.797e-09 879- 899 DM01206B 10.69 4.076e-09 865-885 DM01206B 10.69 7.038e- 09 898-918 DM01206B 10.69 7.949e-09 871- 891 DM01206B 10.69 8.291e-09 767-787
615	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699A 8.91 2.023e- 28 129-158 PD02699C 24.84 1.000e-27 317- 364 PD02699B 18.28 1.000e-17 158-182
616	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455'
617	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 4.086e- 22 288-310 PR00380D 9.93 3.721e-17 486-508 PR00380B 12.64 2.241e- 16 410-428 PR00380C 13.18 2.976e-13 436- 455
618	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 5.143e- 12 531-551 DM01206B 10.69 2.603e-10 535- 555
621	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 3.160e- 21 561-582
622	BL00239	Receptor tyrosine kinase class II proteins.	BL00239F 28.15 3.222e- 10 647-692 BL00239C 18.75 8.304e-10 543- 566
623	PR00407	EUKARYOTIC MOLYBDOPTERIN DOMAIN SIGNATURE	PR00407K 9.94 8.448e- 09 326-339
624	BL00641	Respiratory-chain NADH dehydrogenase 75 Kd	BL00641C 21.10 1.000e- 40 157-202 BL00641E

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		subunit proteins.	24.37 1.000e-40 255- 308 BL00641F 33.12 1.000e-40 571-623 BL00641A 17.15 1.818e- 37 48-80 BL00641B 12.62 5.846e-34 113- 139 BL00641D 13.23 9.308e-29 216-240
627	PR00103	CAMP-DEFENDENT PROTEIN KINASE SIGNATURE	PR00103E 17.80 2.500e- 18 367-380 PR00103B 13.39 2.080e-14 297- 312 PR00103A 9.59 2.957e-14 282-297 PR00103D 10.83 3.077e- 12 346-358 PR00103C 15.68 1.000e-11 334- 344 PR00103B 13.39 1.450e-11 175-190 PR00103A 9.59 1.720e- 10 160-175
630	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	FR00081A 10.53 6.211e- 16 4-22
631	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 8.500e- 14 37-50
632	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 2.233e- 10 1324-1344 DM01206B 10.69 4.822e-10 1276- 1296 DM01206B 10.69 7.658e-10 1328-1348 DM01206B 10.69 8.274e- 10 1280-1300 DM01206B 10.69 4.532e-09 1320- 1340 DM01206B 10.69 7.266e-09 1326-1346
635	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 7.600e- 23 145-176 BL00107B 13.31 2.636e-13 211- 227
636	BL00657	Fork head domain proteins.	BL00657A 19.39 1.545e- 30 101-143 BL00657B 22.27 7.750e-26 149- 192
637	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 10 607-623
643	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 4.913e-09 199-212
647	PF00628	PHD-finger.	PF00628 15.84 2.350e- 13 385-400 PF00628 15.84 3.455e-12 464- 479
648	BL01129	Hypothetical yabO/yceC/sfhB family proteins.	BL01129E 13.25 4.000e- 25 332-357 BL01129C 25.56 8.200e-23 236- 279 BL01129B 12.51 6.118e-13 191-212
649	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 3.908e- 10 455-480
650	BL00027	'Homeobox' domain proteins.	BL00027 26.43 6.684e- 13 771-814
651	BL50002	Src homology 3 (SH3) domain proteins profile.	BL50002A 14.19 1.750e- 12 1026-1045
653	PR00253	GAMMA-AMINOBÚTYRIC ACID (GABA) RECEPTOR SIGNATURE	PR00253A 9.15 4.000e- 24 253-274 PR00253C 13.85 8.800e-24 313- 335 PR00253B 13.47 3.143e-22 279-301 PR00253D 16.68 7.652e-

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654	PD01719	PRECURSOR GLYCOPROTEIN	20 422-443 PD01719A 12.89 4.452e-
	1553/15	SIGNAL RE.	11 969-997 PD01719A 12.89 3.961e-10 128- 156 PD01719A 12.89 7.395e-10 1276-1304 PD01719A 12.89 1.222e- 09 1220-1248
657	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 563-578
658	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 8.397e- 09 580-595
659	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.174e- 13 539-572 DM00215 19.43 4.750e-12 549- 582 DM00215 19.43 9.824e-11 551-584 DM00215 19.43 2.929e- 10 548-581 DM00215 19.43 4.054e-10 550- 583 DM00215 19.43 5.339e-10 552-585 DM00215 19.43 7.107e- 10 544-577
660	PR00688	XYLOSE ISOMERASE SIGNATURE	PR00688I 13.78 9.518e- 09 224-236
661	BL00027	'Homeobox' domain proteins.	BL00027 26.43 5.950e- 23 249-292
662	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
663	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
664	PR00360	C2 DOMAIN SIGNATURE	PR00360B 13.61 7.158e- 10 596-610
666	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 8.988e- 10 704-720
667	BL50040	Elongation factor 1 gamma chain profile.	BL50040C 22.62 2.143e- 16 135-178
668	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019B 11.36 1.360e- 09 139-153 PR00019A 11.19 1.667e-09 94-108 PR00019B 11.36 4.600e- 09 163-177
670	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 3.250e-10 681-694 BL00018 7.41 6.400e-10 717-730
672	PD00131	ATP-BINDING TRANSPORT TRANSMEMBR.	PD00131B 34.97 1.000e- 34 356-410 PD00131C 19.59 1.346e-26 504- 542
673	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	PR00667G 15.33 7.557e- 10 106-123
674	PR00320	G-PROTEIN BETA WD-4C REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 593-608 PR00320B 12.19 4.115e-12 635- 650 PR00320C 13.01 8.435e-11 717-732 PR00320C 13.01 2.800e- 10 635-650 PR00320C 13.01 6.400e-10 593- 608 PR00320B 12.19 3.250e-09 593-608
675	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 4.857e- 13 572-587 PR00320B 12.19 4.115e-12 614-

SEQ ID N	O: ACCESSION	DESCRIPTION	RESULTS*
	NO.		, ALGOLIS
			629 PR00320C 13.01
			8.435e-11 696-711
			PR00320C 13.01 2.800e-
			10 614-629 PR00320C
			13.01 6.400e-10 572-
			587 PR00320B 12.19
676	7770000		3.250e-09 572-587
676	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 9.667e-
679	PF00642	Zinc finger C-x8-C-x5-C-	09 249-263
075	FF00042	x3-H type (and similar).	PF00642 11.59 3.700e- 16 225-236 PF00642
		As a type (and similar):	11.59 7.900e-12 187-
			198
680	PR00308	TYPE I ANTIFREEZE	PR00308C 3.83 8.754e-
		PROTEIN SIGNATURE	10 286-296
681	BL00019	Actinin-type actin-	BL00019D 15.33 4.200e-
		binding domain proteins.	19 227-257
682	PR00700	PROTEIN TYROSINE	PR00700D 12.47 4.000e-
		PHOSPHATASE SIGNATURE	09 99-118
687	PR00049	WILM'S TUMOUR PROTEIN	PR00049D 0.00 8.500e-
		SIGNATURE	10 538-553
689	BL01024	Protein phosphatase 2A	BL01024A 10.26 1.000e-
		regulatory subunit PR55	40 22-69 BL01024B
		proteins.	8.91 1.000e-40 86-127
		,	BL01024C 7.80 1.000e-
			40 146-185 BL01024D
			13.22 1.000e-40 185-
			222 BL01024E 11.96
			1.000e-40 222-266
			BL01024F 9.42 1.000e-
			40 266-317 BL01024G 11.09 1.000e-40 317-
]		349 BL01024H 13.88
			1.000e-40 389-442
691	BL00027	'Homeobox' domain	BL00027 26.43 8.071e-
	1	proteins.	31 152-195
692	BL00211	ABC transporters family	BL00211A 12.23 5.050e-
		proteins.	09 45-57
693	BL00211	ABC transporters family	BL00211A 12.23 5.050e-
·		proteins.	09 45-57
694	BL00211	ABC transporters family	BL00211A 12.23 5.050e-
		proteins.	09 58-70
696	BL00680	Methionine	BL00680 14.37 5.304e-
		aminopeptidase subfamily	17 173-195
697	Dr comus	1 proteins.	
637	BL00741	Guanine-nucleotide	BL00741B 14.27 3.418e-
		dissociation stimulators CDC24 family sign.	11 242-265
698	DM01930	2 kw FINGER SMCX SMCY	DM01930E 15.41 1.367e-
	2001330	YDR096W.	37 170-215 DM01930F
		1-2000000	14.16 B.232e-28 267-
		1	303 DM01930B 19.86
			9.163e-10 37-71
700	PR00869	DNA-POLYMERASE FAMILY X	PR00869A 12.80 1.281e-
		SIGNATURE	16 245-263
701	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 2.174e-
		SIGNATURE	10 77-91 PR00048A
			10.52 6.870e-10 133-
			147 PR00048A 10.52
		1	8.826e-10 105-119
			PR00048A 10.52 5.320e-
			09 161-175
702	BL00523	Sulfatases proteins.	BL00523E 19.27 2.565e-
			25 326-356 BL00523A
			13.36 5.050e-16 38-55
			BL00523B 8.64 5.909e-
			15 86-98 BL00523C
		<u> </u>	12.64 5.500e-13 137-

SEQ ID NO:	ACCESSION	DESCRIPTION	RESULTS*
	NO.		148 BL00523D 9.89
	}		1.844e-11 290-302
			BL00523G 9.46 5.500e-
			10 513-523 BL00523F
			10.85 6.351e-09 413-
			424
703	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 8.412e-
		SIGNATURE	12 376-390 PR00048B
			6.02 1.000e-10 334-344
			PR00048B 6.02 1.474e-
			09 364-374
707	PD00787	SYNTHASE BIOSYNTHESIS	PD00787A 14.84 8.941e-
		TRANSFERASE.	14 66-82
708	PR00761	BINDIN PRECURSOR	PR00761E 14.32 8.500e-
700	11100.02	SIGNATURE	10 822-841
712	DM01354	kw TRANSCRIPTASE REVERSE	DM01354Y 10.69 4.977e-
/12	שבנוטוום	II ORF2.	38 425-465 DM01354X
		II ORIZ.	13.86 7.300e-34 376-
			415 DM01354V 12.97
			4.923e-17 311-358
		•	DM01354W 12.64 5.596e-
			10 356-376
			BL00039D 21.67 7.545e-
713	BL00039	DEAD-box subfamily ATP-	
		dependent helicases	27 450-496 BL00039A
		proteins.	18.44 2.537e-18 147-
		1	186 BL00039C 15.63
			2.216e-14 280-304
			BL00039B 19.19 1.947e-
	1		13 194-220
715	BL00383	Tyrosine specific	BL00383E 10.35 4.981e-
,13	220000	protein phosphatases	10 150-161
	j	proteins.	
717	PF00777	Sialyltransferase	PF00777C 18.60 4.035e-
/1/	Proutt	family.	21 106-161
	D14000033	IMMUNOGLOBULIN V REGION.	DM00031A 16.80 3.750e-
718	DM00031	IMMUNOGLOBULIN V REGION:	39 20-68 DM00031B
			15.41 2.688e-28 84-118
			DM00031C 12.79 1.300e-
	ļ		12 131-142
			BL00243B 17.54 1.000e-
719	BL00243	Integrins beta chain	40 131-172 BL00243C
		cysteine-rich domain	16.42 1.000e-40 172-
		proteins.	
	1		208 BL00243D 24.07
		1	1.000e-40 222-274
			BL00243F 22.63 1.000e-
	1		40 314-358 BL00243I
1			31.77 6.571e-39 607-
Ì			650 BL00243E 16.70
			3.077e-35 274-304 .
1			BL00243G 21.38 3.625e-
1			34 358-400 BL00243H
t			17.53 5.235e-29 567-
			593 BL00243A 17.61
		1	3.250e-21 63-84
1			BL00243H 17.53 7.167e-
1			16 477-503 BL00243H
1			17.53 2.304e-11 524-
			550 BL00243H 17.53
1	1		5.304e-11 606-632
	1	Ì	BL00243I 31.77 1.380e-
		1	
Į.	1		09 610-653
	PR00217	43 KD POSTSYNAPTIC	PR00217C 10.91 8.022e-
720	1	PROTEIN SIGNATURE	09 20-36
720	3		1 DD0000010 11 05 5 0000-
	PR00704	CALPAIN CYSTEINE	PR00704D 11.05 5.909e-
720	PR00704		34 135-161 PR00704F
	PR00704	PROTEASE (C2) FAMILY	
	PR00704		34 135-161 PR00704P
	PR00704	PROTEASE (C2) FAMILY	34 135-161 PR00704F 13.61 7.000e-26 190-

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			PR00704B 17.94 2.241e- 23 75-98 PR00704A 14.68 4.094e-19 30-54 PR00704C 11.88 1.871e- 18 99-116
725	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e- 09 169-187
726	PR00194	TROPOMYOSIN SIGNATURE	PR00194A 7.86 7.652e- 09 169-187
727	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.125e- 13 277-292 PR00320A 16.74 1.310e-11 277- 292 PR00320C 13.01 4.522e-11 323-338 PR00320A 16.74 6.586e- 11 323-338 PR00320B 12.19 4.343e-10 323- 338 PR00320B 12.19 6.914e-10 277-292
731	PR00195	DYNAMIN SIGNATURE	PR00195A 11.94 8.627e- 16 288-307 PR00195E 9.82 3.912e-11 457-474
733	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.082e- 10 787-798
738	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039A 18.44 2.565e- 28 26-65 BL00039D 21.67 2.105e-20 338- 384 BL00039C 15.63 9.100e-13 160-184 BL00039B 19.19 9.617e- 11 73-99
739	BL01289	TSC-22 / dip / bun family proteins.	BL01289A 12.18 8.909e- 31 326-353 BL01289B 10.45 9.571e-17 353- 383
742	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 7.078e- 12 41-81
743	BL00965	Phosphomannose isomerase type I proteins.	BL00965C 23.78 1.000e- 40 256-305 BL00965B 17.77 1.600e-25 126- 153 BL00965A 10.57 6.400e-19 94-113
747	BL00021	Kringle domain proteins.	BL00021D 24.56 4.563e- 25 231-273 BL00021B 13.33 5.345e-21 60-78
74B	BL00612	Osteonectin domain proteins.	BL00612B 11.35 2.034e- 11 93-126
749	PR00450	RECOVERIN FAMILY SIGNATURE	PR00450C 12.22 6.880e- 10 135-157
752	BL00795	Involucrin proteins.	BL00795C 17.06 6.000e- 11 384-429 BL00795C 17.06 9.444e-11 370- 415
754	BL00051	Ribosomal protein L39e proteins.	BL00051 20.92 1.935e- 16 4-50
755	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.723e- 09 171-184
760	BL01020	SAR1 family proteins.	BL01020C 15.35 9.020e- 12 99-150
762	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e- 40 33-88
763	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 9.137e- 10 206-240
764	BL00027	'Homeobox' domain proteins.	BL00027 26.43 8.800e- 29 417-460
767	BL01208	VWFC domain proteins.	BL01208B 15.83 6.063e- 10 309-324 BL01208B 15.83 8.031e-10 165-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
*****			180 BL01208B 15.83
770			4.162e-09 85-100
//0	BL00031	Nuclear hormones receptors DNA-binding	BL00031A 19.55 9.571e- 32 208-241 BL00031B
		region proteins.	22.25 5.500e-27 242-
			274
772	PR00449	TRANSFORMING PROTEIN P21	PR00449A 13.20 1.450e-
		RAS SIGNATURE	18 4-26 PR00449E
			13.50 3.520e-14 142-
			165 PR00449C 17.27
			3.032e-13 44-67
			PR00449D 10.79 8.579e-
			14.34 3.455e-11 27-44
773	BL00523	Sulfatases proteins.	BL00523E 19.27 9.333e-
			23 299-329 BL00523A
			13.36 2.200e-13 47-64
			BL00523B 8.64 2.607e-
			13 91-103 BL00523D
	-		9.89 7.923e-12 224-236
			BL00523C 12.64 4.512e- 10 141-152 BL00523F
			10.85 5.821e-10 373-
			384
775	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
		domain proteins.	09 568-585
776	BL00028	Zinc finger, C2H2 type,	BL00028 16.07 7.686e-
777	BL00028	domain proteins. Zinc finger, C2H2 type,	09 621-638
, , ,	, pronore	domain proteins.	BL00028 16.07 7.686e- 09 595-612
778	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 8.412e-
		region RNP-1 proteins.	11 322-341 BL00030A
			14.39 7.000e-10 220-
			239
779	PR00079	GLUCOSE-6-PHOSPHATE	PR00079B 12.98 2.929e-
		DEHYDROGENASE SIGNATURE	26 193-222 PR00079E
	Ì		16.65 4.150e-23 348- 375 PR00079C 8.68
			6.351e-16 246-264
	İ		PR00079D 13.51 7.070e-
			16 264-281 PR00079A
			16.12 6.769e-13 169-
781	DY 0 0 2 2 5		183
781	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 9.250e- 17 10-35 BL00215A
		cransfer proteins.	15.82 6.000e-16 221-
4			246 BL00215A 15.82
			7.857e-12 108-133
		i	BL00215B 10.44 9.526e-
702	Process	100000000000000000000000000000000000000	11 168-181
783	PD00289	PROTEIN SH3 DOMAIN	PD00289 9.97 6.276e-09
785	BL00690	REPEAT PRESYNA. DEAH-box subfamily ATP-	159-173 BL00690B 13.38 1.000e-
	3200000	dependent helicases	12 147-165 BL00690A
	1	proteins.	6.87 5.320e-10 114-124
]	BL00690C 7.51 3.189e-
			09 218-228
786	PR00449	TRANSFORMING PROTEIN P21	PR00449C 17.27 8.500e-
		RAS SIGNATURE	16 50-73 PR00449A
			13.20 5.235e-14 8-30 PR00449E 13.50 2.853e-
			11 150-173 PR00449D
			10.79 1.545e-09 111-
			125
788	DM01206	CORONAVIRUS NUCLEOCAPSID	DM01206B 10.69 8.767e-
200	D7.000	PROTEIN.	10 1-21
790	BL00915	Phosphatidylinositol 3-	BL00915C 22.43 9.182e-
	į.	and 4-kinases proteins.	39 725-764 BL00915B

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			22.78 5.050e-33 633- 671 BL00915D 27.02 1.529e-21 795-831 BL00915A 10.09 1.000e- 13 395-407
791	PR00208	GLIADIN AND LMW GLUTENÎN SUPERFAMILY SIGNATURE	PRO0208A 12.59 6.294e- 10 120-138 PR00208A 12.59 6.294e-10 121- 139 PR00208A 12.59 6.294e-10 122-140 PR00208A 12.59 6.294e- 10 123-141 PR00208A 12.59 6.294e-10 124- 142 PR00208A 12.59 6.294e-10 125-143 PR00208A 12.59 6.294e- 10 126-144 PR00208A 12.59 6.294e-10 127- 145 PR00208A 12.59 6.294e-10 128-146 PR00208A 12.59 6.294e- 10 129-147 PR00208A 12.59 7.411e-09 130- 148 PR00208A 12.59 7.658e-09 131-149 PR00208A 12.59 7.904e- 09 132-150 PR00208A 12.59 8.274e-09 118- 136 PR00208A 12.59 8.274e-09 119-137
795	PR00205	CADHERIN SIGNATURE	PR00205B 11.39 5.034e- 16 302-320 PR00205A 14.73 1.257e-11 284- 300 PR00205C 13.65 1.333e-11 337-352
796	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 4.000e- 12 196-247 BL00412D 16.54 5.705e-11 197- 248 BL00412D 16.54 7.848e-10 199-250 BL00412D 16.54 1.827e- 09 195-246 BL00412D 16.54 1.918e-09 194- 245 BL00412D 16.54 2.102e-09 201-252
797	BL00021	Kringle domain proteins.	BL00021B 13.33 6.339e- 13 40-58
799	BLÖ1052	Calponin family repeat proteins.	BL01052C 18.51 1.000e- 40 87-127 BL01052A 16.12 1.529e-32 3-35 BL01052B 15.31 1.257e- 25 52-78 BL01052D 10.26 5.737e-25 174- 194
800	BL00348	p53 tumor antigen proteins.	BL00348F 23.19 3.714e- 09 197-240
801	BL00309	Vertebrate galactoside- binding lectin proteins.	BL00309C 18.65 1.621e- 09 62-87
802	PR00245	OLFACTORY RECEPTOR SIGNATURE	PR00245D 10.47 5.224e- 09 187-199
804	PF00774	Dihydropyridine sensitive L-type calcium channel (Beta subuni.	PF00774A 16.47 8.457e- 10 110-156
808	PR00667	RETINAL PIGMENT EPITHELIUM-RETINAL GPCR SIGNATURE	PR00667C 11.71 9.875e- 09 12-28
810	PD02346	PHOTOSYSTEM II PROTEIN PRECURSOR	PD02346F 12.89 4.340e- 09 317-354

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		PHOTOSYNTHESIS.	
811	BL00685	CBF-A/NF-YB subunit proteins.	BL00685B 14.41 6.779e- 14 54-95 BL00685A 11.22 4.798e-13 5-54
812	PR00080	ALCOHOL DEHYDROGENASE SUPERFAMILY SIGNATURE	PR00080A 9.32 9.419e- 10 93-105
813	BL00357	Histone H2B proteins.	BL00357 7.74 1.988e-17 22-65
815	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.923e- 15 158-171 PD00066 13.92 5.200e-14 46-59 PD00066 13.92 7.000e- 14 18-31 PD00066 13.92 7.000e-13 130- 143 PD00066 13.92 7.500e-13 214-227 PD00066 13.92 9.000e- 13 102-115 PD00066 13.92 4.429e-12 186- 199 PD00066 13.92 1.783e-11 74-87
816	BL01195	Peptidyl-tRNA hydrolase proteins.	BL01195C 20.12 3.348e- 20 100-139
820	BLC0520	Interleukin-10 family proteins.	BL00520A 6.21 6.471e- 09 1-14
822	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972A 11.93 8.113e- 09 224-242
825	PR00876	NEMATODE METALLOTHIONEIN SIGNATURE	PR00876B 7.66 2.268e- 10 101-115
829	PD02855	FLAVOPROTEIN PROTEIN DNA/PANTOTHEN.	PD02855A 18.37 4.732e- 28 88-124 PD02855B 8.36 6.478e-09 132-142
830	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 7.000e- 21 44-62 PR00405C 19.41 1.000e-13 65-87 PR00405A 17.71 7.283e- 13 25-45
831	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 1.000e- 09 47-61 PR00019B 11.36 1.720e-09 136- 150 PR00019B 11.36 3.880e-09 44-58
832	PR00011	TYPE III EGF-LIKE SIGNATURE	PR00011B 13.08 3.438e- 16 164-183 PR00011D 14.03 6.850e-16 164- 183 PR00011A 14.06 8.364e-14 164-183 PR00011C 24.25 5.415e- 12 231-260 PR00011D 14.03 9.852e-11 212- 231
834	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 7.000e- 12 232-246
835	PD0030€	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 4.000e- 10 290-304
836	PD00306	PROTEIN GLYCOPROTEIN PRECURSOR RE.	PD00306A 10.26 7.000e- 12 216-230
837	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 3.898e- 09 78-111
839	PD02784	PROTEIN NUCLEAR RIBONUCLEOPROTEIN.	PD02784B 26.46 8.302e- 09 73-116
840	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700B 16.80 5.091e- 22 369-390 PR00700D 12.47 5.765e-21 491- 510 PR00700C 13.17 4.750e-14 449-467 PR00700F 11.18 8.500e-

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			11 538-549 PR00700E 17.57 3.100e-10 522- 538
841	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 5.404e- 13 134-153
844	PD02785	PROTEIN RIBOSOMAL 60S L22 RNA-BINDING HEP.	PD02785B 14.43 1.000e- 40 58-112 PD02785A 15.23 1.915e-28 8-57
845	BL00826	MARCKS family proteins.	BL00826C 7.63 6.738e- 09 203-230
846	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 4.429e- 10 15-24
849	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e- 08 340-349
850	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 6.506e- 09 12-27
851	PD02411	PROTEIN TRANSCRIPTION REGULATION NUCLEAR.	PD02411 21.89 7.000e- 16 246-280
852	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e- 40 723-778 BL00420B 22.67 1.321e-38 933- 988 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e- 27 587-642 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 830-885 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 808- 819 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C 11.90 5.119e-11 1018- 1029 BL00420C 11.90 7.955e-10 567-578
853	BL00420	Speract receptor repeat proteins domain proteins.	BL00420B 22.67 1.000e- 40 756-811 BL00420B 22.67 1.321e-38 966- 1021 BL00420B 22.67 8.457e-28 482-537 BL00420B 22.67 4.500e- 27 620-675 BL00420B 22.67 9.625e-27 270- 325 BL00420B 22.67 4.205e-26 163-218 BL00420B 22.67 5.731e- 23 55-110 BL00420B 22.67 6.464e-20 377- 432 BL00420B 22.67 2.800e-15 863-918 BL00420C 11.90 1.900e- 13 355-366 BL00420C 11.90 1.900e-12 841- 852 BL00420C 11.90 3.550e-12 248-259 BL00420C 11.90 2.831e- 11 141-152 BL00420C 11.90 5.119e-11 1051- 1062 BL00420C 11.90

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	NO.		7.955e-10 567-578
857	PR00388	3',5'-CYCLIC NUCLEOTIDE CLASS II PHOSPHODIESTERASE SIGNATURE	PR00388A 10.45 2.778e- 09 64-83
859	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 2.929e- 13 37-56 BL00030B 7.03 1.900e-11 167-177 BL00030A 14.39 2.000e- 10 128-147
861	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 4.250e- 17 23-41 PR00988C 13.64 8.714e-16 107- 123 PR00988F 12.23 7.828e-15 198-212 PR00988E 8.27 9.769e- 12 176-188 PR00988D 5.95 8.250e-11 163-174 PR00988B 11.60 4.512e- 10 60-72
863	BL00215	Mitochondrial energy transfer proteins.	BL00215B 10.44 8.071e- 12 41-54
864	PR00775	90 KD HEAT SHOCK PROTEIN SIGNATURE	PR00775E 8.06 1.000e- 24 198-221 PR00775B 3.52 1.837e-23 107-130 PR00775D 8.91 4.484e- 17 171-189 PR00775A 9.90 8.342e-17 86-107 PR00775C 10.68 9.379e- 17 153-171 PR00775G 10.64 6.850e-15 267- 286 PR00775F 12.76 6.769e-14 249-267
866	DM01688	2 POLY-IG RECEPTOR.	DM01688G 16.45 9.460e- 09 89-121
867	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 5.596e- 29 14-53
868	BL01287	RNA 3'-terminal phosphate cyclase proteins.	BL01287A 17.95 2.688e- 26 16-48
869	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 6.464e- 10 304-337
872	BL00046	Histone H2A proteins.	BL00046 12.95 1.000e- 40 30-85
874	BL00188	Biotin-requiring enzymes attachment site proteins.	BL00188 30.29 9.036e- 32 665-711
876	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 7.686e- 09 298-315
877	PD02102	SUBUNIT E V-ATPASE VACUOLAR ATP SYNTHASE HYDROL.	PD02102A 16.74 4.176e- 10 97-141
879	BL01189	Ribosomal protein Sl2e proteins.	BL01189A 14.27 1.000e- 40 35-71 BL01189B 13.49 1.000e-40 71-125
882	BL00284	Serpins proteins.	BL00284C 28.56 6.400e- 25 62-104 BL00284B 17.99 6.182e-12 35-56
889	BL00216	Sugar transport proteins.	BL00216B 27.64 4.375e- 21 35-85
896	PR00391	PHOSPHATIDYLINOSITOL TRANSFER PROTEIN SIGNATURE	PR00391E 12.50 7.785e- 15 211-231 PR00391B 8.39 1.000e-13 83-104 PR00391D 12.21 9.328e- 13 191-207 PR00391A 7.83 5.390e-11 16-36
897	PR00327	ICE NUCLEATION PROTEIN	PR00327C 6.37 5.247e-

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	NO.	SIGNATURE	09 313-328
898	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 7.800e-
	3200033	dependent helicases proteins.	26 386-432 BL00039A 18.44 6.674e-16 113- 152 BL00039B 19.19 1.947e-13 153-179 BL00039C 15.63 9.460e-
	1		11 236-260
901	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 8.200e- 16 254-267 PD00066 13.92 8.200e-16 282- 295 PD00066 13.92 8.200e-16 310-323 PD00066 13.92 8.200e- 16 366-379 PD00066 13.92 8.200e-16 394- 407 PD00066 13.92 8.200e-14 338-351
902	BL01115	GTP-binding nuclear	BL01115A 10.22 9.321e-
302	2001113	protein ran proteins.	11 6-50
903	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 9.160e-
904	PROOSEL	KINESIN LIGHT CHAIN SIGNATURE	09 97-111 PR00381E 8.75 6.586e- 25 335-356 PR00381B 18.17 2.667e-24 204- 224 PR00381A 9.55 2.800e-24 107-125 PR00381C 12.48 4.522e- 24 226-245 PR00381D 13.94 1.084e-22 291- 309 PR00381F 9.13 3.288e-22 370-392 PR00381F 9.13 7.181e- 13 286-308 PR00381E 8.75 4.066e-11 251-272 PR00381E 8.75 7.033e- 11 293-314 PR00381E 8.75 8.364e-10 377-398
906	PR00345	STATHMIN FAMILY	PR00381D 13.94 5.230e- 09 333-351 PR00381C 12.48 7.120e-09 310- 329 PR00345C 4.54 8.557e-
		SIGNATURE	09 525-549
907	PR00345	STATHMIN FAMILY SIGNATURE	PR00345C 4.54 8.557e- 09 513-537
908	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 9.308e-11 144-155
910	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.800e- 30 48-87
912	BL01104	Ribosomal protein L13e proteins.	BL01104C 15.14 6.000e- 09 364-392
922	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.842e-09
923	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320C 13.01 2.500e- 09 323-338 PR00320C 13.01 5.500e-09 187- 202
924	PD02181	PROTOCHLOROPHYLLIDE REDUCTASE PHOTOSYNT.	PD02181D 12.85 8.609e-
926	BL00019	Actinin-type actin- binding domain proteins.	BL00019C 14.66 7.453e- 25 108-144 BL00019B 13.34 6.510e-11 61-84 BL00019D 15.33 9.338e- 11 205-235 BL00019A 12.56 2.373e-10 34-45
928	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 9.308e-11

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		proteins proteins.	273-284 BL00678 9.67 1.600e-10 314-325
			BL00678 9.67 7.600e-10 360-371 BL00678 9.67 8.579e-09 206-217
929	BL00518	Zinc finger, C3HC4 type	BL00518 12.23 1.857e-
930	BL01085	(RING finger), proteins. Ribulose-phosphate 3-	10 137-146 BL01085D 16.55 4.600e-
		epimerase family proteins.	24 134-165 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e- 20 172-202 BL01085C 21.81 2.038e-14 66-97
931	BL01085	Ribulose-phosphate 3- epimerase family proteins.	BL01085D 16.55 4.600e- 24 152-183 BL01085B 10.15 5.680e-22 30-52 BL01085E 18.87 8.676e- 20 190-220 BL01085C 21.81 2.038e-14 66-97
933	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301A 10.24 6.400e- 09 160-171
936	PF00168	C2 domain proteins.	PF00168C 27.49 4.000e- 12 336-362
937	BL00415	Synapsins proteins.	BL00415N 4.29 9.519e-
940	PR00862	PROLYL OLIGOPEPTIDASE SERINE PROTEASE (S9A) SIGNATURE	PR00862D 16.17 4.086e- 09 63-84
945	BL01230	RNA methyltransferase trmA family proteins.	BL01230B 11.62 2.373e-
948	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 7.429e- 18 52-68 BL00479A 19.86 2.200e-13 26-49
949	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 1.474e-09
954	PD01311	PROTEIN OXIDOREDUCTASE NAD INTERGENIC RE.	PD01311A 30.23 5.909e-
955	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.250e-
956	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 3.250e-
957	BL00379	CDP-alcohol phosphatidyltransferases proteins.	BL00379 24.64 1.610e- 15 111-148
959	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 1.884e- 10 31-75
960	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 3.438e- 14 110-154
962	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 6.586e- 13 198-236
963	PR00502	MUTT DOMAIN SIGNATURE	PR00502A 15.06 8.200e- 11 210-225
966	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308A 5.90 7.035e-
967	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 1.286e- 12 104-124 DM01206B 10.69 5.299e-11 23-43 DM01206B 10.69 8.274e- 10 73-93 DM01206B 10.69 3.962e-09 108- 128 DM01206B 10.69
969	PF01008	Initiation factor 2 subunit.	5.671e-09 38-58 PF01008B 25.59 4.724e- 31 417-460 PF01008C 12.25 5.333e-18 506- 526 PF01008A 20.14 5.875e-15 369-390

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970	BL01277	Ribonuclease PH proteins.	BL01277C 10.18 7.648e- 10 112-143 BL01277A 17.39 9.806e-10 40-78
975	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 3.605e- 12 130-145 BL01159 13.85 4.122e-10 171- 186
977	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791C 20.98 2.235e- 09 55-94
978	BL01167	Ribosomal protein L17 proteins.	BL01167B 20.66 8.258e- 19 88-127
979	BL00478	LIM domain proteins.	BL00478B 14.79 9.357e- 13 33-48 BL00478B 14.79 7.250e-12 98-113
980	PR00312	CALSEQUESTRIN SIGNATURE	PR00312E 8.32 3.423e- 36 169-199 PR00312I 15.78 5.286e-35 332- 361 PR00312F 15.06 5.865e-35 199-229 PR00312H 13.31 8.313e- 35 263-291 PR00312J 13.73 5.688e-34 363- 392 PR00312D 9.43 2.636e-33 128-158 PR00312C 15.14 8.839e- 33 92-122 PR00312B 15.08 8.941e-33 62-92 PR00312G 11.11 6.657e- 32 230-258 PR00312A 11.70 6.914e-27 35-59
981	PF00992	Troponin.	PF00992A 16.67 8.816e- 09 414-449
982	PR00299	ALPHA CRYSTALLIN SIGNATURE	PR00299F 13.20 2.367e- 09 127-149
983	BL01150	Respiratory-chain NADH dehydrogenase 20 Kd subunit proteins.	BL01150B 17.16 1.000e- 40 156-202 BL01150A 14.10 8.200e-39 100- 138
986	BL00795	Involucrin proteins.	BL00795C 17.06 7.211e- 14 4-49 BL00795C 17.06 1.778e-11 1-46 BL00795C 17.06 3.407e- 10 14-59 BL00795C 17.06 7.802e-10 2-47 BL00795C 17.06 8.640e- 10 19-64 BL00795C 17.06 7.400e-09 11-56 BL00795C 17.06 7.800e- 09 3-48
987	BL00939	Ribosomal protein Lle proteins.	BL00939F 17.27 5.393e- 09 810-840
988	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e- 11 525-541
989	PR00452	SH3 DOMAIN SIGNATURE	PR00452B 11.65 6.538e- 11 497-513
994	BL00027	'Homeobox' domain proteins.	BL00027 26.43 2.500e- 25 146-189
997	BL01304	ubiH/COQ6 monooxygenase family proteins.	BL01304A 8.05 3.893e- 11 65-79
998	DM01767	5 TRANSMITTER DOMAIN.	DM01767B 10.07 7.868e- 09 22-39
1000	PR00926	MITOCHONDRIAL CARRIER PROTEIN SIGNATURE	PR00926C 16.07 1.750e- 24 73-94 PR00926D 10.53 3.250e-23 126- 145 PR00926F 17.75 6.211e-23 217-240 PR00926E 11.70 6.625e-

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			20 174-193 PR00926B 16.07 2.125e-18 24-39 PR00926A 10.41 1.000e- 15 11-25 PR00926F 17.75 5.565e-09 120- 143
1005	BL00406	Actins proteins.	BL00406B 5.47 1.000e- 40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406D 12.58 3.700e- 40 270-325 BL00406E 8.44 7.375e-38 327-377 BL00406A 9.95 3.348e- 29 11-46
1006	BL00406	Actins proteins.	BL00406B 5.47 1.000e- 40 88-143 BL00406C 6.75 1.000e-40 147-202 BL00406E 8.44 1.000e- 35 248-298 BL00406A 9.95 3.348e-29 11-46
1007	PR00304	TAILLESS COMPLEX POLYPEPTIDE 1 (CHAPERONE) SIGNATURE	PR00304D 11.04 8.714e- 22 384-407 PR00304C 8.69 4.667e-20 98-118 PR00304B 11.60 7.577e- 19 68-87 PR00304A 9.20 3.382e-16 46-63 PR00304E 7.79 6.870e- 13 418-431
1009	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.929e- 32 9-48
1011	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.929e- 32 68-107
1012	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.143e- 10 64-73
1016	PD01168	SYNTHETASE LIGASE PROTEIN ALANYL.	PD01168H 12.08 1.000e- 11 174-194
1018	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 1.391e- 32 261-302 PD00930A 25.62 9.550e-22 157- 183
1022	BL00175	Phosphoglycerate mutase family phosphohistidine proteins.	BL00175A 15.42 5.179e- 12 6-26 BL00175C 23.75 8.062e-10 79-111
1025	PR00305	14-3-3 PROTEIN ZETA SIGNATURE	PR00305D 16.34 1.439e- 10 158-185
1026	BL00353	HMG1/2 proteins.	BL00353B 11.47 2.436e- 18 238-288 BL00353C 14.83 8.844e-11 288- 335
1028	BL00183	Ubiquitin-conjugating enzymes proteins.	BL00183 28.97 1.310e- 33 43-91
1033	PF00580	UvrD/REP helicase.	PF00580A 13.37 4.720e- 09 111-133
1034	PR00413	HALOACID DEHALOGENASE/EPOXIDE HYDROLASE FAMILY SIGNATURE	PR00413E 15.78 3.429e- 09 154-171
1037	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.657e- 09 5-44
1038	PD01796	PROTEIN TRANSMEMBRANE COBALT ZINC CADMIU.	PD01796 15.01 4.259e- 11 55-82
1039	BL00299	Ubiquitin domain proteins.	BL00299 28.84 9.036e- 09 17-69
1040	PR00970	ARGININE ADP- RIBOSYLTRANSFERASE	PR00970A 17.73 6.143e- 20 56-78 PR00970D

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		SIGNATURE	9.96 2.154e-18 154-171 PR00970F 12.30 1.000e- 16 224-241 PR00970G 9.97 9.229e-15 242-258 PR00970B 16.37 1.290e- 13 86-105 PR00970C 11.05 1.643e-11 115- 130 PR00970E 11.23 9.820e-11 202-218
1042	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 2.200e-10 243-254
1043	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 6.786e- 13 114-128 PR00048A 10.52 1.000e-09 172- 186
1045	BL00615	C-type lectin domain proteins.	BL00615A 16.68 1.720e- 11 218-236 BL00615B 12.25 1.857e-10 317- 331
1046	BL01092	Adenylate cyclases class-I proteins.	BL01092N 13.54 8.924e- 10 3-40
1047	BL01216	ATP-citrate lyase / succinyl-CoA ligases family proteins.	BL01216D 21.75 4.316e- 28 314-344 BL01216A 13.91 1.000e-10 97-112
1049	DM00031	IMMUNOGLOBULIN V REGION.	DM00031B 15.41 7.618e- 12 102-136
1050	BL01073	Ribosomal protein L24e proteins.	BL01073 24.30 1.000e- 40 12-62
1054	BL00571	Amidases proteins.	BL00571 25.69 5.875e- 31 160-212
1055	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 5.235e- 11 98-117 BL00030B 7.03 4.316e-09 137-147
1058	BL00223	Annexins repeat proteins domain proteins.	BL00223C 24.79 8.754e- 23 262-317 BL00223A 15.59 9.478e-14 46-80 BL00223A 15.59 5.557e- 11 118-152
1060	BL00027	'Homeobox' domain proteins.	BL00027 26.43 3.455e- 35 158-201
1064	BL00455	Putative AMP-binding domain proteins.	BL00455 13.31 6.211e- 13 280-296
1065	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.000e- 09 115-129 PR00019B 11.36 3.880e-09 87-101
1066	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 4.600e- 16 151-172 PR00326C 9.79 1.290e-14 200-216 PR00326B 16.74 8.548e- 14 172-191 PR00326D 19.09 1.257e-13 217- 236
1071	PD02870	RECEPTOR INTERLEUKIN-1 PRECURSOR.	PD02870B 18.83 8.518e- 11 164-197
1072	PF00856	SET domain proteins.	PF00856A 26.14 5.976e- 09 350-387
1075	BL01009	Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 proteins.	BL01009D 14.19 4.300e- 20 127-148 BL01009A 13.75 6.586e-13 57-75 BL01009E 13.50 1.439e- 11 159-175
1077	PR00724	CARBOXYPEPTIDASE C SERINE PROTEASE (S10) FAMILY SIGNATURE	PR00724A 10.91 1.000e- 08 366-379
1078	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 1.000e- 12 170-195 BL00215A 15.82 7.529e-10 79-104
1079	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.316e-09

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	100.	proteins proteins.	298-309
1081	BL00326	Tropomyosins proteins.	BL00326A 14.01 7.398e-
			10 23-57
1094	BL00460	Glutathione peroxidases selenocysteine proteins.	BL00460A 28.67 3.204e- 18 57-92 BL00460B 9.73 6.400e-13 100-118 BL00460D 16.89 9.143e- 12 162-182 BL00460C 14.35 5.500e-09 133-
		·	156
1095	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 67-105 PD02811B 17.07 2.263e-21 118- 151 PD02811C 13.25 5.696e-13 154-167
1096	PD02811	PROTEIN PEPTIDE REDUCTASE MG448 PILB FIMBRIA TRAN.	PD02811A 20.67 3.017e- 22 60-98 PD02811B 17.07 2.263e-21 111- 144 PD02811C 13.25 5.696e-13 147-160
1097	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 6.143e- 09 200-216
1105	PF00881	Nitroreductase family.	PF00881A 27.15 9.229e- 13 111-147
1109	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 3.077e- 10 15-37 PR00449E 13.50 1.857e-09 185- 208 PR00449D 10.79 8.364e-09 131-145
1115	PR00405	HIV REV INTERACTING PROTEIN SIGNATURE	PR00405B 11.83 5.737e- 20 42-60 PR00405A 17.71 2.703e-17 23-43 PR00405C 19.41 6.902e- 10 63-85
1116	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1117	BL00355	HMG14 and HMG17 proteins.	BL00355 5.97 2.528e-25 20-51
1120	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 4.857e- 10 290-306
1123	PR00412	EPOXIDE HYDROLASE SIGNATURE	PR00412F 18.76 9.526e- 12 301-324
1125	PR00186	HEMERYTHRIN SIGNATURE	PR00186A 13.62 2.800e- 09 87-101
1129	BL00170	Cyclophilin-type peptidyl-prolyl cis- trans isomerase signatur.	BL00170C 18.49 3.077e- 33 84-129 BL00170B 20.97 6.838e-25 37-77 BL00170A 17.08 3.455e- 15 10-37
1131	BL00636	Nt-dnaJ domain proteins.	BL00636A 8.07 5.304e- 15 29-46 BL00636B 15.11 1.360e-14 59-80
1132	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1133	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 6.211e-09 29-40
1136	BL00990	Clathrin adaptor complexes medium chain proteins.	BL00990C 18.78 4.176e- 38 235-269 BL00990A 21.44 4.316e-36 94-132 BL00990B 20.15 2.125e- 27 157-187 BL00990D 16.13 5.320e-18 403- 422
1137	PR00314	CLATHRIN COAT ASSEMBLY PROTEIN SIGNATURE	PR00314B 15.68 8.000e- 34 100-128 PR00314D 9.66 3.531e-33 233-261 PR00314C 16.05 8.909e-

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			32 159-188 PR00314A 14.53 1.281e-22 13-34
1139	BL01115	GTP-binding nuclear protein ran proteins.	BL01115A 10.22 6.364e- 13 13-57
1141	BL00107	Protein kinases ATP- binding region proteins.	BL00107A 18.39 4.000e- 19 451-482 BL00107B 13.31 3.077e-12 519- 535
1148	PR00685	TRANSCRIPTION INITIATION FACTOR IIB SIGNATURE	PR00685A 13.62 4.676e- 09 21-42
1155	PD01652	RECEPTOR CELL NK GLYCOPROTEIN IMMUNOGLOB.	PD01652B 8.50 9.396e 10 522-574 PD01652B 8.50 9.463e-10 740-792
1157	PD02894	HYDROLASE N4- PRECURSOR PROTEIN SIGNAL BE.	PD02894A 21.96 7.873e- 28 81-127 PD02894B 13.93 1.188e-27 178- 211
1159	BL00623	GMC oxidoreductases proteins.	BL00623E 15.00 3.531e- 20 391-414 BL00623C 10.86 4.240e-20 155- 176
1161	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA	PD01937A 6.68 3.475e- 09 330-341
1162	PD01937	DNA PROTEIN POLYMERASE ENDONUCLEASE DNA	PD01937A 6.68 3.475e- 09 221-232
1163	PR00624	HISTONE H5 SIGNATURE	PR00624D 11.94 7.455e- 10 214-239 PR00624D 11.94 1.961e-09 312- 337
1167	BL00226	Intermediate filaments proteins.	BL00226B 23.86 7.384e-
1177	BL01032	Protein phosphatase 2C proteins.	BL01032G 8.33 1.422e-
1178	PR00320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PR00320A 16.74 1.794e- 10 205-220 PR00320C 13.01 7.840e-10 205- 220 PR00320B 12.19 8.457e-10 35-50 PR00320A 16.74 7.146e- 09 35-50 PR00320B 12.19 9.100e-09 79-94
1180	PR00454	ETS DOMAIN SIGNATURE	PR00454D 10.89 4.150e- 19 765-784
1181	BL00291	Prion protein.	BL00291A 4.49 8.962e- 11 152-187
1184	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 4.103e- 18 1089-1113
1185	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 4.553e- 13 204-229 BL00215A 15.82 1.429e-12 11-36 BL00215A 15.82 9.809e- 11 104-129
1187	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 2.761e- 10 77-93
1188	BL00878	Orn/DAP/Arg decarboxylases family 2 pyridoxal-P attachment si.	BL00878B 10.95 6.000e- 16 189-204 BL00878C 17.74 8.435e-15 225- 245 BL00878F 19.67 3.625e-13 379-402 BL00878D 16.56 1.621e- 09 270-289
1191	PD02939	PROTEIN GLUTATHIONE SYNTHETASE SY.	PD02939B 10.10 2.723e- 12 203-220 PD02939C 20.01 1.000e-11 224- 252
1193	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e- 28 72-101 PR00345E

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			8.54 7.652e-28 149-174 PR00345C 4.54 9.100e- 28 101-125 PR00345D 10.97 1.964e-24 125- 149 PR00345A 13.46 5.645e-16 43-62
1194	PR00345	STATHMIN FAMILY SIGNATURE	PR00345B 7.12 2.800e- 28 108-137 PR00345E 8.54 7.652e-28 185-210 PR00345C 4.54 9.100e- 28 137-161 PR00345D 10.97 1.964e-24 161- 185 PR00345A 13.46 5.645e-16 79-98
1195	PF00995	Sec1 family.	PF00995B 17.37 1.120e- 13 224-264
1196	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 6.738e- 11 15-47
1197	BL01298	Dihydrodipicolinate reductase proteins.	BL01298A 13.90 5.959e- 09 51-73
1203	BL00061	Short-chain dehydrogenases/reductase s family proteins.	BL00061B 25.79 1.000e- 14 152-190
1204	PR00118	BETA-LACTAMASE CLASS A SIGNATURE	PR00118F 16.42 9.386e- 09 213-229
1206	BL01183	ubiE/COQ5 methyltransferase family proteins.	BL01183B 21.31 1.429e- 37 184-229 BL01183D 27.71 8.535e-27 264- 307 BL01183A 13.25 3.250e-23 51-73 BL01183C 10.77 5.295e- 09 246-258
1208	BL00979	G-protein coupled receptors family 3 proteins.	BL00979L 20.63 2.485e- 09 105-146
1209	PFC0023	Ank repeat proteins.	PF00023A 16.03 4.857e- 11 49-65 PF00023B 14.20 1.818e-09 45-55
1212	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE	PR00048A 10.52 7.750e- 14 227-241 PR00048A 10.52 4.316e-11 199- 213
1213	PR00450	RECOVERIN FAMILY SIGNATURE	PRO0450C 12.22 1.720e- 10 20-42 PR00450C 12.22 3.506e-09 56-78 PR00450D 16.58 6.769e- 09 44-64
1216	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.598e- 10 179-230 PR00456E 3.06 5.348e-
1219	PR00456	RIBOSOMAL PROTEIN P2 SIGNATURE	11 249-264
1222	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 7.231e- 15 295-308 PD00066 13.92 7.231e-15 406- 419 PD00066 13.92 2.286e-12 378-391 PD00066 13.92 7.857e- 12 434-447 PD00066 13.92 3.348e-11 350- 363
1223	BL50058	G-protein gamma subunit profile. Neuromodulin (GAP-43)	BL50058 27.23 1.000e- 40 13-61 BL00412D 16.54 8.439e-
1226	BL00412	proteins.	09 279-330
1227	BL00437	Catalase proximal heme- ligand proteins.	BL00437A 18.82 1.000e- 40 49-101 BL00437B 16.28 1.000e-40 114- 168 BL00437C 21.86

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	NO.		1.000e-40 190-239
			BL00437D 25.72 1.000e-
			40 248-301 BL00437E
			23.95 1.000e-40 327-
		1	379
1230	BL01160	Kinesin light chain	BL01160B 19.54 8.297e-
		repeat proteins.	10 6-60
1231	PR00735	GLYCOSYL HYDROLASE	PR00735A 11.19 6.857e-
		FAMILY 8 SIGNATURE	09 391-405
1232	PR00497	NEUTROPHIL CYTOSOL	PR00497A 6.92 5.553e-
		FACTOR P40 SIGNATURE NEUTROPHIL CYTOSOL	10 158-176 PR00497A 6.92 5.553e-
1233	PR00497	FACTOR P40 SIGNATURE	10 158-176
	BL00866	Carbamoyl-phosphate	BL00866B 36.29 2.776e-
1235	BLOOSE	synthase subdomain	09 75-121
	İ	proteins.	1
1237	BL00027	'Homeobox' domain	BL00027 26.43 1.818e-
123,	2200027	proteins.	21 36-79
1243	PR00403	WW DOMAIN SIGNATURE	PR00403B 12.19 1.184e-
			11 10-25
1246	PD01168	SYNTHETASE LIGASE	PD01168L 9.47 2.837e-
		PROTEIN ALANYL.	10 31-46 PD01168L
			9.47 4.490e-10 174-189
			PD01168L 9.47 7.612e-
			10 183-198 BL00018 7.41 2.800e-10
1249	BL00018	EF-hand calcium-binding domain proteins.	183-196
7.05.4	BL00183	Ubiquitin-conjugating	BL00183 28.97 2.440e-
1254	BLOOLB3	enzymes proteins.	36 96-144
1255	BL01115	GTP-binding nuclear	BL01115A 10.22 5.670e-
1233	DEGITES	protein ran proteins.	11 8-52
1256	BL00373	Phosphoribosylglycinamid	BL00373C 10.35 3.348e-
		e formyltransferase	12 143-156
		proteins.	
1258	PR00011	TYPE III EGF-LIKE	PR00011B 13.08 3.217e-
		SIGNATURE	10 174-193 BL00518 12.23 8.286e-
1259	BL00518	Zinc finger, C3HC4 type	10 31-40
		(RING finger), proteins. DIHYDROFOLATE REDUCTASE	PR00070D 11.63 1,000e-
1261	PR00070	SIGNATURE	15 112-127 PR00070C
		SIGNATURE	13.09 9.500e-15 51-63
			PR00070A 12.92 5.500e-
	Ì		12 16-27
1262	BL00462	Gamma-	BL00462A 20.89 6.438e-
		glutamyltranspeptidase	24 140-183 BL00462B
		proteins.	17.88 5.500e-20 230-
1	1		267 BL00462C 27.41
		Maria Area Desider Ness	2.023e-11 292-347 BL00038B 16.97 9.455e-
1263	BL00038	Myc-type, 'helix-loop- helix' dimerization	11 62-83
		domain proteins.	1 22 02-03
1264	BL01115	GTP-binding nuclear	BL01115A 10.22 5.670e-
1204	1 2001112	protein ran proteins.	12 17-61
1266	PR00837	ALLERGEN V5/TPX-1 FAMILY	PR00837C 17.21 2.714e-
		SIGNATURE	18 165-182 PR00837A
			14.77 4.512e-12 86-105
			PR00837D 11.12 7.577e-
			12 201-215
1269	PR00449	TRANSFORMING PROTEIN P21	PR00449C 17.27 9.308e-
		RAS SIGNATURE	22 40-63 PR00449B
			13.50 1.000e-16 137- 160 PR00449D 10.79
İ			3.520e-11 102-116
1270	5,000	Channel forming collising	BL00276A 8.87 1.500e-
1270	BL00276	Channel forming colicins	09 17-29
1275	PD02327	proteins. GLYCOPROTEIN ANTIGEN	PD02327C 15.47 9.769e-
12/3	FD02321	PRECURSOR IMMUNOGLO.	09 228-243
1276	PR00412	EPOXIDE HYDROLASE	PR00412B 12.59 7.894e-
			

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	NO.		
		SIGNATURE	12 119-135 PR00412C 11.30 1.857e-11 165- 179 PR00412A 13.23
1277	PF00756	Putative esterase.	3.400e-11 100-119 PF00756C 14.12 9.538e-
1279	BL00134	Serine proteases,	10 127-157 BL00134A 11.96 9.325e-
1273	200134	trypsin family, histidine proteins.	13 128-145
1280	BL01220	Phosphatidylethanolamine -binding protein family proteins.	BL01220C 14.75 9.348e- 15 248-276
1285	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 2.286e- 10 33-42
1287	PF00791	Domain present in ZO-1 and Unc5-like netrin receptors.	PF00791B 28.49 7.182e- 11 288-343
1292	PR00802	SERUM ALBUMIN FAMILY SIGNATURE	PR00802B 16.51 1.610e-
1297	PR00716	M-PHASE INDUCER PHOSPHATASE SIGNATURE	PR00716C 17.65 5.696e-
1298	BL00478	LIM domain proteins.	BL00478B 14.79 6.478e-
1301	BL00127	Pancreatic ribonuclease family proteins.	BL00127C 31.49 3.571e- 28 82-126 BL00127B 26.57 8.800e-28 23-68
1302	PR00637	TYPE 3 BOMBESIN RECEPTOR SIGNATURE	PR00637E 11.27 4.250e- 09 290-306
1307	BL00215	Mitochondrial energy transfer proteins.	BL00215A 15.82 5.500e- 17 13-38 BL00215A 15.82 1.000e-16 226- 251 BL00215A 15.82
1308	PR00898	VASOPRESSIN V2 RECEPTOR SIGNATURE	2.658e-13 107-132 PR00898H 11.34 4.682e- 09 552-572
1309	PD00301	PROTEIN REPEAT MUSCLE CALCIUM-BI.	PD00301B 5.49 2.731e- 09 390-401
1310	BL00983	Ly-6 / u-PAR domain proteins.	BL00983C 12.69 9.654e- 13 73-89 BL00983B 8.19 3.132e-09 12-22
1313	BL00194	Thioredoxin family proteins.	BL00194 12.16 1.900e- 11 15-28
1314	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 8.969e-
1316	BL00134	Serine proteases, trypsin family, histidine proteins.	10 53-97 BL00134A 11.96 9.325e- 13 128-145
1320	BL00783	Ribosomal protein L13 proteins.	BL00783C 22.43 6.559e- 24 87-117 BL00783A 14.55 1.600e-19 8-33 BL00783B 12.76 3.500e- 12 74-86
1327	PF00514	Armadillo/beta-catenin- like repeat proteins.	PF00514A 31.30 7.268e- 11 82-120
1329	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 6.294e- 11 129-148 BL00030B 7.03 4.789e-09 168-178
1331	PR00497	NEUTROPHIL CYTOSOL FACTOR P40 SIGNATURE	PR00497A 6.92 7.239e- 09 25-43
1332	PR00161	NICKEL-DEPENDENT HYDROGENASE/B-TYPE CYTOCHROME SIGNATURE	PR00161C 9.51 4.930e- 09 317-337
1333	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 6.769e- 33 10-49
1336	PR00700	PROTEIN TYROSINE PHOSPHATASE SIGNATURE	PR00700D 12.47 2.200e- 09 262-281
1337	PR00700	PROTEIN TYROSINE	PR00700D 12.47 2.200e-

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	NO.	PHOSPHATASE SIGNATURE	09 211-230
1340	PR00860	VERTEBRATE METALLOTHIONEIN SIGNATURE	PR00860A 5.46 5.034e- 13 5-18
1341	BL00893	mutT domain proteins.	BL00893 18.99 6.750e- 16 46-71
1343	BL01282	BIR repeat proteins.	BL01282B 30.49 5.974e- 21 383-422
1344	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 8.313e- 09 417-427
1345	BL00923	Aspartate and glutamate racemases proteins.	BL00923B 11.41 5.935e- 10 135-146
1348	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 7.231e- 13 44-57
1350	PR00193	MYOSIN HEAVY CHAIN SIGNATURE	PR00193D 14.36 3.571e- 32 416-445 PR00193C 12.60 6.318e-31 179- 207 PR00193B 11.69 3.571e-24 133-159 PR00193E 19.47 9.069e- 22 470-499 PR00193A 15.41 1.783e-20 77-97
1352	PR00447	NATURAL RESISTANCE- ASSOCIATED MACROPHAGE PROTEIN SIGNATURE	PR00447E 9.73 1.554e- 15 299-319 PR00447D 13.54 3.408e-15 200- 224 PR00447A 12.73 6.357e-11 97-124 PR00447G 6.69 9.877e- 10 353-373
1353	BL00303	S-100/ICaBP type calcium binding protein.	BL00303A 21.77 6.667e- 26 45-82 BL00303B
1355	BL00039	DEAD-box subfamily ATP-	26.15 1.000e-24 93-130 BL00039D 21.67 5.950e-
		dependent helicases proteins.	29 375-421 BL00039A 18.44 7.136e-29 99-138 BL00039C 15.63 4.000e- 18 225-249 BL00039B 19.19 3.182e-14 141- 167
1357	PF00615	Regulator of G protein signalling domain proteins.	PF00615B 16.25 2.216e- 12 84-101 PF00615C 10.06 8.412e-12 162- 176
1360	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.234e- 29 10-49
1361	PR00925	NONHISTONE CHROMOSOMAL PROTEIN HMG17 FAMILY SIGNATURE	PR00925A 5.47 5.091e- 18 14-29 PR00925B 3.73 6.143e-14 29-42 PR00925C 5.57 4.789e- 12 53-64 PR00925D 6.56 1.857e-10 76-87
1362	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 136-171 BL01272C 11.68 3.314e-25 249- 274 BL01272A 6.49 1.231e-18 99-117
1363	BL01272	Glucokinase regulatory protein family proteins.	BL01272B 19.61 6.870e- 30 113-148 BL01272C 11.68 3.314e-25 226- 251 BL01272A 6.49 1.231e-18 76-94
1364	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.304e- 09 167-177
1368	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.592e- 09 76-96
1370	PR00988	URIDINE KINASE SIGNATURE	PR00988A 6.39 1.794e-

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	+ · · · · · · · · · · · · · · · · · · ·	 	10 1-19
1371	BL00242	Integrins alpha chain proteins.	BL00242B 8.13 8.615e- 09 469-479
1372	PR00625	DNAJ PROTEIN FAMILY SIGNATURE	PR00625B 13.48 7.353e- 19 46-67 PR00625A 12.84 1.391e-16 14-34
1373	BL00434	HSF-type DNA-binding domain proteins.	BL00434C 23.85 3.778e- 09 90-130
1374	PR00962	LETHAL (2) GIANT LARVAE PROTEIN SIGNATURE	PR00962C 8.00 6.337e-
1375	PD02475	MUCIN EPITHELIAL TUMOR- ASSOCIATE.	PD02475A 23.18 8.552e- 10 1111-1150
1376	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.571e- 32 24-63
1380	BL00194	Thioredoxin family proteins.	BL00194 12.16 8.333e- 12 48-61
1381	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 1.458e- 15 1123-1136
1383	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10 243-254
1384	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 7.600e-10 271-282
1385	BL00303	S-100/ICaBP type calcium binding protein.	BL00303B 26.15 6.203e- 10 95-132
1386	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 5.042e- 09 1574-1628
1387	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 1.000e- 11 52-61
1389	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 3.600e- 30 10-49
1390	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 3.512e- 31 32-71
1392	PR00308	TYPE I ANTIFREEZE PROTEIN SIGNATURE	PR00308C 3.83 9.723e- 10 127-137
1393	PR00380	KINESIN HEAVY CHAIN SIGNATURE	PR00380A 14.18 9.625e- 25 8B-110 PR00380D 9.93 2.406e-20 304-326 PR00380B 12.64 4.414e- 16 20B-226 PR00380C 13:18 6.538e-16 243- 262
1394	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.400e- 14 462-475 PD00066 13.92 8.800e-14 348- 361 PD00066 13.92 9.571e-12 405-418 PD00066 13.92 6.087e- 11 490-503 PD00066 13.92 8.043e-11 320- 333
1398	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 6.786e- 32 10-49
1400	DM01206	CORONAVIRUS NUCLEOCAPSID PROTEIN.	DM01206B 10.69 7.038e- 09 270-290
1406	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930A 25.62 7.324e- 15 363-389
1407	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030A 14.39 7.500e- 10 457-476
1408	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PRO0019A 11.19 9.550e- 11 179-193 PR00019A 11.19 8.826e-10 228- 242 PR00019B 11.36 1.360e-09 199-213 PR00019B 11.36 4.960e-

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	NO.		
			09 176-190
1409	PR00510	NEBULIN SIGNATURE	PR00510A 9.09 4.150e-
			12 182-202 PR00510B 12.96 8.767e-12 210-
			230 PR00510F 9.88
			8.172e-10 58-75
			PR00510D 9.21 2.367e-
			09 251-267
1410	PD00078	REPEAT PROTEIN ANK	PD00078B 13.14 5.696e-
		NUCLEAR ANKYR.	09 31-44
1412	BL00358	Ribosomal protein L5	BL00358B 22.76 1.000e-
		proteins.	40 57-103 BL00358C 13.75 6.087e-14 122-
			136 BL00358D 14.26
		ł	5.500e-13 143-158
		ĺ	BL00358A 13.06 1.931e-
		į.	11 33-44
1414	BL00282	Kazal serine protease	BL00282 16.88 7.338e-
		inhibitors family	10 511-534
1415	Dr. o coop	proteins.	
1415	BL00023	Type II fibronectin collagen-binding domain	BL00023 24.31 4.300e-
		proteins.	29 40-77
1417	PR00681	RIBOSOMAL PROTEIN S1	PR00681G 12.54 2.149e-
. –		SIGNATURE	09 38-60
1418	DM00973	3 kw RESISTANCE BENOMYL	DM00973A 21.17 1.462e-
		YLL028W CYCLOHEXIMIDE.	09 171-208
1419	PR00319	BETA G-PROTEIN	PR00319B 11.47 1.571e-
		(TRANSDUCIN) SIGNATURE	09 428-443
1420	PD01941	TRANSMEMBRANE	PD01941A 14.81 1.000e-
		COTRANSPORTER SYMP.	40 142-196 PD01941B 15.02 7.049e-30 400-
			447 PD01941E 15.92
			2.475e-20 817-864
			PD01941C 19.96 3.118e-
			19 488-543 PD01941D
			27.18 9.614e-18 641-
		j	690 PD01941F 28.52
1422	PR00205	CADHERIN SIGNATURE	5.382e-15 1038-1093 PR00205B 11.39 8.043e-
	1200203	GENERIN SIGNATORE	12 199-217
1423	PR00209	ALPHA/BETA GLIADIN	PR00209B 4.88 6.318e-
		FAMILY SIGNATURE	11 1009-1028
1424	BL50002	Src homology 3 (SH3)	BL50002A 14.19 8.200e-
		domain proteins profile.	14 367-386 BL50002A
			14.19 9.250e-12 298-
			317 BL50002A 14.19
			4.462e-11 208-227 BL50002B 15.18 1.000e-
			09 244-258
1425	PF00628	PHD-finger.	PF00628 15.84 3.045e-
			12 330-345
1426	PF00628	PHD-finger.	PF00628 15.84 3.045e-
			12 377-392
1427	PR00405	HIV REV INTERACTING	PR00405B 11.83 5.114e-
		PROTEIN SIGNATURE	16 281-299 PR00405A
			17.71 4.306e-14 262-
1428	BL00039	DEAD-box subfamily ATP-	BL00039D 21.67 5.219e-
		dependent helicases	34 147-193
		proteins.	
1429	PR00320	G-PROTEIN BETA WD-40	PR00320C 13.01 8.920e-
		REPEAT SIGNATURE	10 577-592
1430	PR00378	INOSITOL PHOSPHATASE	PR00378D 16.86 7.563e-
		SIGNATURE	12 295-314 PR00378B
			13.80 8.650e-10 166-
1431	DROGGE	CDAVEG DIGITION CONTROL	186
7437	PR00928	GRAVES DISEASE CARRIER	PR00928B 13.53 3.769e-

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	- NO.	PROTEIN SIGNATURE	10 103-124
1433	BL01113	Clq domain proteins.	BL01113B 18.26 7.049e-
	2001113	ord domain process.	15 14-50 BL01113C 13.18 7.000e-12 82-102
1434	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319B 11.47 7.983e- 10 135-150
1436	BL00030	Eukaryotic RNA-binding	BL00030A 14.39 1.000e-
1438	BL00290	region RNP-1 proteins. Immunoglobulins and	12 84-103 BL00290B 13.17 2.500e-
		major histocompatibility complex proteins.	09 250-268 BL00290A 20.89 4.000e-09 188-
1440	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-
1441	PR00806	VINCULIN SIGNATURE	PR00806B 4.28 4.960e-
1444	BL00422	Granins proteins.	09 88-102 BL00422D 19.48 1.000e-
1445	DD01941	DUOGDUODYI NOD WYNNOD	08 114-138
1445	PD01841	PHOSPHORYLASE KINASE ALPHA MUSCL.	PD01841A 21.71 1.000e- 40 73-123 PD01841B 14.35 1.000e-40 144- 185 PD01841D 17.87 1.000e-40 206-258
			PD01841F 13.36 1.000e- 40 296-345 PD01841G 24.26 1.000e-40 349- 403 PD01841I 23.00
			1.000e-40 494-536 PD01841J 14.94 1.000e- 40 895-932 PD01841L 18.42 1.000e-40 1083-
			1125 PD01841E 18.60 9.719e-38 258-296 PD01841K 14.81 1.000e- 35 1041-1071 PD01841H
			21.30 3.189e-31 435- 472 PD01841C 13.78 1.000e-25 185-206 PD01841M 10.82 1.250e-
1446	PF00816	H-NS histone family.	20 1175-1194 PF00816B 13.84 8.875e-
		•	09 190-220
1447	PR00048	C2H2-TYPE ZINC FINGER	PR00048A 10.52 2.080e-
1447	PR00048	C2H2-TYPE ZINC FINGER SIGNATURE 072 RIBONUCLEASE	PR00048A 10.52 2.080e- 09 402-416
1448	DM00315	SIGNATURE 072 RIBONUCLEASE INHIBITOR.	PR00048A 10.52 2.080e- 09 402-416 DM00315D 18.40 7.393e- 09 23-67
1448	DM00315	SIGNATURE 072 RIBONUCLEASE INHIBITOR. Eukaryotic RNA-binding region RNF-1 proteins.	PR00048A 10.52 2.080e- 09 402-416 DM00315D 18.40 7.393e- 09 23-67 BL00030B 7.03 2.800e- 10 94-104
1448 1451 1454	DM00315 BL00030 DM01688	SIGNATURE 072 RIBONUCLEASE INHIBITOR. Eukaryotic RNA-binding region RNP-1 proteins. 2 POLY-IG RECEPTOR.	PR00048A 10.52 2.080e- 09 402-416 DM00315D 18.40 7.393e- 09 23-67 BL00030B 7.03 2.800e-
1448	DM00315	SIGNATURE 072 RIBONUCLEASE INHIBITOR. Eukaryotic RNA-binding region RNF-1 proteins.	PR00048A 10.52 2.080e- 09 402-416 DM0031SD 18.40 7.393e- 09 23-67 BL00030B 7.03 2.800e- 10 94-104 DM01688D 13.44 7.146e-
1448 1451 1454	DM00315 BL00030 DM01688	SIGNATURE 072 RIBONUCLEASE INHIBITOR. Eukaryotic RNA-binding region RNP-1 proteins. 2 POLY-IG RECEPTOR. Sialyltransferase	PR00048A 10.52 2.080e- 09 402-416 DM00315D 18.40 7.393e- 09 23-67 BL00030B 7.03 2.800e- 10 94-104 DM0168BD 13.44 7.146e- 09 382-405 PF00777C 18.60 2.929e- 22 4-59 BL00927C 10.83 8.085e-
1448 1451 1454 1455	DM00315 BL00030 DM01688 PF00777	SIGNATURE 072 RIBONUCLEASE INHIBITOR. Eukaryotic RNA-binding region RNP-1 proteins. 2 POLY-IG RECEPTOR. Sialyltransferase family.	PR00048A 10.52 2.080e- 09 402-416 DM00315D 18.40 7.393e- 09 23-67 BL00030B 7.03 2.800e- 10 94-104 DM01688D 13.44 7.146e- 09 382-405 PF00777C 18.60 2.929e- 22 4-59 BL00927C 10.83 8.085e- 09 42-53 BL00545C 11.28 7.353e- 17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545B 13.10 3.942e-
1448 1451 1454 1455	DM00315 BL00030 DM01688 PF00777 BL00927	SIGNATURE 072 RIBONUCLEASE INHIBITOR. Eukaryotic RNA-binding region RNP-1 proteins. 2 POLY-IG RECEPTOR. Sialyltransferase family. Trehalase proteins. Aldose 1-epimerase proteins. ANTHRANILATE SYNTHASE	PR00048A 10.52 2.080e- 09 402-416 DM00315D 18.40 7.393e- 09 23-67 BL00030B 7.03 2.800e- 10 94-104 DM01688D 13.44 7.146e- 09 382-405 PF00777C 18.60 2.929e- 22 4-59 BL00927C 10.83 8.085e- 09 42-53 BL00545C 11.28 7.353e- 17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545B 13.10 3.942e- 09 140-153 PR00097C 9.42 9.069e-
1448 1451 1454 1455 1457	DM00315 BL00030 DM01688 PF00777 BL00927 BL00545	SIGNATURE 072 RIBONUCLEASE INHIBITOR. Eukaryotic RNA-binding region RNP-1 proteins. 2 POLY-IG RECEPTOR. Sialyltransferase family. Trehalase proteins. Aldose 1-epimerase proteins. ANTHRANILATE SYNTHASE COMPONENT II SIGNATURE Hypothetical yabO/yceC/sfhB family	PR00048A 10.52 2.080e- 09 402-416 DM00315D 18.40 7.393e- 09 23-67 BL00030B 7.03 2.800e- 10 94-104 DM01688D 13.44 7.146e- 09 382-405 PF00777C 18.60 2.929e- 22 4-59 BL00927C 10.83 8.085e- 09 42-53 BL00545C 11.28 7.353e- 17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545E 13.10 3.942e- 09 140-153 PR00097C 9.42 9.069e- 09 233-245 BL01129E 13.25 5.250e- 22 170-195 BL01129C
1448 1451 1454 1455 1457 1460	DM00315 BL00030 DM01688 PF00777 BL00927 BL00545	SIGNATURE 072 RIBONUCLEASE INHIBITOR. Eukaryotic RNA-binding region RNP-1 proteins. 2 POLY-IG RECEPTOR. Sialyltransferase family. Trehalase proteins. Aldose 1-epimerase proteins. ANTHRANILATE SYNTHASE COMPONENT II SIGNATURE Hypothetical	PR00048A 10.52 2.080e- 09 402-416 DM00315D 18.40 7.393e- 09 23-67 BL00030B 7.03 2.800e- 10 94-104 DM01688D 13.44 7.146e- 09 382-405 PF00777C 18.60 2.929e- 22 4-59 BL00927C 10.83 8.085e- 09 42-53 BL00545C 11.28 7.353e- 17 169-182 BL00545A 10.20 2.071e-15 73-89 BL00545B 13.10 3.942e- 09 140-153 PR00097C 9.42 9.069e- 09 233-245 BL01129E 13.25 5.250e-

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1477	PF00566	Probable rabGAP domain	PF00566A 12.64 7.333e-
		proteins.	10 466-476
1478	BL00030	Eukaryotic RNA-binding region RNP-1 proteins.	BL00030B 7.03 9.400e- 10 43-53 DM00406 7.73 8.541e-10
1479	DM00406	GLIADIN.	292-305
1480	BL00290	Immunoglobulins and major histocompatibility complex proteins.	BL00290B 13.17 2.385e- 15 69-87 BL00290A 20.89 5.091e-11 12-35
1481	PR00150	PHOSPHOENOLPYRUVATE CARBOXYLASE SIGNATURE	PR00150F 10.45 9.039e- 09 21-51
1482	PF00780	Domain found in NIK1- like kinases, mouse citron and yeast ROM.	PF00780Î 14.69 4.825e- 09 107-137
1483	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 1.153e- 09 108-162
1485	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 5.909e- 25 17-56
1486	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.529e- 09 34-50
1488	BL00039	DEAD-box subfamily ATP- dependent helicases proteins.	BL00039D 21.67 9.586e- 10 116-162
1490	BL00166	Enoyl-CoA hydratase/isomerase proteins.	BL00166D 22.87 2.607e- 24 190-226 BL00166C 18.93 5.500e-14 140- 167 BL00166B 16.92 9.357e-11 93-115
1491	BL00452	Guanylate cyclases proteins.	BL00452D 28.59 3.700e- 31 63-106 BL00452E 11.92 3.045e-13 115- 131
1492	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 3.667e- 09 532-546
1497	BL00107	Protein kinases ATP- binding region proteins.	BL00107B 13.31 1.000e- 11 384-400 BL00107A 18.39 5.345e-11 322- 353
1500	PF00876	Ogre family.	PF00876E 7.99 1.947e- 10 107-117
1502	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e- 24 112-155
1503	BL00027	'Homeobox' domain proteins.	BL00027 26.43 4.789e- 24 112-155
1505	BL01177	Anaphylatoxin domain proteins.	BL01177E 20.64 5.800e- 24 448-475 BL01177C 17.39 5.333e-19 402- 421 BL01177B 13.61 7.840e-16 155-171 BL01177D 17.50 1.900e- 15 427-445
1506	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 5.500e- 14 311-336 BL00972A 11.93 7.429e-14 48-66 BL00972E 20.72 8.759e- 10 341-363
1512	BL00523	Sulfatases proteins.	BL00523E 19.27 4.536e- 22 76-106 BL00523D 9.89 1.563e-11 40-52 BL00523F 10.85 4.162e- 09 159-170 BL00523G 9.46 5.333e-09 256-266
1516	BL00914	Syntaxin / epimorphin family proteins.	BL00914 24.91 7.045e- 14 168-218
1518	BL00600	Aminotransferases class- III pyridoxal-phosphate attachment si.	BL00600A 17.98 6.143e- 19 98-122 BL00600E 16.43 1.771e-17 302-

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			331 BL00600G 12.43 9.625e-17 377-396 BL00600B 19.60 5.091e- 15 160-186 BL00600C 16.18 6.040e-12 190- 206 BL00600F 8.77 1.000e-11 343-356 BL00600D 8.71 1.000e- 10 281-295
1523	PD00930	PROTEIN GTPASE DOMAIN ACTIVATION.	PD00930B 33.72 9.600e- 18 41-82
1528	PRO0320	G-PROTEIN BETA WD-40 REPEAT SIGNATURE	PRO0320B 12.19 4.774e- 11 192-207 PR00320B 12.19 8.839e-11 272- 287 PR00320B 12.19 9.743e-10 106-121 PR00320A 16.74 1.878e- 09 192-207 PR00320A 16.74 2.317e-09 106- 121 PR00320A 16.74 8.683e-09 272-287 PR00320C 13.01 8.800e- 09 106-121
1538	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 4.508e-
1539	PF00781	Diacylglycerol kinase catalytic domain proteins (presumed).	PF00781D 11.11 7.593e- 10 103-127
. 1540	PR00965	OCULAR ALBINISM TYPE 1 PROTEIN SIGNATURE	PR00965H 10.73 1.231e- 29 312-334 PR00965E 12.93 5.846e-29 172- 195 PR00965F 5.98 1.123e-28 209-231 PR00965C 15.04 1.000e- 27 131-151 PR00965D 5.84 1.000e-27 150-170 PR00965G 8.52 2.440e- 27 258-279 PR00965B 4.80 8.650e-26 88-109 PR00965A 12.52 1.000e- 25 35-55 PR00965I 3.91 6.442e-25 385-406
1541	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 9.719e- 17 163-207
1543	PD02699	PROTEIN DNA-BINDING BINDING DNA.	PD02699C 24.84 1.000e- 40 599-646 PD02699A 8.91 2.286e-34 219-248 PD02699B 18.28 6.143e- 21 485-509
1544	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 7.857e- 10 182-197 PR00049D 0.00 7.102e-09 67-82
1547	BL00951	ER lumen protein retaining receptor proteins.	BL00951C 19.35 1.000e- 40 93-142 BL00951D 13.94 8.714e-40 142- 177 BL00951A 15.10 1.000e-38 2-38 . BL00951B 14.23 6.250e- 33 38-69
1548	BL00536	Ubiquitin-activating enzyme proteins.	BL00536F 13.65 8.920e- 30 279-318 BL00536D 22.91 5.737e-24 21-65 BL00536B 16.94 4.696e- 18 248-279
1549	PR00139	ASPARAGINASE/GLUTAMINASE FAMILY SIGNATURE	PR00139C 11.72 9.679e- 09 550-569
1553	PR00049	WILM'S TUMOUR PROTEIN SIGNATURE	PR00049D 0.00 5.119e- 09 58-73

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1556	BL00061	Short-chain	BL00061B 25.79 6.276e-
		dehydrogenases/reductase s family proteins.	13 67-105
1557	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1558	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1559	BL01228	Hypothetical cof family proteins.	BL01228D 17.44 8.105e- 12 107-132
1562	BL00522	DNA polymerase family X proteins.	BL00522C 11.90 6.600e- 18 412-436 BL00522B 27.30 1.738e-16 364- 410 BL00522A 25.52 6.000e-16 279-326 BL00522E 19.63 6.123e- 14 502-532 BL00522F 14.90 2.385e-13 551- 575
1563	PF00651	BTB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 1.947e- 11 46-59
1564	BL00299	Ubiquitin domain proteins.	BL00299 28.84 2.823e- 10 324-376
1566	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 8.594e- 17 184-228 BL01013C 9.97 4.906e-12 14-24
1567	BL00678	Trp-Asp (WD) repeat proteins proteins.	BL00678 9.67 3.400e-10 378-389 BL00678 9.67 5.800e-10 418-429 BL00678 9.67 8.800e-10 295-306
1570	BL00479	Phorbol esters / diacylglycerol binding domain proteins.	BL00479B 12.57 5.235e- 17 297-313 BL00479A 19.86 6.625e-15 271- 294 BL00479A 19.86 2.667e-14 147-170 BL00479B 12.57 6.294e- 12 173-189
1576	PR00665	OXYTOCIN RECEPTOR SIGNATURE	PR00665G 12.36 4.673e- 24 364-384 PR00665D 9.93 1.200e-22 138-155 PR00665F 11.73 4.000e- 22 337-354 PR00665C 5.89 1.000e-20 65-80 PR00665B 5.29 4.337e- 19 24-39 PR00665E 5.60 2.929e-15 246-260 PR00665A 5.99 5.622e- 15 11-25
1577	DM00099	4 kw A55R REDUCTASE TERMINAL DIHYDROPTERIDINE.	DM00099B 14.73 9.308e- 10 127-137
1579	BL00524	Somatomedin B domain proteins.	BL00524A 9.65 6.776e- 14 52-73
1580	PD02894	HYDROLASE N4 - PRECURSOR PROTEIN SIGNAL BE.	PD02894B 13.93 6.959e- 16 182-215 PD02894A 21.96 2.125e-10 57-103
1581	BL00411	Kinesin motor domain proteins.	BL00411C 15.04 5.292e- 12 32-54 BL00411H 15.66 4.441e-11 245- 276
1582	PR00604	CLASS IA AND IB CYTOCHROME C SIGNATURE	PR00604A 11.13 2.440e-
1584	PF00651	BTB (also known as BR-C/Ttk) domain proteins.	PF00651 15.00 1.000e- 10 225-238
1585	DM01551	kw OSTEOINDUCTIVE YOPM MEMBRANE OUTER.	DM01551C 14.62 9.455e-
1586	DM01354	kw TRANSCRIPTASE REVERSE II ORF2.	DM01354S 11.61 7.750e- 09 474-495

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1507	PR00072	MALIC ENZYME SIGNATURE	PR00072B 13.77 7.955e- 33 180-210 PR00072A 12.75 6.040e-25 120- 145 PR00072C 11.42 2.286e-24 216-239 PR00072D 10.77 3.400e- 22 276-295 PR00072E 10.54 1.360e-19 301- 318 PR00072G 10.45 5.304e-19 433-450 PR00072F 8.87 5.935e- 15 332-349
1589	BL00191	Cytochrome b5 family, heme-binding domain proteins.	BL00191H 15.64 1.537e- 22 61-113 BL00191K 17.38 9.027e-12 398- 442
1590	DM01970	0 kw ZK632.12 YDR313C ENDOSOMAL III.	DM01970B 8.60 7.716e- 13 211-224 DM01970B 8.60 2.157e-12 94-107
1591	DM00517	5 kw NUCLEAR 60.7 NUP1 CHROMOSOME.	DM00517B 10.96 6.625e- 16 1175-1193 DM00517A 8.21 1.000e-11 1015- 1026
1592	BL00037	Myb DNA-binding domain proteins repeat proteins proteins.	BL00037B 15.92 3.250e- 27 116-142 BL00037A 16.68 2.500e-24 83-107 BL00037A 16.68 3.250e- 12 31-55 BL00037B 15.92 3.526e-11 64-90 BL00037C 16.86 9.654e- 10 146-164
1595	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 1.514e- 09 110-127
1598	PF00628	PHD-finger.	PF00628 15.84 3.250e- 11 1667-1682
1599	PR00014	FIBRONECTIN TYPE III REPEAT SIGNATURE	PR00014D 12.04 5.500e- 09 980-995
1600	BL00518	Zinc finger, C3HC4 type (RING finger), proteins.	BL00518 12.23 6.571e- 10 30-39
1602	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.402e- 10 136-187
1605	PF00651	ETB (also known as BR- C/Ttk) domain proteins.	PF00651 15.00 3.571e- 10 44-57
1607	BL00252	Interferon alpha, beta and delta family proteins.	BL00252A 18.49 6.657e- 23 20-57 BL00252B 19.78 9.125e-16 58-109
1610	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 1.000e- 08 61-94
1611	BL00904	Protein prenyltransferases alpha subunit repeat proteins proteins.	BL00904C 8.98 7.353e- 10 91-125 BL00904D 1.47 6.018e-09 127-168
1612	PF00168	C2 domain proteins.	PF00168C 27.49 3.250e- 09 365-391
1613	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 6.051e- 09 932-983 BL00412D 16.54 7.153e-09 933- 984
1614	BL00559	Eukaryotic molybdopterin oxidoreductases proteins.	BL00559I 13.63 3.531e- 25 54-83 BL00559K 13.17 2.957e-18 197- 224 BL00559J 19.63 6.870e-16 124-176 BL00559L 13.60 9.000e- 16 266-284
1615	PD01427	TRANSFERASE METHYLTRANSFERASE BI.	PD01427B 22.45 3.025e- 22 500-541 PD01427A 19.94 8.773e-18 439-

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			472
1616	BL00115	Eukaryotic RNA	BL00115Z 3.12 7.485e-
		polymerase II	09 152-201 BL00115Z
		heptapeptide repeat	3.12 9.603e-09 145-194
		proteins.	
1617	BL00303	S-100/ICaBP type calcium	BL00303B 26.15 7.750e-
		binding protein.	32 51-88 BL00303A
			21.77 1.947e-31 4-41
1618	BL01254	Fetuin family proteins.	BL01254F 10.02 8.754e-
			09 137-147
1619	PD01888	PEPTIDE REDUCTASE	PD01888B 25.10 1.000e-
	120000	PROTEIN METHI.	40 47-97 PD01888C
			21.56 7.000e-30 125-
			155 PD01888A 12.84
		ļ	8.800e-15 7-23
1621	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239E 1.58 3.455e-
1021	PR00239	1	1
		TERMINAL TAIL SIGNATURE	09 692-704 PR00239E
			1.58 4.580e-09 697-709
			PR00239E 1.58 4.580e-
			09 702-714 PR00239E
	1		1.58 5.193e-09 703-715
1622	PR00860	VERTEBRATE	PR00860B 7.04 1.900e-
		METALLOTHIONEIN	18 27-41 PR00860C
		SIGNATURE	9.61 1.474e-14 41-51
			PR00860A 5.46 1.720e-
			14 5-18
1624	PR00784	MITOCHONDRIAL BROWN FAT	PR00784D 15.86 8.027e-
		UNCOUPLING PROTEIN	11 77-95
		SIGNATURE	}
1626	BL00325	Actin-depolymerizing	BL00325B 21.66 1.000e-
		proteins.	40 93-139 BL00325A
		-	24.83 6.786e-23 61-93
1631	BL00064	L-lactate dehydrogenase	BL00064B 23.57 1.000e-
		proteins.	40 82-130 BL00064C
			17.28 1.000e-40 137-
			182 BL00064E 27.20
			1.000e-40 223-275
			BL00064F 25.14 7.882e-
	1		36 286-331 BL00064A
			21.16 1.000e-33 22-60
			BL00064D 14.19 6.500e-
			31 182-212
1632	PR00063	RIBOSOMAL PROTEIN L27	PR00063B 15.24 9.700e-
1032	1 TROUGH	SIGNATURE	11 59-84 PR00063A
		SIGNATURE	11.71 1.614e-09 34-59
1634	PR00239	MOLLUSCAN RHODOPSIN C-	PR00239D 0.00 1.105e-
1034	FR00239	TERMINAL TAIL SIGNATURE	11 36-49 PR00239C
		TERMINAL TATE SIGNATURE	3.51 2.538e-09 37-45
1636	BL01210	Ganalina mahaina	•
1030	PUOTSTO	Caveolins proteins.	BL01210B 13.92 9.531e-
1737	DT 00000	I Distanted to the second of t	10 133-183
1637	BL00982	Bacterial-type phytoene	BL00982A 18.41 5.388e-
	\	dehydrogenase proteins.	11 11-43
1639	BL01183	ubiE/COQ5	BL01183B 21.31 8.144e-
	1	methyltransferase family	12 132-177
27.2	<u> </u>	proteins.	
1640	PR00015	GRAM-POSITIVE COCCUS	PR00015B 9.84 8.468e-
		SURFACE PROTEIN ANCHOR	10 128-149
		SIGNATURE	
1641	PR00320	G-PROTEIN BETA WD-40	PR00320B 12.19 5.935e-
	İ	REPEAT SIGNATURE	11 364-379 PR00320A
			16.74 7.828e-11 364-
	1	,	379 PR00320C 13.01
	1		2.800e-10 279-294
	1		PR00320C 13.01 2.800e-
	1		10 364-379 PR00320B
	1		12.19 5.114e-10 279-
	1		294 PR00320A 16.74
	i	1	1.659e-09 279-294
	J		

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
			PR00320A 16.74 2.098e-
			PF00023A 16.03 6.464e;
1642	PF00023	Ank repeat proteins.	09 114-130
1643	PR00169	POTASSIUM CHANNEL SIGNATURE	PR00169A 16.77 1.806e- 11 74-94
1644	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 2.200e-10
2018		proteins proteins.	109-120 BL00678 9.67 5.737e-09 528-539
1645	BL01108	Ribosomal protein L24 proteins.	BL01108A 20.33 7.366e- 17 56-89
1646	PR00380	KINESIN HEAVY CHAIN	PR00380A 14.18 9.270e-
		SIGNATURE	21 103-125 PR00380D 9.93 6.308e-18 386-408 PR00380C 13.18 7.923e- 16 332-351 PR00380B 12.64 6.657e-15 292-
			310
1647	DM01242	3 THREONINETRNA LIGASE.	DM01242C 17.15 9.791e- 37 340-381 DM01242E 23.00 5.071e-31 463- 505 DM01242D 23.29 3.925e-30 420-463 DM01242B 23.57 8.054e- 18 265-314 DM01242F 10.61 7.618e-14 526- 540
1649	PD00126	PROTEIN REPEAT DOMAIN TPR NUCLEA.	PD00126A 22.53 5.500e- 10 13-34
1651	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 6.720e- 11 431-485
1652	BL00933	FGGY family of carbohydrate kinases proteins.	BL00933A 17.50 4.673e- 12 11-35 BL00933E 13.80 9.217e-09 456- 472
1653	BL00795	Involucrin proteins.	BL00795C 17.06 2.988e- 10 70-115
1654	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 302-334
1655	BL00982	Bacterial-type phytoene dehydrogenase proteins.	BL00982A 18.41 7.750e- 17 282-314
1656	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 1.391e- 16 607-630
1657	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 7.938e- 11 114-136
1658	PR00910	LUTEOVIRUS ORF6 PROTEIN SIGNATURE	PR00910A 2.51 8.889e- 10 442-455
1659	BL00972	Ubiquitin carboxyl- terminal hydrolases family 2 proteins.	BL00972D 22.55 4.140e- 12 376-401 BL00972E 20.72 5.629e-09 446- 468
1660	BL00406	Actins proteins.	BL00406D 12.58 8.767e- 15 188-243
1661	PR00105	CYTOSINE-SPECIFIC DNA METHYLTRANSFERASE SIGNATURE	PR00105A 10.36 4.900e- 13 1140-1157 PR00105B 12.32 2.800e-12 1259- 1274 PR00105C 10.86 1.000e-10 1305-1319
1662	BL00280	Pancreatic trypsin inhibitor (Kunitz) family proteins.	BL00280 24.61 3.172e- 33 3119-3163
1663	PR00319	BETA G-PROTEIN (TRANSDUCIN) SIGNATURE	PR00319D 11.64 6.625e- 23 107-125 PR00319C 13.41 5.714e-20 89-105 PR00319A 15.27 5.286e- 19 51-68 PR00319B 11.47 8.200e-19 70-85

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1664	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 5.050e-10
1667	PD01066	PROTEIN ZINC FINGER	PD01066 19.43 8.500e-
2007	1001000	ZINC-FINGER METAL- BINDING NU.	38 7-46
1669	BL01153	NOL1/NOP2/sun family	BL01153D 19.69 1.188e-
	220222	proteins.	17 115-141 BL01153C
		-	13.67 8.977e-15 66-80
			BL01153B 20.52 1.885e-
			10 13-37
1671	PR00678	PI3 KINASE P85	PR00678H 9.13 3.100e-
		REGULATORY SUBUNIT SIGNATURE	10 1146-1169
1672	BL00598	Chromo domain proteins.	BL00598 14.45 8.500e- 20 27-49
1673	PR00326	GTP1/OBG GTP-BINDING	PR00326A 8.75 8.329e-
		PROTEIN FAMILY SIGNATURE	09 686-707
1674	PR00049	WILM'S TUMOUR PROTEIN	PR00049D 0.00 7.580e-
		SIGNATURE	11 343-358 PR00049D
		į	0.00 1.286e-10 342-357
1676	PR00747	GLYCOSYL HYDROLASE	PR00747H 12.76 8.636e-
		FAMILY 47 SIGNATURE	19 427-448 PR00747G
		1	14.50 2.286e-18 368-
	i		393 PR00747C 12.06
			7.500e-18 112-131
			PR00747A 14.05 4.600e-
			17 42-63 PR00747D
			15.23 8.759e-17 163-
		· ·	183 PR00747E 15.13
			8.244e-15 254-272
			PR00747B 7.65 5.355e-
			13 75-90 PR00747F 13.56 8.714e-10 311-
		ł.	328
1677	PR00747	GLYCOSYL HYDROLASE	PR00747H 12.76 8.636e-
10//	FROOTET	FAMILY 47 SIGNATURE	19 309-330 PR00747G
	ļ		14.50 2.286e-18 250-
			275 PR00747C 12.06
			7.500e-18 112-131
			PR00747A 14.05 4.600e-
			17 42-63 PR00747B
	į		7.65 5.355e-13 75-90
			PR00747F 13.56 8.714e-
			10 193-210
1680	BL00678	Trp-Asp (WD) repeat	BL00678 9.67 4.600e-10
		proteins proteins.	406-417 BL00678 9.67
1607	77.00670	Trp-Asp (WD) repeat	6.684e-09 320-331
1681	BL00678	proteins proteins.	BL00678 9.67 4.600e-10 329-340 BL00678 9.67
		processa process.	6.684e-09 243-254
1683	PR00326	GTP1/OBG GTP-BINDING	PR00326A 8.75 1.346e-
1003	***************************************	PROTEIN FAMILY SIGNATURE	13 389-410
1685	PR00646	RDC1 ORPHAN RECEPTOR	PR00646H 6.32 4.188e-
		SIGNATURE	09 755-771
1690	BL01160	Kinesin light chain	BL01160B 19.54 6.644e-
		repeat proteins.	09 75-129
1691	PR00456	RIBOSOMAL PROTEIN P2	PR00456E 3.06 7.281e-
		SIGNATURE	10 418-433 PR00456E
			3.06 7.281e-10 419-434
			PR00456E 3.06 8.125e-
	<u> </u>		10 420-435
1.000		RIBOSOMAL PROTEIN P2	PR00456E 3.06 7.281e-
1692	PR00456		
1692	PR00456	SIGNATURE	10 487-502 PR00456B
1692	PR00456		3.06 7.281e-10 488-503
1692	PR00456		3.06 7.281e-10 488-503 PR00456E 3.06 8.125e-
		SIGNATURE	3.06 7.281e-10 488-503 PR00456E 3.06 8.125e- 10 489-504
1693	PR00456		3.06 7.281e-10 488-503 PR00456E 3.06 8.125e-

SEQ ID N	O: ACCESSION	DESCRIPTION	RESULTS*
	NO.		
			4.46 4.000e-23 241-263 BL00674D 23.41 8.560e- 18 338-385 BL00674E 15.24 1.720e-15 414- 434
1697	PR00409	PHTHALATE DIOXYGENASE REDUCTASE FAMILY SIGNATURE	PR00409F 12.70 4.388e- 10 427-447
1698	PR00466	CYTOCHROME B-245 HEAVY CHAIN SIGNATURE	PR00466C 10.17 3.443e- 13 187-208 PR00466B 5.03 5.500e-11 162-186 PR00466F 9.16 6.159e- 09 498-517
1699	BL00028	Zinc finger, C2H2 type, domain proteins.	BL00028 16.07 9.217e- 12 283-300 BL00028 16.07 3.769e-11 255- 272 BL00028 16.07 5.154e-11 171-188 BL00028 16.07 5.500e- 11 227-244 BL00028 16.07 1.600e-10 199- 216
1700	BL01019	ADP-ribosylation factors family proteins.	BL01019A 13.20 3.348e- 15 62-102 BL01019B 19.49 4.000e-15 107- 162
1703	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 2.484e- 12 200-239
1707	PR00109	TYROSINE KINASE CATALYTIC DOMAIN SIGNATURE	PR00109B 12.27 4.558e- 14 134-153
1710	PR00019	LEUCINE-RICH REPEAT SIGNATURE	PR00019A 11.19 2.565e- 10 116-130 PR00019B 11.36 4.600e-09 113- 127 PR00019B 11.36 7.120e-09 204-218
1711	BL01159	WW/rsp5/WWP domain proteins.	BL01159 13.85 6.523e- 11 232-247 BL01159 13.85 5.408e-10 613- 628
1712	PF00023	Ank repeat proteins.	PF00023A 16.03 7.000e- 10 187-203
1713	PF00642	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e- 11 230-241
1714	PF00642 BL01115	Zinc finger C-x8-C-x5-C-x3-H type (and similar).	PF00642 11.59 9.550e- 11 230-241
1510		GTP-binding nuclear protein ran proteins.	BL01115A 10.22 7.129e- 09 7-51
1/18	BL00353	HMG1/2 proteins.	BL00353C 14.83 6.018e- 10 136-183 BL00353B 11.47 8.866e-09 86-136
1719	BL00412	Neuromodulin (GAP-43) proteins.	BL00412D 16.54 5.408e- 09 432-483
1721	BL00038	Myc-type, 'helix-loop- helix' dimerization domain proteins.	BL00038B 16.97 8.448e- 12 79-100 BL00038A 13.61 4.000e-11 52-68
1723	PD00567	PROTEIN RNA-BINDING RNA REPEAT HYD.	PD00567C 9.17 8.500e-
1724	BL01279	Protein-L- isoaspartate (D- aspartate) O- methyltransferase signa.	BL01279A 24.27 5.663e- 12 233-281
1728	BL00018	EF-hand calcium-binding domain proteins.	BL00018 7.41 2.059e-11 73-86 BL00018 7.41 4.176e-11 157-170
1730	BL00594	Aromatic amino acids permeases proteins.	BL00594A 16.75 1.089e- 09 17-61
		1.	03 17 01

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1731	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e~ 10 296-350
1732	BL01160	Kinesin light chain repeat proteins.	BL01160B 19.54 9.676e- 10 316-370
1733	PF00850	Histone deacetylase family.	PF00850F 15.70 4.349e- 22 246-279 PF00850D 14.76 6.850e-20 177- 201 PF00850E 8.88 8.691e-18 209-235 PF00850G 22.75 4.098e- 14 281-323
1734	BL00354	HMG-I and HMG-Y DNA- binding domain proteins (Ahook).	BL00354C 6.61 5.932e- 09 292-307
1735	DM00179	w KINASE ALPHA ADHESION T-CELL.	DM00179 13.97 5.263e- 10 492-502
1743	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e- 11 5-27 PR00449D 10.79 2.241e-10 109- 123 PR00449E 13.50 9.289e-10 144-167
1744	PR00449	TRANSFORMING PROTEIN P21 RAS SIGNATURE	PR00449A 13.20 1.188e- 11 5-27 PR00449D 10.79 2.241e-10 109- 123 PR00449E 13.50 9.289e-10 144-167
1745	BL00720	Guanine-nucleotide dissociation stimulators CDC25 family sign.	BL00720B 16.57 8.297e- 15 136-160
1746	PR00081	GLUCOSE/RIBITOL DEHYDROGENASE FAMILY SIGNATURE	PR00081B 10.38 6.727e- 11 45-57 PR00081E 17.54 3.935e-10 150- 168
1747	BL00439	Acyltransferases ChoActase / COT / CPT family proteins.	BL00439H 18.24 8.435e- 14 65-91 BL00439G 13.40 2.895e-12 3-14
1749	PR00819	CBXX/CFQX SUPERFAMILY SIGNATURE	PR00819B 10.83 7.158e- 11 4-20
1751	PD00066	PROTEIN ZINC-FINGER METAL-BINDI.	PD00066 13.92 3.400e- 14 33-46 PD00066 13.92 1.000e-13 89-102 PD00066 13.92 7.000e- 13 61-74 PD00066 13.92 6.571e-12 117- 130
1753	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 6.516e- 18 33-77
1754	BL00790	Receptor tyrosine kinase class V proteins.	BL00790I 20.01 2.393e- 09 490-521 BL00790I 20.01 2.821e-09 60-91 BL00790I 20.01 6.357e- 09 287-318
1756	PD01066	PROTEIN ZINC FINGER ZINC-FINGER METAL- BINDING NU.	PD01066 19.43 9.750e- 35 10-49
1758	DM00406	GLIADIN.	DM00406 7.73 7.600e-09 653-666
1762	PD02929	ADHESION GLYCOPROTEIN PRECURSOR I.	PD02929A 28.27 4.529e- 09 224-278
1765	PR00326	GTP1/OBG GTP-BINDING PROTEIN FAMILY SIGNATURE	PR00326A 8.75 5.950e- 11 146-167
1775	PF00023	Ank repeat proteins.	PF00023A 16.03 3.077e- 14 523-539
1776	BL00942	glpT family of transporters proteins.	BL00942F 15.07 4.343e- 10 371-389 BL00942B 20.36 8.040e-09 94-137
1777	DM00215	PROLINE-RICH PROTEIN 3.	DM00215 19.43 2.373e- 09 279-312

SEQ ID NO:	ACCESSION NO.	DESCRIPTION	RESULTS*
1778	BL00084	Copper type II, ascorbate-dependent monooxygenases proteins.	BL00084D 25.11 3.700e- 20 169-224 BL00084B 24.26 8.134e-16 10-58 BL00084C 27.71 8.412e- 11 107-158
1779	BL01013	Oxysterol-binding protein family proteins.	BL01013D 26.81 3.758e- 18 611-655 BL01013A 25.14 2.881e-15 344- 380 BL01013C 9.97 6.308e-13 435-445 BL01013B 11.33 3.717e- 12 409-420
1783	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515
1784	BL00741	Guanine-nucleotide dissociation stimulators CDC24 family sign.	BL00741B 14.27 8.138e- 13 492-515

^{*} results include in order: accession number subtype; raw score; p-value; postion of signature in amino acid sequence.

TRADOCS:1416223.1(%CRU011.DOC)

TABLE 4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORE
2	ig	Immunoglobulin domain	2.1e-32	109.5
3	pkinase	Eukaryotic protein kinase domain	1.3e-29	110.7
4	zf-C2H2	Zinc finger, C2H2 type	1.6e-21	84.9
5	fn3	Fibronectin type III domain	0	1097.1
6	fn3	Fibronectin type III domain	0	1035.0
7	fn3	Fibronectin type III domain	0	1090.4
8	fn3	Fibronectin type III domain	0	1097.1
9	TBC	TBC domain	4e-40	146.7
10	p450	Cytochrome P450	9.5e-17	62.0
12	ank	Ank repeat	6e-20	79.7
14	ig	Immunoglobulin domain	1.7e-05	22.7
15	zf-MYND	MYND finger	1.3e-06	35.4
16	zf-MYND	MYND finger	1.3e-06	35.4
17	zf-C2H2	Zinc finger, C2H2 type	1.7e-99	343.9
18	CAP GLY	CAP-Gly domain	1.2e-25	98.7
20	IMPDH C	IMP dehydrogenase / GMP	1.6e-119	410.5
	_	reductase C terminus		1
21	IMPDH_C	IMP dehydrogenase / GMP reductase C terminus	4.3e-102	352.6
22	pkinase	Eukaryotic protein kinase	2.4e-79	277.0
23	pkinase	domain Eukaryotic protein kinase	8.4e-74	258.6
23	prinase	domain	0.46-74	250.0
25	RNA_pol_A	RNA polymerase alpha subunit	0	1077.7
26	Clq	Clq domain	1.9e-10	44.4
27	Ribosomal_L2	Ribosomal protein L23	7.8e-32	111.2
28	Ribosomal_L2	Ribosomal protein L23	le-29	104.2
30	zf-A20	A20-like zinc finger	1.5e-10	48.5
31	zf-A20	A20-like zinc finger	1.5e-10	48.5
32	FMN_dh	FMN-dependent dehydrogenase	5.4e-179	608.1
34	PID	Phosphotyrosine interaction domain (PTB/PID)	3.8e-59	209.9
35	ig	Immunoglobulin domain	1.4e-13	48.8
36	ig	Immunoglobulin domain	1.4e-13	48.8
40	kinesin	Kinesin motor domain	6.7e-76	265.6
44	Ets	Ets-domain	1.4e-56	182.1
45	Ets	Ets-domain	1.4e-56	182.1
46	LRR	Leucine Rich Repeat	1.7e-13	58.3
48	zf-C2H2	Zinc finger, C2H2 type	2.3e-162	552.8
49	ITAM	Immunoreceptor tyrosine-based activation mot	1.4e-05	31.9
50	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	1.1e-26	102.0
51	UCH-2	Ubiquitin carboxyl-terminal	1.1e-26	102.0
52	ras	Ras family	8.5e-45	162.3
53	PRK	Phosphoribulokinase	2.1e-65	230.7
54	myb_DNA-	Myb-like DNA-binding domain	0.096	15.2
55	binding voltage CLC	Voltage gated chlorida characle	2 30 106	631 0
		Voltage gated chloride channels	3.3e-186	631.9
56	sugar_tr	Sugar (and other) transporter	0.00015	-64.3
57	TBC	TBC domain	2.2e-37	137.6
58	ank	Ank repeat	5.9e-25	96.3
59 67	ank PMP22_Claudi	Ank repeat PMP-22/EMP/MP20/Claudin family	5.9e-25 7.9e-49	96.3 175.6
	n			
68	C2	C2 domain	7.9e-54	192.2
69	C2	C2 domain	2.3e-54	194.0
70	Kelch	Kelch motif	9.4e-99	341.5
72	ig	Immunoglobulin domain	8.2e-28	94.7
73	pkinase	Eukaryotic protein kinase	8e-69	242.1

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
		domain		- BCOKE
74	pkinase	Eukaryotic protein kinase domain	2.8e-38	140.6
76	zf- C4 Topoisom	Topoisomerase DNA binding C4 zinc fing	5.4e-54	192.8
83	Peptidase S9	Prolyl oligopeptidase family	4.3e-10	36.8
84	fn3	Fibronectin type III domain	4.1e-51	183.2
86	SH2	Src homology domain 2	3.1e-22	67.7
88	ig	Immunoglobulin domain	0.0091	14.0
89	WD40	WD domain, G-beta repeat	2.1e-21	84.6
92	laminin_G	Laminin G domain	6.1e-27	98.5
93	AMP-binding	AMP-binding enzyme	2.4e-13	-37.2
95	pkinase	Eukaryotic protein kinase domain	1.4e-59	211.4
96	pkinase	Eukaryotic protein kinase domain	2.6e-51	183.9
97	adh_short	short chain dehydrogenase	2e-61	217.5
98	kinesin	Kinesin motor domain	2.2e-86	300.4
101	IRS	PTB domain (IRS-1 type)	5.4e-36	133.0
102	AAA	ATPases associated with various cellular act	6.8e-05	-5.2
104	pkinase	Eukaryotic protein kinase domain	2.7e-73	256.9
106	ras	Ras family	8.3e-24	92.5
107	FYVE	FYVE zinc finger	5.4e-27	100.7
108	Cyt_reductas e	FAD/NAD-binding Cytochrome reductase	7.7e-61	215.5
109	zf-C2H2	Zinc finger, C2H2 type	2.3e-122	420.0
113	pkinase	Eukaryotic protein kinase domain	4e-88	306.2
116	PH	PH domain	3.1e-11	45.2
117	lipocalin	Lipocalin / cytosolic fatty- acid binding pr	2.4e-14	53.5
118	pkinase	Eukaryotic protein kinase domain	4.5e-20	76.3
120	WD40	WD domain, G-beta repeat	2.4e-14	61.1
121	WD40	WD domain, G-beta repeat	2.4e-14	61.1
123	IF5_eIF4_eIF 2	eIF4-gamma/eIF5/eIF2-epsilon	1e-32	122.2
124	ig	Immunoglobulin domain	6.5e-08	30.6
127	mito_carr	Mitochondrial carrier proteins	3e-16	58.6
128	PP2C ATP1G1_PLM_M AT8	Protein phosphatase 2C ATPIGI/PLM/MAT8 family	2.2e-71 3.1e-20	250.6 80.6
130	pfkB	pfkB family carbohydrate kinase	4.5e-42	137.1
133	ACBP	Acyl CoA binding protein	4.6e-22	86.7
134	rrm	RNA recognition motif.	1.2e-31	118.5
135	IQ	IQ calmodulin-binding motif	2.6e-08	41.0
136	ATP1G1_PLM_M AT8	ATP1G1/PLM/MAT8 family	9.3e-22	85.7
139	WH2	Wiskott Aldrich syndrome homology region 2	0.0067	23.1
140	zf-C2H2	Zinc finger, C2H2 type	1.7e-82	287.5
141	Peptidase_S2 6	Signal peptidase I	5.7e-10	35.7
143	arf	ADP-ribosylation factor family	1.2e-39	145.2
146	KRAB	KRAB box	7.3e-30	112.6
148	DUF6	Integral membrane protein DUF6	0.096	8.0
149	PDEase	3'5'-cyclic nucleotide phosphodiesterase	3.8e-80	231.1
151	S4	S4 domain	1.1e-08	42.3
153	tRNA-synt_1d	tRNA synthetases class I (R)	3.8e-103	356.1
154	Cyt_reductas e	FAD/NAD-binding Cytochrome reductase	7.8e-60	212.2
155	ras	Ras family	3.6e-28	107.0
157	actin	Actin	3.8e-26	87.1

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORE
158	Jacalin	Jacalin-like lectin domain	0.09	-24.9
160	Zn_carbOpept	Zinc carboxypeptidase	5e-138	471.9
L65	pkinase	Eukaryotic protein kinase domain	5.1e-67	236.1
167	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-07	27.0
168	Ribosomal_S1	Ribosomal protein \$15	1.1e-06	29.0
169	DEAD	DEAD/DEAH box helicase	le-48	157.0
171	DUF59	Domain of unknown function DUF59	0.07	-17.4
172	pkinase	Eukaryotic protein kinase domain	3.7e-15	58.6
173	globin	Globin	4.6e-18	67.4
174	WW	WW domain	7.3e-06	32.9
175	ras	Ras family	1e-31	118.8
178	ATPIG1_PLM_M AT8	ATPIG1/PLM/MAT8 family	2.5e-17	71.0
179	zf-C2H2	Zinc finger, C2H2 type	1.5e-99	344.2
180	Clq	Clq domain	8.8e-72	251.9
190	Y_phosphatas e	Protein-tyrosine phosphatase	4.9e-287	967.0
191	efhand	EF hand	7.5e-16	66.1
193	pkinase	Eukaryotic protein kinase domain	6.5e-82	285.6
194	bromodomain	Bromodomain	5.8e-31	111.4
195	PALP	Pyridoxal-phosphate dependent enzyme	2.5e-64	227.1
197	DnaJ	DnaJ domain	1.6e-3B	141.4
199	RrnaAD	Ribosomal RNA adenine dimethylases	0.00018	16.9
200	acid_phospha	Histidine acid phosphatase	2.5e-10	37.2
201	WH2	Wiskott Aldrich syndrome homology region 2	0.00048	26.9
204	vATP- synt_AC39	ATP synthase (C/AC39) subunit	1.3e-159	543.7
205	vATP- synt_AC39	ATP synthase (C/AC39) subunit	1.6e-139	476.9
206	ldl_recept_a	Low-density lipoprotein receptor domain	2.4e-25	97.6
209	ank	Ank repeat	1.4e-19	78.4
210	Rhomboid	Rhomboid family	0.0035	1.2
211	Clq	Clq domain	1.6e-70	247.7
212	UQ_con	Ubiquitin-conjugating enzyme	7.4e-74	258.8
213	UQ_con	Ubiquitin-conjugating enzyme	le-53	191.9
215	DEAD	DEAD/DRAH box helicase	1.8e-43	140.4
216	PMP22_Claudi n	PMP-22/EMP/MP20/Claudin family	4.5e-21	83.4
218	Glycos_trans f_2	Glycosyl transferases	4e-21	83.6
219	ig	Immunoglobulin domain	0.092	10.7
222	WD40	WD domain, G-beta repeat	7.4e-23	89.4
224	TPR	TPR Domain	1.2e-08	42.1
225	DnaJ_CXXCXGX G	DnaJ central domain (4 repeats)	1.5e-38	141.5
226	DnaJ_CXXCXGX G	DnaJ central domain (4 repeats)	1.5e-38	141.5
229	HSP70	Hsp70 protein	2.4e-54	194.0
230	GSHPx	Glutathione peroxidases	3.4e-47	170.2
231	tsp_1	Thrombospondin type 1 domain	0.0075	17.1
233	cyclin	Cyclin	4.6e-144	492.0
234	ras	Ras family	4.8e-50	179.7
	LRR	Leucine Rich Repeat	1.2e-30	115.3
235			1	
235 236	LRR	Leucine Rich Repeat	6.7e-29	109.4
		Leucine Rich Repeat PDZ domain (Also known as DHR	6.7e-29 1.7e-09	109.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
244	dCMP_cyt_dea	Cytidine and deoxycytidylate	2.5e-05	31.1
	m	deaminase Immunoglobulin domain	6.7e-08	30.5
45	ig	Immunogiobulin domain	9.1e-270	742.6
248	wnt	wnt family of developmental signaling protei		
250	mito_carr	Mitochondrial carrier proteins	1.3e-55	193.6
254	adenylatekin ase	Adenylate kinase	1.8e-14	55.7
255	Cation_efflu	Cation efflux family	2.8e-33	124.0
256	SH3	SH3 domain	3.9e-14	60.4
257	Aa_trans	Transmembrane amino acid transporter protein	2.6e-52	187.2
258	adenylatekin	Adenylate kinase	2.1e-110	380.2
259	HIT	HIT family	8.2e-07	25.3
		PQQ enzyme repeat	1.6e-15	65.0
260	Bacterial_PQ Q			
262	proteasome	Proteasome A-type and B-type	6.5e-64	225.7
267	pkinase	Eukaryotic protein kinase domain	6.3e-27	
270	filament	Intermediate filament proteins	3.2e-150	512.5
271	Choline_kina	Choline/ethanolamine kinase	2e-67	237.4
277	Ribosomal_S7	Ribosomal protein S7p/S5e	3.3e-20	80.6
279	pkinase	Eukaryotic protein kinase	3.3e-77	269.9
280	WD40	WD domain, G-beta repeat	7.8e-73	255.4
281	WD40	WD domain, G-beta repeat	7.8e-73	255.4
284	zf-DHHC	DHHC zinc finger domain	4.6e-24	93.4
287	Exonuclease	Exonuclease	1.4e-67	238.0
291	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
292	SAM	SAM domain (Sterile alpha motif)	0.034	11.2
294	zf-C2H2	Zinc finger, C2H2 type	1.4e-29	111.7
295	zf-C2H2	Zinc finger, C2H2 type	2.2e-125	430.0
296	mito carr	Mitochondrial carrier proteins	4.1e-59	205.5
297	HMG box	HMG (high mobility group) box	6.7e-29	109.4
302	Glycos_trans f 4	Glycosyl transferase	5e-87	302.5
304	tRNA-synt_2	tRNA synthetases class II (D, K and N)	1.1e-84	294.8
305	KRAB	KRAB box	2e-44	161.0
306	rrm	RNA recognition motif.	2.7e-44	160.6
308	7tm_1	7 transmembrane receptor (rhodopsin family)	5.2e-39	126.1
309	DNA_polymera	DNA polymerase X family	2.4e-64	227.2
311	F-box	F-box domain.	9.5e-08	39.2
312	ig	Immunoglobulin domain	6.8e-19	65.9
313	Ets	Ets-domain	8.1e-60	192.3
315	Kelch	Kelch motif	1.3e-106	367.6
317	arf	ADP-ribosylation factor family	3.2e-35	130.4
318	sugar tr	Sugar (and other) transporter	0.0003	-73.1
320	pkinase	Eukaryotic protein kinase domain	8.1e-83	288.6
322	pkinase	Eukaryotic protein kinase domain	4.9e-81	282.6
324	Xlink	Extracellular link domain	4.5e-143	331.5
326	ARID	ARID DNA binding domain	5.1e-37	136.4
	HMG box	HMG (high mobility group) box	6.7e-29	109.4
	cadherin	Cadherin domain	B.1e-81	281.9
327				
328 331	chromo	'chromo' (CHRromatin Organization MOdifier)	4e-18	66.7

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
335	vwa	von Willebrand factor type A	2.3e-07	37.9
	ļ	Ras family	7.8e-07	-59.1
339	ras		8.2e-64	225.4
340	zf-C2H2	Zinc finger, C2H2 type	2.4e-85	297.0
342	zf-C2H2	Zinc finger, C2H2 type		. 1
343	ig	Immunoglobulir domain	0.0005	18.0
346	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
347	pkinase	Eukaryotic protein kinase domain	6.5e-65	229.1
351	EGF	EGF-like domain	8.5e-20	79.2
352	ank	Ank repeat	2.5e-101	350.0
	TBC	TBC domain	5.1e-15	63.3
354			3.2e-07	37.4
355	PHD	PHD-finger		
358	DUF6	Integral membrane protein DUP6	0.033	15.8
359	zf-C2H2	Zinc finger, C2H2 type	7.4e-20	79.4
361	ank	Ank repeat	6.6e-34	126.1
362	ArfGap	Putative GTP-ase activating protein for Arf	4.7e-53	189.7
363	efhand	BF hand	5.4e-10	46.6
367	LRR	Leucine Rich Repeat	8.8e-44	158.9
368	laminin G	Laminin G domain	1.5e-33	121.7
		Protein phosphatase 2C	5.3e-20	73.9
369	PP2C		9.9e-15	57.1
372	LIM	LIM domain containing proteins		90.0
373	KRAB	KRAB box	4.8e-23	1 2 2
376	ion_trans	Ion transport protein	2.9e-09	-4.2
377	Beach	Beige/BEACH domain	4.9e-208	704.5
380	pkinase	Eukaryotic protein kinase domain	1.6e-94	327.5
381	AMP-binding	AMP-binding enzyme	1.4e-07	-140.3
382	HECT	HECT-domain (ubiquitin- transferase).	1.3e-07	-13.5
384	ank	Ank repeat	2.5e-101	350.0
	1	Immunoglobulin domain	9.5e-06	23.6
386	ig		1.7e-42	154.6
388	zf-C2H2	Zinc finger, C2H2 type		
389	ig	Immunoglobulin domain	2.8e-15	54.3
390	mito_carr	Mitochondrial carrier proteins	3.5e-67	233.2
392	TPR	TPR Domain	6.1e-17	69.7
393	SH3	SH3 domain	3.5e-09	43.9
394	AAA	ATPases associated with various cellular act	4.1e-21	83.6
396	spectrin	Spectrin repeat	2.1e-67	237.3
397	zf-C2H2	Zinc finger, C2H2 type	0.0066	23.1
		Fibronectin type III domain	4.1e-102	352.6
399	fn3		0.00049	26.8
400	WD40	WD domain, G-beta repeat	1	1
401	El_dehydrog	Dehydrogenase E1 component	3e-119	409.6
402	£n3	Fibronectin type III domain	0	1719.6
404	LRR	Leucine Rich Repeat	2.1e-10	48.0
405	cadherin	Cadherin domain	8.1e-81	281.9
406	zf-CXXC	CXXC zinc finger	5e-15	63.4
410	RhoGEF	RhoGEF domain	1.1e-23	92.1
411	F-box	F-box domain.	4.2e-06	33.7
411	SNF2_N	SNF2 and others N-terminal	5.8e-16	61.6
415	CPSase_L_cha	domain Carbamoyl-phosphate synthase	1.5e-172	586.6
	in	(CPSase)	3.8e-24	93.6
418	LRR	Leucine Rich Repeat	1	
419	DENN	DENN (AEX-3) domain	2e-58	207.5
420	RasGEF	RasGEF domain	8.1e-43	155.7
421	ank	Ank repeat	1.4e-153	523.7
424	G-patch	G-patch domain	le-19	78.9
425	pkinase	Eukaryotic protein kinase	2.2e-31	117.1
		domain		24.6
426	Plexin_repea	Plexin repeat	0.0023	
427	Plexin repea	Plexin repeat	0.0023	24.6

SEQ ID	PFAM NAME	DESCRIPTION		
NO:	<u> </u>	DESCRIPTION	p-value	PFAM SCORE
429	zf-C3HC4			
		Zinc finger, C3HC4 type (RING finger)	8.6e-11	39.2
431	DEAD	DEAD/DEAH box helicase	1e-66	214.0
432	SH3	SH3 domain	3.4e-16	67.2
433	GTP_CDC	Cell division protein	2.1e-114	393.5
436	Collagen	Collagen triple helix repeat (20 copies)	4.6e-194	658.1
438	Ricin_B_lect	Similarity to lectin domain of ricin b	0.0085	10.5
441	Alpha_adapti n C	Alpha adaptin carboxyl-terminal	1.2e-256	866.0
442	Alpha_adapti	Alpha adaptin carboxyl-terminal domai	1.8e-235	795.7
443	PDZ	PDZ domain (Also known as DHR or GLGF).	1.9e-65	230.9
445	LON	ATP-dependent protease La (LON) domain	0.00012	-17.1
446	ig	Immunoglobulin domain		_
451	sushi	Immunograbulin domain	0.00011	20.1
452	fn3	Sushi domain (SCR repeat)	1.4e-18	75.2
454		Fibronectin type III domain	1.5e~06	35.2
	pyridoxal_de C	Pyridoxal-dependent decarboxylase conse	8.3e-14	50.3
456	kinesin	Kinesin motor domain	4.9e-217	734.4
457	neur_chan	Neurotransmitter-gated ion- channel	le-175	597.1
458	Josephin	Josephin	0.0002	18.7
468	bZIP	bZIP transcription factor	1.7e-07	31.8
470	NTP_transfer ase	Nucleotidyl transferase	6.3e-06	-26.3
471	WD40	WD domain, G-beta repeat	2e-28	107.9
473	LIM	LIM domain containing proteins	0.00021	20.7
477	zf-RanBP	Zn-finger in Ran binding protein and others.	0.028	21.0
479	WD40	WD domain, G-beta repeat	6.5e-18	73.0
480	KRAB	KRAB box	le-31	118.8
481	ArfGap	Putative GTP-ase activating	8.4e-66	232.0
485	SH2	protein for Arf Src homology domain 2		L
486	Clg	Clq domain	0.011	11.4
487	dsrm	Double-stranded RNA binding	4.3e-74 1.1e-47	259.6 171.9
		motif		
489	zf-C2H2	Zinc finger, C2H2 type	4.8e-153	521.9
490	Alpha_adapti n_C	Alpha adaptin carboxyl-terminal domai	3.4e-222	751.6
492	SKI	Shikimate kinase	1.2e-10	48.8
497	ENV_polyprot ein	ENV polyprotein (coat polyprotein)	2.6e-22	77.6
498	abhydrolase_ 2	Phospholipase/Carboxylesterase	0.041	-48.1
500	rrm	RNA recognition motif.	5.4e-34	126.4
501	WW	WW domain	4.6e-18	73.4
502	ig	Immunoglobulin domain	1.1e-10	
504	abhydrolase	alpha/beta hydrolase fold	0.045	39.5
505	vwa	von Willebrand factor type A domain	7.1e-62	-3.6 219.0
508	Na_K_ATPase_ C	Na+/K+ ATPase C-terminus	2.3e-145	496.3
509	Exonuclease	Exonuclease	1.3e-56	201 5
510	Glycos_trans f 1	Glycosyl transferases group 1	2.9e-06	201.5
511	Glycos_trans f 1	Glycosyl transferases group 1	2.9e-06	27.0
512	Glycos_trans f 1	Glycosyl transferases group 1	1.9e-09	38.5
514	pro_isomeras e	Cyclophilin type peptidyl- prolyl cis-tr	1.8e-63	221.4

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SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:				SCORE
515	EGF	EGF-like domain	1.9e-18	74.7
516	Surp	Surp module	4.3e-38	140.0
523	ig	Immunoglobulin domain	3.3e-06	25.0
526	UBX	UBX domain	1.1e-34	128.6
528	adh zinc	Zinc-binding dehydrogenases	2.7e-34	127.4
530	SAM	SAM domain (Sterile alpha	0.046	10.0
		motif)		
531	adh short	short chain dehydrogenase	0.0025	-34.1
532	mito carr	Mitochondrial carrier proteins	2.5e-8I	281.7
533	mito carr	Mitochondrial carrier proteins	2e-61	213.5
534	thiolase	Thiolase	3.5e-183	622.0
535	FMO-like	Flavin-binding monooxygenase-	0	1153.7
		like		
536	SCAN	SCAN domain	4e-55	196.6
537	tRNA-synt_1	tRNA synthetases class I (I, L,	3.1e-136	466.0
		M and V)		
538	tRNA-synt 1	tRNA synthetases class I (I, L,	3.1e-136	466.0
550		M and V)		
539	tRNA-synt 1	tRNA synthetases class I (I, L,	1.9e-117	403.6
J		M and V)		
540	tRNA-synt 1	tRNA synthetases class I (I, L,	3.1e-136	466.0
320		M and V)	3.20 130	
541	vATP-synt E	ATP synthase (E/31 kDa) subunit	5.9e-85	295.7
543	zf-C2H2	Zinc finger, C2H2 type	5.5e-69	242.6
544	DUF101	Protein of unknown function	8.5e-38	139.0
544	DOFIUL	DUF101	6.56-36	139.0
545	MOTI	TGF-beta propeptide	1.1e-67	238.2
545	TGFb_propept ide	TGr-beca propeptide	1.16-67	230.2
547	WD40	WD domain, G-beta repeat	2.6e-32	120.8
	RHD	Rel homology domain (RHD).	1.6e-238	686.2
548	1	GTPase of unknown function	5.4e-67	236.0
549	MMR HSR1	HECT-domain (ubiquitin-	4.3e-127	435.6
551	HECT		4.3e-12/	435.6
	- 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1	transferase). Class II histocompatibility	3.5e-74	259.8
554	MHC_II_alpha	antigen, alp	3.5e-74	259.8
555	zf-UBR1	Putative zinc finger in N-	3.3e-16	67.3
555	ZI-UBRI	recognin	3.36-16	67.3
556	Kelch	Kelch motif	5.5e-29	109.7
		AMP-binding enzyme	2.8e-06	-163.7
561	AMP-binding		4.9e-38	139.8
562	PABP	Poly-adenylate binding protein,	4.9e-38	139.8
		unique domai	 	238.2
564	Gag_p30	Gag P30 core shell protein	1.2e-67	
566	PWWP	PWWP domain	8.1e-16	66.0
567	SCAN	SCAN domain	7.3e-68	238.9
569	pkinase	Eukaryotic protein kinase	1.5e-84	294.3
	<u> </u>	domain		
570	pkinase	Bukaryotic protein kinase	1.5e-84	294.3
		domain		
571	CN_hydrolase	Carbon-nitrogen hydrolase	0.00081	-79.7
572	myosin_head	Myosin head (motor domain)	0	1495.2
573	myosin_head	Myosin head (motor domain)	0	1490.4
575	Surp	Surp module	1.7e-23	91.5
576	Surp	Surp module	1.7e-23	91.5
577	DNA_pol_B	DNA polymerase family B	0	1138.6
578	PDZ	PDZ domain (Also known as DHR	8.3e-09	42.7
	1	or GLGF).		
579	LRR	Leucine Rich Repeat	4.9e-21	83.3
580 ·	neur_chan	Neurotransmitter-gated ion-	5.9e-177	601.3
		channel		
583	sushi	Sushi domain (SCR repeat)	0	1673.0
584	DEAD	DRAD/DEAH box helicase	7.3e-36	116.3
586	KH-domain	KH domain	2.9e-13	57.5
587	G-patch	G-patch domain	2.3e-14	61.2
589	LIM	LIM domain containing proteins	2.3e-36	133.4
590	bromodomain	Bromodomain	6.6e-32	114.7
591	bromodomain	Bromodomain	6.6e-32	114.7
	Promodomatil	I PTOUCHUMETH	, 0.05-34	1 444.7

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:	<u> </u>			SCORE
592	hormone_rec	Ligand-binding domain of nuclear hormone	3.5e-22	87.1
593	PHD	PHD-finger	3.8e-12	53.8
594	cadherin	Cadherin domain	4.2e-99	342.7
596	pkinase	Eukaryotic protein kinase	5e-92	319.2
		domain		02212
597	WD40	WD domain, G-beta repeat	0.00054	26.7
600	FG-GAP	FG-GAP repeat	4.3e-75	262.9
602	G_Adapt_CT	Gamma-adaptin, C-terminus	1.1e-53	191.8
603	pkinase	Eukaryotic protein kinase domain	2.3e-86	300.4
605	Collagen	Collagen triple helix repeat (20 copies)	8e-42	152.4
606	mito_carr	Mitochondrial carrier proteins	6.3e-67	232.3
608	PWWP	PWWP domain	2.6e-28	107.5
609	PWWP	PWWP domain	2.6e-28	107.5
613	CAP_GLY	CAP-Gly domain	0.0046	20.1
615	RFX_DNA_bind ing	RFX DNA-binding domain	5.2e-54	192.9
616	kinesin kinesin	Kinesin motor domain	1.1e-81 8.4e-80	284.8
617 618	zf-C3HC4	Kinesin motor domain Zinc finger, C3HC4 type (RING	0.0098	278.5 13.1
	<u> </u>	finger)		
620	MATH	MATH domain Protein-tyrosine phosphatase	7.8e-05 1.4e-32	121.6
	Y_phosphatas e			
622	pkinase	Eukaryotic protein kinase domain	4.4e-40	146.6
623	BNR	BNR repeat	2.1e-11	51.3
624	molybdopteri n	Prokaryotic molybdopterin oxidoreductas	1.4e-12	42.2
625	TPR	TPR Domain	1.1e-17	72.2
627	cNMP_binding	Cyclic nucleotide-binding domain	3.7e-58	206.6
630	adh_short	short chain dehydrogenase	5e-17	70.0
631	zf-C2H2	Zinc finger, C2H2 type	2.1e-88	307.1
632 635	rrm pkinase	RNA recognition motif. Eukaryotic protein kinase	4e-05 1.6e-104	30.5
635	pkinase	domain	1.66-104	360.7
636	Fork head	Fork head domain	5.9e-27	103.0
637	pkinase	Eukaryotic protein kinase domain	3.8e-70	246.5
642	TPR	TPR Domain	4.8e-08	40.1
643	efhand	EF hand	1.9e-27	104.6
647	SNF2_N	SNF2 and others N-terminal domain	1.2e-101	351.1
648	PseudoU_synt h_2	RNA pseudouridylate synthase	1.9e-55	197.6
650	zf-C2H2	Zinc finger, C2H2 type	0.0087	22.7
651	ank	Ank repeat	1.3e-17	71.9
652	I_LWEQ	I/LWEQ domain	9.5e-101	341.0
653	neur_chan	Neurotransmitter-gated ion- channel	4.1e-171	581.8
654	tsp_1	Thrombospondin type 1 domain	4.1e-47	169.9
659	FH2	Formin Homology 2 Domain	1e-107	371.2
661	pou	Pou domain - N-terminal to homeobox domain	5.3e-45	162.9
662	C2	C2 domain	6.7e-19	76.2
663	C2	C2 domain	6.7e-19	76.2
664	C2	C2 domain	6.7e-19	76.2
667 668	GST	Glutathione S-transferases.	9.3e-34	114.4
670	LRR spectrin	Leucine Rich Repeat Spectrin repeat	9.3e-31 4e-57	115.6
671	I LWEQ	I/LWEQ domain	9.5e-101	341.0
672	ABC tran	ABC transporter	5.3e-60	212.8

NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
NO: 675		WD domain, G-beta repeat	4.8e-24	93.3
	WD40	Leucine Rich Repeat	0.0015	25.2
676	LRR	Zinc finger C-x8-C-x5-C-x3-H	2.6e-29	107.7
679	zf-CCCH	type	2.66-29	
680	zf-C2H2	Zinc finger, C2H2 type	5.2e-05	30.1
681	CH	Calponin homology (CH) domain	2.4e-17	71.1
682	DSPc	Dual specificity phosphatase, catalytic doma	4.3e-43	156.6
683	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	0.051	10.8
687	Synapsin	Synapsin	10	1890.8
689	PR55	Protein phosphatase 2A regulatory subunit PR	0	1038.8
691	homeobox	Homeobox domain	8.5e-30	112.4
696	Peptidase_M2	metallopeptidase family M24	2.6e-59	210.5
C07	4	RhoGEF domain	9.5e-35	128.9
697	RhoGEF	I	9.5e-35 0.008	9.3
698	PHD	PHD-finger	5.5e-123	422.0
701	zf-C2H2	Zinc finger, C2H2 type	3e-231	781.6
702	Sulfatase	Sulfatase		
703	zf-C2H2	Zinc finger, C2H2 type	5.7e-20	79.8
707	Acyl_transf	Acyl transferase domain	1.1e-22	88.8
708	WD4 0	WD domain, G-beta repeat	4.8e-19	76.7
710	Ran_BP1	RanBP1 domain.	8.4e-06	-7.3
713	DEAD	DEAD/DEAH box helicase	9.9e-42	134.9
714	PH	PH domain	1.6e-09	39.0
715	DSPc	Dual specificity phosphatase, catalytic doma	1.5e-37	138.2
717	Sialyltransf	Sialyltransferase family	7.5e-31	115.9
718	iq	Immunoglobulin domain	1e-29	100.8
719	integrin B	Integrins, beta chain	0	1125.4
720	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	1.1e-08	32.4
722	Peptidase_C2	Calpain family cysteine protease	3e-145	495.9
723	ig	Immunoglobulin domain	2.2e-05	22.4
724	F-box	F-box domain.	0.007	23.0
725	Мор	Putative snoRNA binding domain	8.1e-58	205.5
726	Non	Putative snoRNA binding domain	8.1e-58	205.5
726	Nop WD40	Putative snoRNA binding domain	8.1e-58 7.5e-26	205.5
726 727 730	Nop WD40 dsrm	WD domain, G-beta repeat Double-stranded RNA binding	8.1e-58 7.5e-26 0.027	205.5 99.3 12.1
727 730	WD40 dsrm	WD domain, G-beta repeat Double-stranded RNA binding motif	7.5e-26 0.027	99.3
727	WD40	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H	7.5e-26	99.3
727 730 731 733	WD40 dsrm dynamin zf-CCCH	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol	7.5e-26 0.027 4.2e-16	99.3 12.1 66.9
727 730 731 733 735	WD40 dsrm dynamin zf-CCCH CDP- OH P transf	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26	99.3 12.1 66.9 41.7
727 730 731 733 735	WD40 dsrm dynamin zf-CCCH CDP- OH P transf DEAD	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57	99.3 12.1 66.9 41.7 100.1
727 730 731 733 735 738 739	WD40 dsrm dynamin zf-CCCH CDP- OH P_transf DEAD TSC22	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32	99.3 12.1 66.9 41.7 100.1 182.5 119.5
727 730 731 733 735 738 739 742	WD40 dsrm dynamin zf-CCCH CDP- OH P transf DEAD TSC22 ras	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family Ras family	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32 2.2e-100	99.3 12.1 66.9 41.7 100.1 182.5 119.5 346.9
727 730 731 733 735 738 739 742 743	WD40 dsrm dynamin zf-CCCH CDP- OH_P_transf DEAD TSC22 ras PMI_typeI	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family Ras family Phosphomannose isomerase type I	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32 2.2e-100 1.2e-243	99.3 12.1 66.9 41.7 100.1 182.5 119.5 346.9 822.9
727 730 731 733 735 736 739 742 743 747	WD40 dsrm dynamin zf-CCCH CDP- OH_P_transf DEAD TSC22 ras PMI_typeI trypsin	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family Ras family Phosphomannose isomerase type I Trypsin	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32 2.2e-100 1.2e-243 6.4e-88	99.3 12.1 66.9 41.7 100.1 182.5 119.5 346.9 822.9 279.4
727 730 731 733 735 738 739 742 743 747	WD40 dsrm dynamin zf-CCCH CDP-OH_P transf DEAD TSC22 ras PMI_typeI trypsin kazal	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family Ras family Phosphomannose isomerase type I Trypsin Kazal-type serine protease inhibitor domain	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32 2.2e-100 1.2e-243 6.4e-88 2.2e-52	99.3 12.1 66.9 41.7 100.1 182.5 119.5 346.9 822.9 279.4 187.4
727 730 731 733 735 738 739 742 743 747	WD40 dsrm dynamin zf-CCCH CDP- OH_P_transf DEAD TSC22 ras PMI_typeI trypsin	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family Ras family Phosphomannose isomerase type I Trypsin Kazal-type serine protease	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32 2.2e-100 1.2e-243 6.4e-88	99.3 12.1 66.9 41.7 100.1 182.5 119.5 346.9 822.9 279.4
727 730 731 733 735 738 739 742 743 747	WD40 dsrm dynamin zf-CCCH CDP-OH_P transf DEAD TSC22 ras PMI_typeI trypsin kazal	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family Ras family Phosphomannose isomerase type I Trypsin Kazal-type serine protease inhibitor domain EF hand PHD-finger	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32 2.2e-100 1.2e-243 6.4e-88 2.2e-52	99.3 12.1 66.9 41.7 100.1 182.5 119.5 346.9 822.9 279.4 187.4
727 730 731 733 735 738 739 742 743 747 748	WD40 dsrm dynamin zf-CCCH CDP-OH_P transf DEAD TSC22 ras PMI_typeI trypsin kazal efhand	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family Ras family Phosphomannose isomerase type I Trypsin Kazal-type serine protease inhibitor domain EF hand	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32 2.2e-100 1.2e-243 6.4e-88 2.2e-52 6.3e-06	99.3 12.1 66.9 41.7 100.1 182.5 119.5 346.9 822.9 279.4 187.4
727 730 731 733 735 738 739 742 743 747 748	WD40 dsrm dynamin zf-CCCH CDP-OH_P_transf DEAD TSC22 ras PMI_typeI trypsin kazal efhand PHD	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family Ras family Phosphomannose isomerase type I Trypsin Kazal-type serine protease inhibitor domain EF hand PHD-finger Zinc finger, C2H2 type haloacid dehalogenase-like	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32 2.2e-100 1.2e-243 6.4e-88 2.2e-52 6.3e-06 4.9e-16	99.3 12.1 66.9 41.7 100.1 182.5 119.5 346.9 822.9 279.4 187.4
727 730 731 733 735 738 739 742 743 747 748 749 751	WD40 dsrm dynamin zf-CCCH CDP- OH_P_transf DEAD TSC22 ras PMI_typeI trypsin kazal efhand PHD zf-C2H2 Hydrolase Ribosomal_L3	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family Ras family Phosphomannose isomerase type I Trypsin Kazal-type serine protease inhibitor domain EF hand PHD-finger Zinc finger, C2H2 type	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32 2.2e-100 1.2e-243 6.4e-88 2.2e-52 6.3e-06 4.9e-16 3.2e-21	99.3 12.1 66.9 41.7 100.1 182.5 119.5 346.9 822.9 279.4 187.4 33.1 66.7 83.9
727 730 731 733 735 738 739 742 743 747 748 749 751 752 753	WD40 dsrm dynamin zf-CCCH CDP- OH_P transf DEAD TSC22 ras PMI_typeI trypsin kazal efhand PHD zf-C2H2 Hydrolase Ribosomal_L3 9	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family Ras family Phosphomannose isomerase type I Trypsin Kazal-type serine protease inhibitor domain EF hand PHD-finger Zinc finger, C2H2 type haloacid dehalogenase-like hydrolase Ribosomal L39 protein	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32 2.2e-100 1.2e-243 6.4e-88 2.2e-52 6.3e-06 4.9e-16 3.2e-21 6.1e-11 0.00018	99.3 12.1 66.9 41.7 100.1 182.5 119.5 346.9 822.9 279.4 187.4 33.1 66.7 83.9 49.8
727 730 731 733 735 738 739 742 743 747 748 749 751 752 753 754	WD40 dsrm dynamin zf-CCCH CDP-OH_P_transf DEAD TSC22 ras PMI_typeI trypsin kazal efhand PHD zf-C2H2 Hydrolase Ribosomal_L3 9 PH	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family Ras family Phosphomannose isomerase type I Trypsin Kazal-type serine protease inhibitor domain EF hand PHD-finger Zinc finger, C2H2 type haloacid dehalogenase-like hydrolase Ribosomal L39 protein	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32 2.2e-100 1.2e-243 6.4e-88 2.2e-52 6.3e-06 4.9e-16 3.2e-21 6.1e-11 0.00018 3.6e-14	99.3 12.1 66.9 41.7 100.1 182.5 119.5 346.9 822.9 279.4 187.4 33.1 66.7 83.9 49.8 26.7
727 730 731 733 735 738 739 742 743 747 748 749 751 752 753 754 755 758	WD40 dsrm dynamin zf-CCCH CDP- OH_P_transf DEAD TSC22 ras PMI_typeI trypsin kazal efhand PHD zf-C2H2 Hydrolase Ribosomal_L3 9 PH SCAN	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family Ras family Phosphomannose isomerase type I Trypsin Kazal-type serine protease inhibitor domain EF hand PHD-finger Zinc finger, C2H2 type haloacid dehalogenase-like hydrolase Ribosomal L39 protein PH domain SCAN domain	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32 2.2e-100 1.2e-243 6.4e-88 2.2e-52 6.3e-06 4.9e-16 3.2e-21 6.1e-11 0.00018 3.6e-14 1.4e-53	99.3 12.1 66.9 41.7 100.1 182.5 119.5 346.9 822.9 279.4 187.4 33.1 66.7 83.9 49.8 26.7
727 730 731 733 735 738 739 742 743 747 748 749 751 752 753 754	WD40 dsrm dynamin zf-CCCH CDP-OH_P_transf DEAD TSC22 ras PMI_typeI trypsin kazal efhand PHD zf-C2H2 Hydrolase Ribosomal_L3 9 PH	WD domain, G-beta repeat Double-stranded RNA binding motif Dynamin family Zinc finger C-x8-C-x5-C-x3-H type CDP-alcohol phosphatidyltransferase DEAD/DEAH box helicase TSC-22/dip/bun family Ras family Phosphomannose isomerase type I Trypsin Kazal-type serine protease inhibitor domain EF hand PHD-finger Zinc finger, C2H2 type haloacid dehalogenase-like hydrolase Ribosomal L39 protein	7.5e-26 0.027 4.2e-16 2.8e-10 4.2e-26 8.6e-57 6.5e-32 2.2e-100 1.2e-243 6.4e-88 2.2e-52 6.3e-06 4.9e-16 3.2e-21 6.1e-11 0.00018 3.6e-14	99.3 12.1 66.9 41.7 100.1 182.5 119.5 346.9 822.9 279.4 187.4 33.1 66.7 83.9 49.8 26.7

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
762	histone	Core histone H2A/H2B/H3/H4	9.9e-53	188.6
763	zf-MYND	MYND finger	4.1e-14	60.3
764	pou	Pou domain - N-terminal to	le-52	188.6
702	Pou	homeobox domain	10 32	100.0
767	vwc	von Willebrand factor type C domain	2.9e-34	127.3
769	efhand	EF hand	4.8e-11	50.1
770	zf-C4	Zinc finger, C4 type (two	2.4e-53	181.6
	21-04	domains)		L
772	ras	Ras family	7e-90	312.0
773	Sulfatase	Sulfatase	le-142	487.5
775	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
776	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
777	zf-C2H2	Zinc finger, C2H2 type	1.1e-12	55.5
778	rrm	RNA recognition motif.	2.1e-32	121.1
779	G6PD ·	Glucose-6-phosphate dehydrogenase	1.5e-76	236.6
780	spectrin	Spectrin repeat	3.7e-29	110.3
781	mito carr	Mitochondrial carrier proteins	4.6e-57	198.5
782	SCAN	SCAN domain	1.3e-24	95.2
783	PDZ	PDZ domain (Also known as DHR or GLGF).	4.1e-07	37.1
785	DEAD	DEAD/DEAH box helicase	6e-06	21.7
786	ras	Ras family	5.3e-39	143.0
787	RNase HII	Ribonuclease HII	2.5e-67	237.1
790	PI3 PI4 kina	Phosphatidylinositol 3- and 4-	5.4e-108	372.2
,,,,	se	kinases		İ
795	cadherin	Cadherin domain	2.5e-40	147.4
796	ARID	ARID DNA binding domain	1.6e-20	81.6
797	trypsin	Trypsin	9.9e-20	64.8
799	CH	Calponin homology (CH) domain	3.7e-15	63.8
801	Gal- bind lectin	Vertebrate galactoside-binding lectin	4.1e-25	88.7
803	WD40	WD domain, G-beta repeat	0.00082	26.1
806	TBC	TBC domain	1.8e-26	101.4
807	TBC	TBC domain	1.8e-26	101.4
808	CN hydrolase	Carbon-nitrogen hydrolase	8.8e-80	278.5
811	CBFD_NFYB_HM	Histone-like transcription	6e-14	59.8
	F	factor	B.1e-20	79.3
812	adh_short	short chain dehydrogenase Domain of unknown function	3.3e-71	250.0
814	zf-C2H2	Zinc finger, C2H2 type	8.2e-66	232.1
815 816	Pept_tRNA_hy	Peptidyl-tRNA hydrolase	1.6e-37	138.0
	dro		 	+=
817 826	ARID IF5_eIF4_eIF	ARID DNA binding domain eIF4-gamma/eIF5/eIF2-epsilon	2.5e-18 1.6e-32	74.3
830	2 ArfGap	Putative GTP-ase activating	1.5e-53	191.3
	_	protein for Arf		
831	LRR	Leucine Rich Repeat	2.1e-26	101.1
832	laminin_EGF	Laminin EGF-like (Domains III and V)	2e-57	204.2
839	rrm	RNA recognition motif.	1.3e-22	88.5
840	Y_phosphatas	Protein-tyrosine phosphatase	2.6e-119	409:8
841	e pkinase	Eukaryotic protein kinase	3.4e-100	346.3
844	Ribosomal L2	domain Ribosomal L22e protein family	le-64	228.4
044	2e	ATDOSOMAT DAZE PROCESH SAMILY	16-04	220.4
846	IBR	IBR domain	9e-15	62.5
849	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.4e-07	26.5
850	zf-C3HC4	Zinc finger, C3HC4 type (RING	0.00016	18.9
		finger)	1	
851	SET	SET domain	5e-30	113.2

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:			p varue	SCORE
		rich domain	 	
853	SRCR	Scavenger receptor cysteine- rich domain	0	1025.4
857	lactamase_B	Metallo-beta-lactamase superfamily	0.012	-6.0
858	COX6A	Cytochrome c oxidase subunit	3.4e-58	206.7
859	rrm	RNA recognition motif.	5.4e-45	162.9
861	PRK	Phosphoribulokinase	5.1e-62	219.4
863	mito carr	Mitochondrial carrier proteins	2.9e-53	185.5
864	HSP90	Hsp90 protein	4.7e-158	538.5
866	ig	Immunoglobulin domain	4e-12	44.1
867	zf-C2H2	Zinc finger, C2H2 type	7e-135	461.5
872	histone	Core histone H2A/H2B/H3/H4	4.9e-41	149.8
874	CPSase_L_cha	Carbamoyl-phosphate synthase (CPSase)	2.1e-218	739.0
879	Ribosomal_S1 2e	Ribosomal protein S12e	2.1e-98	340.3
882	serpin	Serpins (serine protease inhibitors)	2.5e-42	145.7
883	Patatin	Patatin	+1-2	1
884	RA	Ras association (RalGDS/AF-6)	1.2e-51 0.044	182.0
887	DUF92	domain		
889	sugar tr	Integral membrane protein DUF92	2.7e-12	54.3
893	DUF28	Sugar (and other) transporter Domain of unknown function	8.2e-63	222.1
		DUF28	1.3e-43	158.3
896	IP_trans	Phosphatidylinositol transfer protein	6.5e-98	338.7
898	DEAD	DEAD/DEAH box helicase	1.5e-48	156.5
899	KE2	KE2 family protein	7e-61	215.7
900	KE2	KE2 family protein	4.3e-51	183.2
901 902	zf-C2H2	Zinc finger, C2H2 type	2.7e-57	203.8
902	ras TPR	Ras family	2.3e-75	263.8
906	GBP	TPR Domain	3.2e-22	87.2
907	GBP	Guanylate-binding protein Guanylate-binding protein	8.9e-253	853.1
908	WD40	WD domain, G-beta repeat	1.1e-239	809.6
909	PH	PH domain	2.6e-26	100.8
910	zf-C2H2	Zinc finger, C2H2 type	1.3e-09 2.5e-39	39.4
913	Epimerase	NAD dependent	5e-07	144.1
		epimerase/dehydratase family	3e-07	-88.5
921 922	TBC	TBC domain	1.5e-09	30.7
922	WD40	WD domain, G-beta repeat	1.6e-25	98.2
924	Hydrolase	WD domain, G-beta repeat	8.2e-07	36.1
	-	haloacid dehalogenase-like hydrolase	2.9e-05	29.1
925	UQ_con	Ubiquitin-conjugating enzyme	0.00033	-27.6
926	CH	Calponin homology (CH) domain	3.3e~53	190.2
928	WD40	WD domain, G-beta repeat	5.9e-48	172.7
929	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	3.1e-10	37.4
930	Ribul_P_3_ep im	Ribulose-phosphate 3 epimerase family	7.2e-105	361.8
931	Ribul_P_3_ep im	Ribulose-phosphate 3 epimerase family	1.2e-96	334.4
936	C2	C2 domain	2.2e-62	220.7
937	NAP_family	Nucleosome assembly protein (NAP)	1.1e-22	84.6
40	abhydrolase	alpha/beta hydrolase fold	0.011	ا ا
144	Tropomyosin	Tropomyosins		3.1
48	pkinase	Eukaryotic protein kinase domain	3.2e-07 3.4e-75	25.1
	WD40	WD domain, G-beta repeat		
14.9 I				
949	Acyltransfer	Acyltransferase	1.8e-27 1.6e-07	38.4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
951	SAM	SAM domain (Sterile alpha motif)	0.014	14.5
954	GFO IDH MocA	Oxidoreductase family	1.3e-11	52.0
955	BTB	BTB/POZ domain	7e-22	86.1
956	BTB	BTB/POZ domain	7e-22	86.1
957	CDP-	CDP-alcohol	0.053	-22.2
	OH_P_transf	phosphatidyltransferase		
959	ras	Ras family	2.4e-97	336.8
960	ras	Ras family	8.4e-43	155.6
961	Acetyltransf	Acetyltransferase (GNAT) family	1.2e-08	42.2
962	adh short	short chain dehydrogenase	2.4e-31	117.6
963	mutT	Bacterial mutT protein	5.6e-06	26.2
969	IF-2B	Initiation factor 2 subunit family	8.4e-193	653.9
970	RNase PH	3' exoribonuclease family	9e-24	92.4
975	WW	WW domain	5.7e-25	96.4
977	PDZ	PDZ domain (Also known as DHR or GLGF).	3.6e-21	83.7
978	Ribosomal_L1	Ribosomal protein L17	2.4e-20	81.0
979	LIM	LIM domain containing proteins	5.8e-42	152.8
980	Calsequestri	Calsequestrin	1.7e-297	1001.7
982	HSP20	Hsp20/alpha crystallin family	1.2e-10	43.2
983	oxidored_q6	NADH ubiquinone oxidoreductase, 20 Kd sub	4.8e-63	222.9
988	TBC	TBC domain	2.2e-50	180.8
989	TBC	TBC domain	2.2e-50	180.8
993	tRNA_int_end	tRNA intron endonuclease	0.0017	-34.2
994	homeobox	Homeobox domain	4e-18	73.6
997	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	0.012	11.6
1000	mito carr	Mitochondrial carrier proteins	9.7e-123	1
1001	RA RA	Ras association (RalGDS/AF-6)	1.2e-15	65.4
1004	DUF81	Domain of unknown function	0.099	10.2
1005	actin	Actin	1.3e-174	574.3
1006	actin	Actin	3.1e-130	428.6
1007	cpn60_TCP1	TCP-1/cpn60 chaperonin family	3.7e-130	661.8
1008	TPR	TPR Domain		
1009	zf-C2H2	Zinc finger, C2H2 type	8.1e-44 3.6e-61	159.0 216.6
1011	zf-C2H2	Zinc finger, C2H2 type	3.6e-61	
1012	zf-C3HC4	Zinc finger, C3HC4 type (RING	4.7e-15	216.6
		finger)		53.1
1016	tRNA-synt_2c RhoGAP	tRNA synthetases class II (A) RhoGAP domain	2.3e-15	55.2
			1.6e-78	274.3
1022	PGAM	Phosphoglycerate mutase family	3.8e-18	69.7
1026	HMG_box	HMG (high mobility group) box	8.4e-20	79.2
1027	TBC	TBC domain	7.3e-45	162.5
1028 1032	UQ_con PDZ	Ubiquitin-conjugating enzyme PDZ domain (Also known as DHR	1.4e-49 0.028	178.1
1034	Hydrolase	or GLGF). haloacid dehalogenase-like	2e-21	84.6
1037	KRAB	hydrolase	4 5	
1038	Cation_efflu	KRAB box Cation efflux family	4.8e-06 7.1e-42	32.4 152.5
1040	ART	NAD:arginine ADP-	4.7e-47	169.1
1040	LUD 4.0	ribosyltransferase		
1042	WD40	WD domain, G-beta repeat	1.9e-18	74.7
1043	zf-C2H2	Zinc finger, C2H2 type	3.7e-24	93.7
1045	lectin_c	Lectin C-type domain	1.9e-28	108.0
1046	Glucosamine_	Glucosamine-6-phosphate	0.00013	-25.1
	igo	isomerase		4

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
NO:		<u> </u>	Final	SCORE
1047	ligase-CoA	CoA-ligases	4.5e-80	279.4
1049	ig	Immunoglobulin domain	1.7e-09	35.6
1050	Ribosomal_L2 4e	Ribosomal protein L24e	2e-33	124.5
1054	Amidase	Amidase	4.3e-152	518.7
1055	rrm	RNA recognition motif.	3.8e-26	100.3
1058	annexin	Annexin	6.9e-44	159.2
1059	PMP22_Claudi n	PMP-22/EMP/MP20/Claudin family	0.023	-23.6
1060	homeobox	Homeobox domain	3.2e-31	117.2
1062	Acyltransfer ase	Acyltransferase	0.00065	10.5
1064	AMP-binding	AMP-binding enzyme	6.6e-100	345.3
1065	LRR	Leucine Rich Repeat	3.3e-14	60.6
1066	GTP1_OBG	GTP1/OBG family	4.8e-41	141.8
1071	ig	Immunoglobulin domain	8.4e-48	159.1
1072	PHD	PHD-finger	6.Be-07	36.3
1074	DENN	DENN (AEX-3) domain	8.3e-33	121.5
1075	SCP	SCP-like extracellular protein	4.7e-41	149.8
1077 .	OLF	Olfactomedin-like domain	2.2e-66	234.0
1078	mito_carr	Mitochondrial carrier proteins	1e-42	149.3
1079	WD40	WD domain, G-beta repeat	6.2e-45	162.7
1087	START	START domain	1.5e-48	174.7
1093	DSPc	Dual specificity phosphatase, catalytic doma	3.3e-63	223.4
1094	GSHPx	Glutathione peroxidases	9.6e-41	148.8
1095	DUF25	Domain of unknown function DUF25	2e-75	264.0
1096	DUF25	Domain of unknown function DUF25	6e-75	262.4
1105	Nitroreducta se	Nitroreductase family	1.3e-13	58.6
1106	PTE	Phosphotriesterase family	1.3e-179	610.1
1107	DAGKC	Diacylglycerol kinase catalytic domain	0.00049	19.6
1109	ras	Ras family	1.3e-15	40.7
1115	ArfGap	Putative GTP-ase activating protein for Arf	9.7e-47	168.7
1116	HMG14_17	HMG14 and HMG17	4.4e-21	83.5
1117	HMG14_17	HMG14 and HMG17	9.9e-12	52.4
1119	FAA_hydrolas e	Fumarylacetoacetate (FAA) hydrolase fam	2e-83	290.6
1120	pkinase	Eukaryotic protein kinase domain	1.4e-94	327.6
1123	abhydrolase	alpha/beta hydrolase fold	9.2e-23	89.0
1129	pro_isomeras e	Cyclophilin type peptidyl- prolyl cis-tr	2.2e-56	197.1
1131	DnaJ	DnaJ domain	1.6e-30	114.9
1132	WD40	WD domain, G-beta repeat	1.3e-19	78.6
1133	WD40	WD domain, G-beta repeat	1.8e-15	64.9
1134	PH	PH domain	0.0015	17.8
1136	Adap_comp_su b	Adaptor complexes medium subunit family	1.2e-256	866.0
1137	Adap_comp_su b	Adaptor complexes medium subunit family	2.5e-209	708.8
1139	ras	Ras family	1.5e-86	301.0
1141	pkinase	Eukaryotic protein kinase domain	9.4e-74	258.4
1152	Acyltransfer ase	Acyltransferase	1.2e-05	29.9
1153	IRS	PTB domain (IRS-1.type)	5.4e-55	196.1
1155	ig	Immunoglobulin domain	1.3e-31	106.9
1157	Asparaginase	Asparaginase	6.4e-72	252.3
1159	GMC_oxred	GMC oxidoreductases	4.7e-142	485.3

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM
1163	linker_histo	linker histone H1 and H5 family	3.8e-14	60.4
1164	ne DED	Death effector domain	3.9e-05	30.5
1165	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1166	IRS	PTB domain (IRS-1 type)	2.6e-43	157.3
1168	SAM	SAM domain (Sterile alpha	0.04	10.5
	,	motif)	i	-
1170	abhydrolase	alpha/beta hydrolase fold	0.098	-7.5
1174	SAP	SAP domain	3.9e-10	47.1
1177	PP2C	Protein phosphatase 2C	5.3e-31	112.5
1178	WD40	WD domain, G-beta repeat	4.7e-35	129.9
1180	Ets	Ets-domain	1.8e-09	33.3
1181	Collagen	Collagen triple helix repeat (20 copies)	0.00016	24.7
1182	TCL1_MTCP1	TCL1/MTCP1 family	9.5e-56	198.6
1184	RasGEF	RasGEF domain	1.7e-88	307.4
1185	mito_carr	Mitochondrial carrier proteins	1.5e-62	217.3
1187	UPAR_LY6	u-PAR/Ly-6 domain	0.0042	15.6
1188	Orn_DAP_Arg_ deC	Pyridoxal-dependent decarboxylase	6.2e-128	430.6
1193	Stathmin	Stathmin family	1.8e-90	314.0
1194	Stathmin	Stathmin family	1.8e-90	314.0
1195	Sec1	Secl family	3.2e-183	622.1
1196	pyr_redox	Pyridine nucleotide-disulphide oxidoreducta	3.1e-32	111.8
1197	Glyco_transf	Glycosyl transferase family 8	1.2e-09	45.5
1202	K_tetra	K+ channel tetramerisation domain	0.022	-16.8
1203	adh_short	short chain dehydrogenase	8.3e-45	162.3
1206	Ubie_methylt ran	ubiE/COQ5 methyltransferase family	1.3e-121	417.4
1208	7tm_3	7 transmembrane receptor	7.2e-09	29.0
1209	ank	Ank repeat	3.9e-15	63.7
1210	vATP- synt_AC39	ATP synthase (C/AC39) subunit	2.5e-128	439.7
1212	zf-C2H2	Zinc finger, C2H2 type	5.5e-17	69.9
1213	efhand	EF hand	3.2e-07	37.4
1219	rrm	RNA recognition motif.	2.1e-40 0.015	147.7
1220	DUF6	Integral membrane protein DUF6 SCAN domain	1.5e-71	251.1
1222	SCAN G-gamma	GGL domain	3.6e-36	129.5
1223 1227	G-gamma catalase	Catalase	0	1158.9
1232	PX	PX domain	2.2e-15	64.5
1232	PX	PX domain	2.2e-15	64.5
1236	FCH	Fes/CIP4 homology domain	3.3e-09	44.0
1241	Peptidase_M2	Peptidase family M20/M25/M40	2e-63	224.1
1243	WW	WW domain	0.044	17.9
1247	UPF0006	Metalloenzyme of unknown function UPF0006	6.3e-61	215.8
1248	Glycos_trans f_2	Glycosyl transferases	4.5e-10	46.9
1249	efhand	BF hand	4e-11	50.4
1254	UQ_con	Ubiquitin-conjugating enzyme	2.1e-73	257.3
1255	ras	Ras family	2.2e-62	220.7
1256	formyl_trans	Formyl transferase	4.9e-30	108.3
1259	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.3e-13	46.4
1261	DiHfolate_re	Dihydrofolate reductase	2.1e-69	241.7
1262	G_glu_transp ept	Gamma-glutamyltranspeptidase	1.8e-110	380.4
1263	PAS	PAS domain	1.3e-08	36.9
1265	LRR	Leucine Rich Repeat	4.2e-22	86.9

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM
1266	1000	000 121 - 11 1		SCORE
1266	SCP	SCP-like extracellular protein	6e-29	108.0
	K_tetra	K+ channel tetramerisation domain	2.8e-27	104.0
1269	ras	Ras family	1.3e-85	297.9
1275	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	4.2e-10	37.0
1276	abhydrolase	alpha/beta hydrolase fold	5.4e-23	89.8
1277	abhydrolase	alpha/beta hydrolase fold	5.6e-21	83.1
1279	trypsin	Trypsin	4.4e-41	132.0
1280	PBP	Phosphatidylethanolamine- binding protein	1.3e-13	58.7
1285	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	5.6e-14	49.6
1287	ank	Ank repeat	1.7e-52	187.8
1294	fn3	Fibronectin type III domain	0.026	20.9
1295	GBP	Guanylate-binding protein	0.00026	-70.0
1296	PMP22_Claudi n	PMP-22/EMP/MP20/Claudin family	6.9e-41	149.3
1297	Rhodanese	Rhodanese-like domain	3.2e-14	60.7
1298	LIM	LIM domain containing proteins	5.8e-21	79.1
1301	rnaseA	Pancreatic ribonucleases	4.9e-43	145.2
1307	mito_carr	Mitochondrial carrier proteins	2.1e-53	186.0
1308	WD40	WD domain, G-beta repeat	1.6e-17	71.6
1310	UPAR_LY6	u-PAR/Ly-6 domain	7.1e-20	75.5
1313	thiored	Thioredoxin	3.6e-05	21.6
1314	Aa_trans	Transmembrane amino acid transporter protein	1.5e-67	237.9
1316	trypsin	Trypsin	4.4e-41	132.0
1320	Ribosomal_L1	Ribosomal protein L13	3.9e-62	219.8
1327	Armadillo_se	Armadillo/beta-catenin-like repeats	0.0054	23.4
1328	KRAB	KRAB box	0.052	-5.6
1329	rrm	RNA recognition motif.	2.1e-40	147.7
1330	Bcl-2	Apoptosis regulator proteins, Bcl-2 family	0.014	-1.6
1331	PX	PX domain	2.1e-10	48.0
1333	KRAB	KRAB box	1.8e-36	134.6
1334	UPP_syntheta se	Putative undecaprenyl diphosphate synt	2.3e-89	310.3
1335	UPP_syntheta	Putative undecaprenyl diphosphate synt	1.8e-59	211.0
1336	DSPc	Dual specificity phosphatase, catalytic doma	1.2e-31	118.6
1337	DSPc	Dual specificity phosphatase, catalytic doma	2.3e-12	54.5
1338	TPR	TPR Domain	0.00021	28.1
1340	metalthio	Metallothionein	0.013	20.3
1341	mutT	Bacterial mutT protein	5.8e-09	36.5
1343	Band 41	FERM domain (Band 4.1 family)	1.3e-38	122.5
1344	Kelch	Kelch motif	1.4e-44	161.5
1345	Antifreeze	Antifreeze protein	1.2e-10	48.8
1347	3Beta HSD	3-beta hydroxysteroid	1	-177.2
T3#1	355642.155	dehydrogenase/isomera	0.086	-1/7.2
1347	BTB	dehydrogenase/isomera		
_	<u> </u>	dehydrogenase/isomera ETB/POZ domain	5.3e-28	106.5
1348	BTB	dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6		106.5
1348 1349	BTB DUF6	dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated	5.3e-28 0.033	106.5
1348 1349 1350	BTB DUF6 myosin_head	dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium	5.3e-28 0.033	106.5 15.8 1088.7
1348 1349 1350 1352	BTB DUF6 myosin_head Nramp S_100	dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/TCaBP type calcium binding domain	5.3e-28 0.033 0 1.2e-202 5.3e-23	106.5 15.8 1088.7 686.6
1348 1349 1350 1352 1353	BTB DUF6 myosin_head Nramp S_100 DEAD	dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain DRAD/DEAH box helicase	5.3e-28 0.033 0 1.2e-202 5.3e-23	106.5 15.8 1088.7 686.6 89.9
1348 1349 1350 1352 1353 1355 1356	BTB DUF6 myosin_head Nramp S_100 DEAD C2	dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain DRAD/DEAH box helicase C2 domain	5.3e-28 0.033 0 1.2e-202 5.3e-23 3.6e-65 2.4e-15	106.5 15.8 1088.7 686.6 89.9
1348 1349 1350 1352 1353	BTB DUF6 myosin_head Nramp S_100 DEAD	dehydrogenase/isomera BTB/POZ domain Integral membrane protein DUF6 Myosin head (motor domain) Natural resistance-associated macrophage pro S-100/ICaBP type calcium binding domain DRAD/DEAH box helicase	5.3e-28 0.033 0 1.2e-202 5.3e-23	106.5 15.8 1088.7 686.6 89.9

		DESCRIPTION	p-value	PFAM
SEQ ID	PFAM NAME	DESCRIPTION	p-varue	SCORE
NO:	SIS	STS domain	3.8e-30	113.6
1362	SIS	SIS domain	1.3e-28	108.5
1363	1	Immunoglobulin domain	0.00026	19.0
1364	ig K tetra	K+ channel tetramerisation	1.1e-16	68.9
1368		domain		
1371	Collagen	Collagen triple helix repeat (20 copies)	2.2e-113	390.1
1372	DnaJ	DnaJ domain	6.6e-36	132.7
1376	KRAB	KRAB box	2.1e-38	141.0
1378	ELM2	ELM2 domain	2e-23	91.3
1380	thiored	Thioredoxin	1.2e-23	82.8
1381	ank	Ank repeat	2.3e-83	290.4
1382	ВТВ	BTB/POZ domain	3e-11	50.8
1383	WD40	WD domain, G-beta repeat	1.6e-19	78.3
1384	WD40	WD domain, G-beta repeat	6.3e-24	92.9
1387	zf-C3HC4	Zinc finger, C3HC4 type (RING	1.1e-09	35.6
	-4 02112	finger)	5.5e-50	179.5
1389	zf-C2H2	Zinc finger, C2H2 type Zinc finger, C2H2 type	2.5e-85	296.9
1390	zf-C2H2	Kinesin motor domain	7.8e-188	637.4
1393	kinesin	Zinc finger, C2H2 type	1.2e-49	178.4
1394	zf-C2H2 KRAB	KRAB box	5.1e-22	86.6
1398		bZIP transcription factor	0.035	13.1
1402	bZIP	Sugar (and other) transporter	0.033	-101.5
1405	sugar_tr		8.9e-47	168.8
1406	RhoGAP	RhoGAP domain RNA recognition motif.	le-35	132.1
1407	rrm		2.1e-13	58.0
1408	LRR	Leucine Rich Repeat Nebulin repeat	6e-54	192.6
1409	Nebulin_repe at	Nebulin repeat		
1410	ank	Ank repeat	1.6e-17	71.6
1412	Ribosomal_L5	ribosomal LSP family C-terminus	8.2e-58	205.5
1415	trypsin	Trypsin	4.7e-85	.270.4
1416	aminotran 1	Aminotransferases class-I	4.4e-05	-91.2
1417	S1	S1 RNA binding domain	1.6e-07	33.1
1419	WD40	WD domain, G-beta repeat	2.2e-09	44.6
1422	cadherin	Cadherin domain	8.3e-42	152.3
1424	SH3	SH3 domain	2.5e-80	280.3
1425	PHD	PHD-finger	3.2e-17	70.6
1426	PHD	PHD-finger	3.2e-17	70.6
1427	ArfGap	Putative GTP-ase activating protein for Arf	1e-37	138.8
1428	helicase_C	Helicases conserved C-terminal	1e-26	102.2
		domain	l	1
1429	WD40	WD domain, G-beta repeat	3.9e-07	37.2
1430	inositol_P	Inositol monophosphatase family	2.5e-10	40.2
1431	mito_carr	Mitochondrial carrier proteins	4.3e-83	287.7
1433	Clq	Clq domain	2.9e-16	66.2
1434	WD40	WD domain, G-beta repeat	1.6e-13	58.3
1435	Inos-1-	Myo-inositol-1-phosphate	7e-228	770.4
	P_synth	synthase	1 42 34	130 3
1436	rrm	RNA recognition motif.	1.4e-34	128.3
1438	ig	Immunoglobulin domain	1.3e-12	45.6
1440	G_Adapt_CT	Gamma-adaptin, C-terminus	3.4e-67	236.7
1441	C 14 CO	Gamma-adaptin, C-terminus	3.4e-67	236.7
	G_Adapt_CT			1 2 X 7
1443	Kelch	Kelch motif	0.00013	
1446	Kelch ARID	ARID DNA binding domain	1.8e-21	84.7
	Kelch ARID zf-C2H2	ARID DNA binding domain Zinc finger, C2H2 type	1.8e-21 9.4e-28	84.7
1446	Kelch ARID	ARID DNA binding domain Zinc finger, C2H2 type AMP-binding enzyme	1.8e-21 9.4e-28 2.6e-07	84.7 105.6 -145.1
1446 1447	Kelch ARID zf-C2H2	ARID DNA binding domain Zinc finger, C2H2 type AMP-binding enzyme RNA recognition motif.	1.8e-21 9.4e-28 2.6e-07 6.5e-21	84.7 105.6 -145.1 82.9
1446 1447 1448	Kelch ARID zf-C2H2 AMP-binding	ARID DNA binding domain Zinc finger, C2H2 type AMP-binding enzyme	1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44	84.7 105.6 -145.1 82.9 146.7
1446 1447 1448 1451	Kelch ARID zf-C2H2 AMP-binding rrm	ARID DNA binding domain Zinc finger, C2H2 type AMP-binding enzyme RNA recognition motif.	1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21	84.7 105.6 -145.1 82.9 146.7 83.2
1446 1447 1448 1451 1454	Kelch ARID zf-C2H2 AMP-binding rrm ig	ARID DNA binding domain Zinc finger, C2H2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain	1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21 1.9e-35	84.7 105.6 -145.1 62.9 146.7 83.2 131.2
1446 1447 1448 1451 1454 1455	Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf	ARID DNA binding domain Zinc finger, C2H2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family	1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21	84.7 105.6 -145.1 62.9 146.7 83.2 131.2 73.6
1446 1447 1448 1451 1454 1455 1460	Kelch ARID zf-C2H2 AMP-binding rrm ig Sialyltransf Aldose_epim	ARID DNA binding domain Zinc finger, C2H2 type AMP-binding enzyme RNA recognition motif. Immunoglobulin domain Sialyltransferase family Aldose 1-epimerase	1.8e-21 9.4e-28 2.6e-07 6.5e-21 5.6e-44 5.4e-21 1.9e-35	84.7 105.6 -145.1 82.9 146.7 83.2 131.2

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
 -	h 2	 	 	
1474	DENN	DENN (AEX-3) domain	1.3e-44	161.6
1475	Cation_efflu x	Cation efflux family	4.6e-49	176.4
1477	TBC	TBC domain	8e-47	169.0
1478	rrm	RNA recognition motif.	2e-21	84.6
1480	ig	Immunoglobulin domain	5.5e-06	24.3
1484	Telo_bind_al pha	Telomere-binding protein alpha subuni	0.028	-225.9
1485	zf-C2H2	Zinc finger, C2H2 type	1.8e-68	240.9
1486	pkinase	Eukaryotic protein kinase domain	9.5e-13	49.9
1488	helicase_C	Helicases conserved C-terminal domain	1.4e-15	65.2
1489	DUF89	Protein of unknown function DUF89	0.079	-132.4
1490	ECH	Enoyl-CoA hydratase/isomerase family	5.2e-41	149.7
1491	guanylate_cy c	Adenylate and Guanylate cyclase catalyt	5.9e-46	166.1
1492	LRR	Leucine Rich Repeat	3.4e-19	77.2
1495	zf-C3HC4	Zinc finger, C3HC4 type (RING finger)	7.1e-10	36.3
1497	pkinase	Eukaryotic protein kinase domain	1e-22	85.8
1500	SH3	SH3 domain	9.3e-05	27.2
1502 1503	homeobox	Homeobox domain	0.084	13.8
1503	homeobox	Homeobox domain EGF-like domain	0.084	13.8
1505	UCH-2	Ubiquitin carboxyl-terminal	2.7e-23	90.B
1508	Peptidase M2	hydrolase family Peptidase family M20/M25/M40	2.7e-21	84.2
1511	Peptidase_m2 0		2.8e-28	101.8
1512	Sulfatase	PX domain Sulfatase	1.9e-11	130.7
1516	Syntaxin	Syntaxin	2.8e-35 0.011	-62.3
1518	aminotran_3	Aminotransferases class-III pyridoxal-pho	9.7e-106	305.6
1520	ig	Immunoglobulin domain	0.075	11.0
1521	RA	Ras association (RalGDS/AF-6) domain	0.013	13.3
1523	RhoGAP	RhoGAP domain	2.5e-05	18.7
1528	WD40	WD domain, G-beta repeat	5.4e-24	93.1
1535	IMS	impB/mucB/samB family	7.8e-95	328.5
1538	FYVE	FYVE zinc finger	3.2e-27	101.5
1539	DAGKc	Diacylglycerol kinase catalytic domain	6e-07	36.5
1540	Ocular_alb	Ocular albinism type 1 protein	0	1184.7
1653	SAP Amino_oxidas	SAP domain Flavin containing amine oxidase	3.2e-43	33.2 157.0
1655	Amino_oxidas	Flavin containing amine oxidase	3.2e-43	157.0
1656	RhoGEF	RhoGEF domain	1.4e-24	95.1
1657	MMR HSR1	GTPase of unknown function	0.0011	-45.5
1659	UCH-2	Ubiquitin carboxyl-terminal hydrolase family	2.5e-11	51.1
1660	actin	Actin	6.6e-21	69.9
1661	BAH	BAH domain	1.7e-82	287.5
1662	vwa	von Willebrand factor type A domain	0	1909.4
1663	WD40	WD domain, G-beta repeat	1.4e-67	237.9
1667	zf-C2H2	Zinc finger, C2H2 type	1.3e-93	324.4
1669	Nol1_Nop2_Su	NOL1/NOP2/sun family	1.3e-23	84.3
	l n			

SEQ ID	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1672	chromo	'chromo' (CHRromatin	2.1e-18	67.7
1672	CITOMO	Organization MOdifier)	2.10	0,.,
1674	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H	0.0025	17.6
1074	22 000	type		} - · · · ·
1676	Glyco_hydro_	Glycosyl hydrolase family 47	1.8e-187	636.2
1677	Glyco_hydro_	Glycosyl hydrolase family 47	4.5e-74	259.5
1680	WD40	WD domain, G-beta repeat	1.1e-27	105.5
1681	WD40	WD domain, G-beta repeat	1.le-27	105.5
1683	MMR HSR1	GTPase of unknown function	1.8e-78	274.1
1691	rrm	RNA recognition motif.	1.8e-37	137.9
1692	rrm	RNA recognition motif.	1.8e-37	137.9
1693	AAA	ATPases associated with various cellular act	1.3e-81	284.5
1697	Ferric_reduc	Ferric reductase like transmembrane com	8.4e-82	285.2
1698	Ferric_reduc	Ferric reductase like transmembrane com	3.5e-53	190.1
1699	zf-C2H2	Zinc finger, C2H2 type	4.4e-34	126.6
1700	arf	ADP-ribosylation factor family	9e-19	75.8
1702	GTP_EFTU	Elongation factor Tu family	0.014	11.4
1703	SCAN	SCAN domain	1.8e-54	194.4
1707	pkinase	Eukaryotic protein kinase domain	1.2e-88	307.9
1709	WD40	WD domain, G-beta repeat	0.0035	24.0
1710	LRR	Leucine Rich Repeat	1.2e-30	115.3
1711	WW	WW domain	7.6e-12	52.8
1712	ank	Ank repeat	4.2e-34	126.7
1713	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1714	zf-CCCH	Zinc finger C-x8-C-x5-C-x3-H type	2.6e-09	38.3
1715	ras	Ras family	4.4e-41	149.9
1718	HMG_box	HMG (high mobility group) box	8.3e-21	82.6
1719	TBC	TBC domain	1.1e-45	165.2
1721	HLH	Helix-loop-helix DNA-binding domain	9.2e-10	45.9
1723	dsrm	Double-stranded RNA binding motif	2.9e-05	30.9
1724	RrnaAD	Ribosomal RNA adenine dimethylases	0.045	9.2
1725	CIDE-N	CIDE-N domain	5.9e-40	146.2
1726	HAT	HAT (Half-A-TPR) repeats	2.9e-44	160.5
1728	efhand	EF hand	5.1e-20	79.9
1733	Hist_deacety	Histone deacetylase family	1.7e-104	360.6
1735	LRR	Leucine Rich Repeat	4.6e-34	126.6
1739	PI-PLC-X	Phosphatidylinositol-specific phospholipase	0.0023	16.1
1743	ras	Ras family	3.7e-10	-21.3
1744	ras	Ras family	3.7e-10	-21.3
1745	RasGEF	RasGEF domain	3.2e-49	176.9
1746	adh_short	short chain dehydrogenase	7.1e-08	34.6
1751	zf-C2H2	Zinc finger, C2H2 type	9e-39	142.2
1754	fn3	Fibronectin type III domain	5.5e-101	348.9
1756	zf-C2H2	Zinc finger, C2H2 type	6.3e-93	322.1
1758	rrm	RNA recognition motif.	0.017	21.2
1760	Nop	Putative snoRNA binding domain	6.1e-95	328.8
1761	Nop	Putative snoRNA binding domain	6.1e-95	328.8
1765	MMR HSR1	GTPase of unknown function	6.4e-41	149.4
1769	CN_hydrolase	Carbon-nitrogen hydrolase	3e-06	-43.9
1775	ank	Ank repeat	4.1e-07	37.1
1779	Oxysterol_BP	Oxysterol-binding protein	4.7e-56	199.6
1783	RhoGEF	RhoGEF domain	1.6e-23	91.6
1784	RhoGBF	RhoGEF domain	1.6e-23	91.6

SEQ ID NO:	PFAM NAME	DESCRIPTION	p-value	PFAM SCORE
1785	rrm	RNA recognition motif.	6.4e-14	59.7

TRADOCS:1416227.1(%CRN01!.DOC)

TABLE 5

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
DEQ 15 NO.	SIGNAL IN AMINO	SCORE)	SCORE)
	ACID SEQUENCE	·	}
1	1-21	0.991	0.955
2	1-31	0.995	0.944
3	1-33	0.949	0.736
4	1-19	0.970	0.951
5	1-26	0.971	0.863
6	1-26	0.971	0.863
7	1-26	0.971	0.863
8	1-26	0.971	0.863
9	1-46	0.982	0.901
10	1-21	0.991	0.955
11	1-23	0.989	0.899
12	1-25	0.955	0.803
13	1-18	0.932	0.625
14	1-18	0.938	0.876
15	1-25	0.941	0.811
16	1-17	0.972	0.939
17	1-27	0.964	0.777
18	1-16	0.914	0.657
19	1-19	0.935	0.840
20	1-20	0.935	0.850
21	1-22	0.961	0.850
23	1-19	0.991	0.959
24	1-31	0.995	0.944
25	1-22	0.976	0.935
26	1-27	0.996	0.928
27	1-24	0.953	0.739
28	1-21	0.906	0.688
29	1-31	0.986	0.841
30	1-28	0.980	0.893
31	1-19	0.993	0.976
32	1-22	0.998	0.909
35	1-33	0.949	0.736
36	1-33	0.949	0.736
46	1-19	0.970	0.951
67	1-25	0.968	0.848
71	1-18	0.949	0.845
72	1-30	0.991	0.919
75	1-29	0.958	0.854
88	1-20	0.986	0.945
94	1-33	0.994	0.943
97	1-46	0.964	0.595
103	1-49	0.983	0.570
108	1-26	0.978	0.885
111	1-23	0.989	0.899
126	1-25	0.955	0.803
129	1-19	0.963	0.918
138	1-29	0.971	0.844
143	1-18	0.914	0.628
148	1-20	0.969	0.904
156	1-25	0.941	0.811
158	1-22	0.979	0.927
160	1-17	0.972	0.939
161	1-48	0.903	0.571
162	1-25	0.937	0.729
168	1-16	0.939	0.826
171	1-27	0.964	0.777
178	1-21	0.945	0.825
180	1-27	0.981	0.941
187	1-28	0.982	0.936
190	1-19	0.953	0.840
196	1-22	0.975	0.916
197	1-22	0.963	0.936

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
	SIGNAL IN AMINO	SCORE)	SCORE)
	ACID SEQUENCE	- 035	0.001
199	1-20	0.935	0.701
200	1-23	0.984	0.773
207	1-19	0.990	0.924
208	1-22	0.974	0.850
210	1-40	0.940	0.670
211	1-28	0.971	0.849
216	1-24	0.986	0.956
218	1-33	0.961	0.895
219	1-19	0.970	0.871
221	1-19	0.904	0.553
222	1-21	0.917	0.555
230	1-19	0.991	0.959
231	1-26	0.953	0.800
232	1-25	0.988	0.826
239	1-23	0.969	0.828
240	1-17	0.982	0.955
241	1-17	0.982	0.955
245	1-30	0.970	0.722
248	1-22	0.976	0.935
249	1-23	0.968	0.940
252	1-18	0.971	0.923
261	1-24	0.883	0.587
265	1-18	0.939	0.868
283	1-24	0.953	0.739
284	1-21	0.997	0.688
290	1-31	0.986	0.841
302	1-28	0.980	0.893
304	1-16	0.907	0.635
312	1-19	0.993	0.976
313	1-17	0.930	0.753
323	1-22	0.998	0.909
324	1-17	0.982	0.954
328	1-19	0.971	0.865
329	1-22	0.963	0.924
330	1-33	0.978	0.841
331	1-24	0.920	0.712
332	1-24	0.975	0.881
333	1-19	0.984	0.941
334	1-20	0.899	0.567
335	1-27	0.942	0.813
336	1-20	0.952	0.850
337	1-38	0.942	0.653
338	1-27	0.973	0.772
339	1-36	0.979	0.804
340	1-27	0.888	0.597
343	1-19	0.971	0.865
345	1-22	0.994	0.928
346	1-17	0.936	0.822
347	1-19	0.963	0.924
349	1-24	0.982	0.966
351	1-21	0.918	0.815
352	1-31	0.988	0.912
354	1-31	0.974	0.839
355	1-29	0.932	0.632
356	1-15	0.994	0.969
357	1-33	0.935	0.726
360	1-27	0.938	0.827
361	1-25	0.954	0.674
362	1-22	0.929	0.788
363	1-21	0.881	0.715
364	1-33	0.978	0.841
365	1-33	0.978	0.841
			·

SEQ ID NO:	POSITION OF SIGNAL IN AMINO	Maxs (MAXIMUM SCORE)	MeanS (MEAN SCORE)
	ACID SEQUENCE	0.016	0.820
366	1-21	0.916	0.820
367	1-19	0.936	0.874
368	1-29	0.972	0.712
370	1-24	0.920	0.712
371	1-24	0.961	0.768
372	1-27	0.919	
373	1-19	0.986	0.945
375	1-32	0.994	0.932
376	1-34	0.987	0.810
377	1-17	0.995	0.950
378	1-49	0.971	0.749
380	1-20	0.968	0.874
381	1-20	0.928	0.782
382	1-19	0.986	0.934
383	1-28	0.965	0.829
384	1-39	0.970	0.551
386	1-24	0.975	0.881
388	1-30	0.989	0.868
389	1-19	0.984	0.941
390	1-26	0.971	0.782
392	1-20	0.981	0.900
393	1-16	0.968	0.890
394	1-23	0.937	0.701
397	1-22	0.985	0.854
399	1-46	0.977	0.698
401	1-20	0.899	0.567
402	1-22	0.967	0.931
403	1-27	0.992	0.934
404	1-19	0.991	0.973
405	1-23	0.994	0.921
407	1-35	0.987	0.658
408	1-39	0.976	0.551
409	1-33	0.897	0.570
410	1-25	0.990	0.962
411	1-38	0.977	0.827
412	1-20	0.944	0.768
413	1-20	0.988	0.965
414	1-46	0.993	0.638
415	1-23	0.981	0.940
417	1-29	0.941	0.672
418	1-20	0.952	0.850
419	1-19	0.986	0.967
420	1-29	0.965	0.861
421	1-22	0.889	0.785
422	1-48	0.982	0.862
424	1-19	0.979	0.933
428	1-38	0.942	0.653
430	1-18	0.947	0.595
432	1-33	0.957	0.789
433	1-26	0.979	0.904
434	1-27	0.962	0.777
435	1-24	0.998	0.977
436	1-27	0.973	0.772
443	1-15	0.966	0.940
448	1-36	0.979	0.804
453	1-41	0.958	0.609
455	1-33	0.943	0.606
457	1-27		0.597
457	1-16	0.925	0.681
	1-27	0.925	0.845
486	1-24	0.917	0.636
495			0.890
498	1-26	0.993	0.890
505	1-20	0.976	
507	1-17	0.966	0.687
510	1-23	0.930	0.593

SEQ ID NO: POSITION OF SIGNAL IN AMINO SCORE SCO	000 70 10	DOCTOR OF	Mane /Maytuffe	Means /MEAN
ACID SEQUENCE	2EG ID NO:			1
511 1-23 0.930 0.593 512 1-23 0.950 0.593 515 1-18 0.978 0.956 523 1-19 0.936 0.924 545 1-24 0.962 0.966 550 1-30 0.933 0.711 552 1-21 0.973 0.912 554 1-23 0.969 0.784 571 1-21 0.918 0.815 574 1-31 0.988 0.912 574 1-31 0.988 0.912 580 1-39 0.955 0.556 608 1-29 0.932 0.632 609 1-29 0.932 0.632 610 1-21 0.990 0.948 621 1-15 0.994 0.969 623 1-33 0.935 0.726 623 1-33 0.935 0.784 621 1-15 0.990 0.948			SCORE)	SCORE
512 1-23 0.978 0.593 523 1-19 0.936 0.822 529 1-24 0.982 0.966 550 1-30 0.933 0.713 550 1-30 0.933 0.713 552 1-21 0.973 0.912 554 1-23 0.969 0.784 571 1-21 0.918 0.815 574 1-31 0.988 0.932 574 1-31 0.988 0.932 580 1-39 0.925 0.556 594 1-31 0.974 0.839 608 1-29 0.932 0.632 609 1-29 0.932 0.632 610 1-21 0.990 0.948 621 1-15 0.994 0.956 623 1-33 0.935 0.726 633 1-27 0.938 0.827 668 1-22 0.929 0.798				10.503
515 1-18 0.978 0.956 523 1-19 0.936 0.822 529 1-22 0.963 0.924 545 1-24 0.982 0.966 550 1-30 0.933 0.713 552 1-21 0.973 0.912 554 1-23 0.969 0.784 571 1-21 0.918 0.815 574 1-31 0.988 0.912 580 1-39 0.925 0.6556 584 1-31 0.974 0.839 609 1-29 0.932 0.632 609 1-29 0.932 0.632 610 1-21 0.990 0.948 621 1-15 0.994 0.959 623 1-33 0.935 0.726 623 1-33 0.935 0.726 633 1-27 0.938 0.827 668 1-22 0.929 0.786				
523 1-19 0.936 0.822 529 1-22 0.963 0.924 5545 1-24 0.982 0.966 550 1-30 0.933 0.713 552 1-21 0.973 0.912 554 1-23 0.969 0.784 571 1-21 0.918 0.815 574 1-31 0.988 0.912 580 1-39 0.925 0.556 594 1-31 0.974 0.839 608 1-29 0.932 0.632 609 1-29 0.932 0.632 610 1-21 0.990 0.946 621 1-15 0.994 0.969 623 1-33 0.935 0.726 623 1-33 0.935 0.726 633 1-27 0.938 0.827 668 1-22 0.929 0.788 677 1-16 0.948 0.807				
529 1-22 0.962 0.924 545 1-24 0.982 0.966 550 1-30 0.933 0.713 552 1-21 0.973 0.912 554 1-23 0.969 0.784 571 1-21 0.918 0.815 574 1-31 0.988 0.912 580 1-39 0.925 0.656 608 1-29 0.932 0.632 608 1-29 0.932 0.632 609 1-29 0.932 0.632 610 1-21 0.990 0.948 621 1-15 0.994 0.969 623 1-33 0.935 0.776 623 1-33 0.935 0.726 633 1-27 0.938 0.827 668 1-22 0.929 0.768 677 1-16 0.948 0.807 685 1-21 0.961 0.972				
54S 1-24 0.982 0.966 55D 1-30 0.933 0.713 552 1-21 0.973 0.912 554 1-23 0.969 0.784 571 1-71 0.918 0.815 574 1-31 0.988 0.912 580 1-39 0.935 0.556 594 1-31 0.974 0.839 608 1-29 0.932 0.632 610 1-21 0.990 0.948 6201 1-15 0.994 0.969 623 1-33 0.935 0.726 621 1-15 0.994 0.969 623 1-33 0.935 0.726 621 1-16 0.938 0.827 668 1-22 0.939 0.786 677 1-16 0.948 0.807 677 1-16 0.948 0.807 685 1-21 0.881 0.715				
S50	529	1-22	0.963	0.924
552 1-21 0.973 0.912 554 1-23 0.969 0.784 571 1-21 0.918 0.815 574 1-31 0.988 0.912 580 1-39 0.925 0.556 594 1-31 0.974 0.839 608 1-29 0.932 0.632 610 1-21 0.990 0.948 621 1-15 0.994 0.969 623 1-33 0.935 0.726 623 1-27 0.938 0.827 668 1-22 0.939 0.948 623 1-33 0.935 0.726 653 1-27 0.938 0.827 668 1-22 0.929 0.768 677 1-16 0.948 0.807 677 1-16 0.948 0.807 685 1-21 0.881 0.715 699 1-22 0.975 0.816	545	1-24	0.982	0.966
554 1-23 0.969 0.784 571 1-21 0.918 0.815 574 1-31 0.988 0.912 580 1-39 0.925 0.556 594 1-31 0.974 0.839 608 1-29 0.932 0.632 609 1-29 0.932 0.632 610 1-21 0.990 0.948 621 1-15 0.994 0.969 623 1-33 0.935 0.726 653 1-27 0.938 0.827 668 1-22 0.929 0.788 677 1-16 0.948 0.807 685 1-21 0.891 0.715 685 1-21 0.891 0.715 685 1-21 0.891 0.715 687 1-22 0.975 0.816 707 1-16 0.800 0.562 713 1-25 0.966 0.743	550	1-30	0.933	0.713
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864 1-20 0.928 0.782 866 1-19 0.986 0.934 873 1-23 0.948 0.886 681 1-28 0.965 0.829 887 1-39 0.970 0.551 927 1-30 0.989 0.868 934 1-48 0.988 0.777 939 1-39 0.994 0.889 944 1-26 0.971 0.782 950 1-29 0.957 0.845 963 1-20 0.981 0.900 964 1-20 0.886 0.558 973 1-16 0.968 0.890 980 1-34 0.961 0.749 981 1-20 0.953 0.622 984 1-12 0.938 0.780 1015 1-22 0.985 0.854 1040 1-46 0.977 0.698 1052 1-18 0.969 0.842	827	1-49	0.971	
866 1-19 0.986 0.934 873 1-23 0.948 0.886 881 1-28 0.965 0.829 887 1-39 0.970 0.551 927 1-30 0.989 0.868 934 1-48 0.988 0.777 939 1-39 0.994 0.889 944 1-26 0.971 0.782 950 1-29 0.957 0.845 963 1-20 0.981 0.900 964 1-20 0.886 0.558 973 1-16 0.968 0.890 980 1-34 0.961 0.749 981 1-20 0.953 0.622 984 1-12 0.938 0.780 1015 1-22 0.985 0.854 1040 1-46 0.977 0.698 1052 1-18 0.969 0.842 1059 1-20 0.927 0.867 <td>848</td> <td>1-20</td> <td>0.968</td> <td>0.874</td>	848	1-20	0.968	0.874
873 1-23 0.948 0.886 681 1-28 0.965 0.829 887 1-39 0.970 0.551 927 1-30 0.989 0.868 934 1-48 0.988 0.777 939 1-39 0.994 0.889 944 1-26 0.971 0.782 950 1-29 0.957 0.845 963 1-20 0.981 0.900 964 1-20 0.886 0.558 973 1-16 0.968 0.890 980 1-34 0.961 0.749 981 1-20 0.953 0.822 984 1-12 0.938 0.780 1015 1-22 0.985 0.854 1040 1-46 0.977 0.698 1052 1-18 0.969 0.842 1059 1-20 0.927 0.867	864	1-20	0.928	0.782
881 1-28 0.965 0.829 887 1-39 0.970 0.551 927 1-30 0.989 0.868 934 1-48 0.968 0.777 939 1-39 0.994 0.889 944 1-26 0.971 0.782 950 1-29 0.957 0.845 963 1-20 0.961 0.900 964 1-20 0.886 0.558 973 1-16 0.968 0.890 980 1-34 0.961 0.749 981 1-20 0.953 0.822 984 1-12 0.938 0.780 1015 1-22 0.985 0.854 1040 1-46 0.977 0.698 1052 1-18 0.969 0.842 1059 1-20 0.927 0.867	866	1-19	0.986	0.934
887 1-39 0.970 0.551 927 1-30 0.989 0.868 934 1-48 0.988 0.777 939 1-39 0.994 0.889 944 1-26 0.971 0.782 950 1-29 0.957 0.845 963 1-20 0.961 0.900 964 1-20 0.886 0.558 973 1-16 0.968 0.890 980 1-34 0.961 0.749 981 1-20 0.953 0.822 984 1-12 0.938 0.780 1015 1-22 0.985 0.854 1040 1-46 0.977 0.698 1052 1-18 0.969 0.842 1059 1-20 0.927 0.867	873	1-23	0.948	0.886
887 1-39 0.970 0.551 927 1-30 0.989 0.868 934 1-48 0.988 0.777 939 1-39 0.994 0.889 944 1-26 0.971 0.782 950 1-29 0.957 0.845 963 1-20 0.961 0.900 964 1-20 0.886 0.558 973 1-16 0.968 0.890 980 1-34 0.961 0.749 981 1-20 0.953 0.822 984 1-12 0.938 0.780 1015 1-22 0.985 0.854 1040 1-46 0.977 0.698 1052 1-18 0.969 0.842 1059 1-20 0.927 0.867	881	1-28	0.965	0.829
927 1-30 0.989 0.868 934 1-48 0.988 0.777 939 1-39 0.994 0.889 944 1-26 0.971 0.782 950 1-29 0.957 0.845 963 1-20 0.981 0.900 964 1-20 0.886 0.558 973 1-16 0.968 0.890 980 1-34 0.961 0.749 981 1-20 0.953 0.822 984 1-12 0.938 0.780 1015 1-22 0.985 0.854 1040 1-46 0.977 0.698 1052 1-18 0.969 0.842 1059 1-20 0.927 0.867		1-39		
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980 1-34 0.961 0.749 981 1-20 0.953 0.822 984 1-12 0.938 0.780 1015 1-22 0.985 0.854 1040 1-46 0.977 0.698 1052 1-18 0.969 0.842 1059 1-20 0.927 0.867				
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984 1-12 0.938 0.780 1015 1-22 0.985 0.854 1040 1-46 0.977 0.698 1052 1-18 0.969 0.842 1059 1-20 0.927 0.867				
1015 1-22 0.985 0.854 1040 1-46 0.977 0.698 1052 1-18 0.969 0.842 1059 1-20 0.927 0.867				
1040 1-46 0.977 0.698 1052 1-18 0.969 0.842 1059 1-20 0.927 0.867	984	1-12	0.938	0.780
1052 1-18 0.969 0.842 1059 1-20 0.927 0.867	1015	1-22	0.985	0.854
1052 1-18 0.969 0.842 1059 1-20 0.927 0.867	1040	1-46		0.698
1059 1-20 0.927 0.867				
1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	L			
1069 1-22 0.993 0.935				

SEQ ID NO:	POSITION OF	MaxS (MAXIMUM	MeanS (MEAN
· · · • · · · · · · · · · · · · · · ·	SIGNAL IN AMINO	SCORE)	SCORE)
	ACID SEQUENCE		,
1075	1-27	0.992	0.934
1080	1-19	0.931	0.829
1092	1-19	0.991	0.973
1094	1-46	0.992	0.653
1095	1-30	0.974	0.929
1105			
	1-23	0.994	0.921
1123	1-35	0.987	0.658
1138	1-32	0.954	0.613
1140	1-38	0.989	0.789
1142	1-33	0.897	0.570
1152	1-25	0.990	0.962
1170	1-38	0.977	0.827
1176	1-20	0.944	0.768
1187	1-20	0.988	0.965
1189	1-35	0.967	0.839
1192	1-46	0.993	0.638
1193	1-16	0.925	0.710
1197	1-29	0.985	0.853
1208	1-23	0.981	0.940
1225	1-29	0.941	0.672
1245	1-19	0.986	0.872
1258	1-29	0.965	0.861
1265	1-22		_L
1266		0.889	0.785
	1-20	0.944	0.809
1276	1-48	0.982	0.862
1292	1-19	0.979	0.933
1296	1-21	0.984	0.944
1297	1-19	0.984	0.953
1332	1-38	0.942	0.653
1358	1-18	0.947	0.595
1371	1-33	0.957	0.789
1380	1-26	0.979	0.904
1397	1-27	0.962	0.777
1399	1-23	0.997	0.960
1404	1-24	0.998	0.977
1410	1-15	0.946	0.845
1414	1-24	0.913	0.588
1415	1-19	0.982	0.929
1416	1-12	0.931	0.891
1418	1-30	0.933	0.563
1420	1-20	0.881	0.561
1421	1-19	0.990	0.968
1423	1-17	0.968	
1424	4		0.863
	1-21	0.885	0.591
1425	1-24	0.913	0.588
1426	1-24	0.913	0.588
1428	1-25	0.967	0.899
1430	1-34	0.977	0.819
1431	1-28	0.979	0.923
1432	1-36	0.957	0.613
1433	1-32	0.921	0.753
1434	1-39	0.983	0.621
1435	1-25	0.910	0.631
1436	1-42	0.988	0.868
1437	1-22	0.998	0.980
1442	1-20	0.918	0.753
1448	1-12	0.931	0.891
1462	1-18	0.968	0.888
1490	1-20	0.9881	
1518	1-17		0.561
		0.968	0.863
1525	1-21	0.885	0.591
1547	1-28	0.974	0.891
1561	1-25	0.967	0.899
	<u> </u>		<u>1</u>
1580 1593	1-17 1-28	0.923	0.824

SEQ ID NO:	POSITION OF SIGNAL IN AMINO ACID SEQUENCE	MaxS (MAXIMUM SCORE)	MeanS (MEAN SCORE)
1596	1-16	0.929	0.709
1601	1-36	0.957	0.613
1606	1-22	0.979	0.831
1607	1-20	0.974	0.770
1608	1-32	0.921	0.753
1614	1-33	0.969	0.829
1616	1-20	0.959	0.869
1625	1-39	0.983	0.621
1632	1-25	0.910	0.631
1636	1-33	0.897	0.591
1639	1-42	0.988	0.868
1645	1-20	0.927	0.568
1647	1-17	0.923	0.742
1648	1-22	0.998	0.980

TRADOCS:1416234.1(%CR%01!.DOC)

TABLE 6

TABLE 6					
SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	
	sequence			application	
1	1787	3573	5359	784CIP2_1	1103
2	1788	3574	5360	784CIP2_2	2673
3	1789	3575	5361	784CIP2_3	4117
4	1790	3576	5362	784CIP2_4	5556
5	1791	3577	5363	784CIP2_5	5562 5562
6	1792	3578	5364	784CIP2_6 784CIP2_7	5562
7	1793	3579	5365 5366	784CIP2_7 784CIP2_8	5562
8	1794	3580	1		5563
9	1795	3581	5367	784CIP2_9	5564
10	1796	3582	5368	784CIP2_10	5565
11	1797	3583	5369	784CIP2_11 784CIP2_12	5689
1.2	1798	3584	5370 5371	784CIP2_12 784CIP2_13	5729
13	1799	3585	5372	784CIP2_13	5745
14	1800	3586	5373	784CIP2_14 784CIP2_15	5777
15	1801 1802	3587 3588	5374	784CIP2_15	5777
16	1802	3588	5375	784CIP2_18	5789
18	1803	3589	5376	784CIP2_17	5792
19	1804	3590	5377	784CIP2_18	5804
20	1806	3592	5378	784CIP2 20	5805
21	1807	3593	5379	784CIP2 21	5805
22	1808	3594	5380	784CIP2 22	5844
23	1809	3595	5381	784CIP2 23	5844
24	1810	3596	5382	784CIP2 24	5850
25	1811	3597	5383	784CIP2 25	5867
26	1812	3598	5384	784CIP2 26	5973
27	1813	3599	5385	784CIP2 27	5995
28	1814	3600	5386	784CIP2 28	5995
29	1815	3601	5387	784CIP2 29	6005
30	1816	3602	5388	784CIP2 30	6007
31	1817	3603	5389	784CIP2 31	6007
32	1818	3604	5390	784CIP2 32	6009
33	1819	3605	5391	784CIP2 33	6012
34	1820	3606	5392	784CIP2 34	6015
35	1821	3607	5393	784CIP2 35	6016
36	1822	3608	5394	784CIP2 36	6016
37	1823	3609	5395	784CIP2_37	6018
38	1824	3610	5396	784CIP2_38	6018
39	1825	3611	5397	784CIP2_39	6018
40	1826	3612	5398	784CIP2_40	6023
41	1827	3613	5399	784CIP2_41	6070
42	1828	3614	5400	784CIP2_42	6081
43	1829	3615	5401	784CIP2_43	6089
44	1830	3616	5402	784CIP2_44	6118
45	1831	3617	5403	784CIP2_45	6118
46	1832	3618	5404	784CIP2_46	6130
47	1833	3619	5405	784CIP2_47	6177
48	1834	3620	5406	784CIP2_48	6189
49	1835	3621	5407	784CIP2_49	6191
50	1836	3622	5408	784CIP2_50	6204
51	1837	3623	5409	784CIP2_51 ·	6204
52	1838	3624	5410	784CIP2_52	6284
53	1839	3625	5411	784CIP2_53	6367
54	1840	3626	5412	784CIP2_54	6436
55	1841	3627	5413	784CIP2_55	6442
56	1842	3628	5414	784CIP2_56	6445
57	1843	3629	5415	784CIP2_57	6457
58	1844	3630	5416	784CIP2_58	6458
59	1845	3631	5417	784CIP2_59	6458

SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
of full-	NO: of	of contig	NO:	docket number_	NO:in
length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
sequence	peptide		sequence	priority	
	sequence			application	
60	1846	3632	5418	784CIP2_60	6462
61	1847	3633	5419	784CIP2_61	6472
62	1848	3634	5420	784CIP2_62	6499
63	1849	3635	5421	784CIP2_63	6 4 99
64	1850	3636	5422	784CIP2_64	6505
65	1851	3637	5423	784CIP2_65	6534
66	1852	3638	5424	784CIP2_66	6534
67	1853	3639	5425	784CIP2_67	6540
68	1854	3640	5426	784CIP2_68	6550
69	1855	3641	5427	784CIP2_69	6550
70	1856	3642	5428	784CIP2_70	6592
71	1857	3643	5429	784CIP2_71	6645
72 73	1858	3644	5430	784CIP2_72	6671
73	1859	3645	5431	784CIP2_73	6763
	1860	3646	5432	784CIP2_74	6763
75 76	1861	3647	5433	784CIP2_75	6786
76	1862 1863	3648	5434	784CIP2_76	6824
78		3649	5435	784CIP2_77	6830
79	1864	3650	5436	784CIP2_78	6831
80	1865 1866	3651 3652	5437	784CIP2_79	6832
81	1867	3652	5438 5439	784CIP2_80	6834
82	1868	3654	5439	784CIP2_81	6834 6835
83	1869	3655	5441	784CIP2_82 784CIP2_83	6835
84	1870	3656	5442	784CIP2_83	6843
85	1871	3657	5443	784CIP2_84	6859
86	1872	3658	5444	784CIP2_86	6915
87	1873	3659	5445	784CIP2_87	6932
88	1874	3660	5446	784CIP2_87	6957
89	1875	3661	5447	784CIP2 89	6961
90	1876	3662	5448	784CIP2 90	6973
91	1877	3663	5449	784CIP2 91	6973
92	1878	3664	5450	784CIP2 93	7007
93	1879	3665	5451	784CIP2 94	7018
94	1880	3666	5452	784CIP2 95	7019
95	1881	3667	5453	784CIP2 96	7020
96	1882	3668	5454	784CIP2 97	7020
97	1883	3669	5455	784CIP2 98	7021
98	1884	3670	5456	784CIP2 99	7023
99	1885	3671	5457	784CIP2 100	7027
100	1886	3672	5458	784CIP2 101	7028
101	1887	3673	5459	784CIP2 102	7029
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103	1889	3675	5461	784CIP2 104	7032
104	1890	3676	5462	784CIP2 105	7033
105	1891	3677	5463	784CIP2_106	7035
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107	1893	3679	5465	784CIP2_108	7039
108	1894	3680	5466	784CIP2_109	7043
109	1895	3681	5467	784CIP2_110	7044
110	1896	3682	5468	784CIP2 111	7046
111	1897	3683	5469	784CIP2_112	7054
112	1898	3684	5470	784CIP2 113	7061
113	1899	3685	5471	784CIP2_114	7077
114	1900	3686	5472	784CIP2 115	7092
115	1901	3687	5473	784CIP2 116	7094
116	1902	3688	5474	784CIP2 117	7106
117	1903	3689	5475	784CIP2 118	7107
	1904	3690	5476	784CIP2 119	7111
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	1904	3691	5477	784CIP2 120	7123
118					

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Sequence 1908 3694 5860 784CHP2 133 7154 123 1909 3695 5481 784CHP2 133 7169 124 1310 3695 5482 784CHP2 132 7169 125 1311 3697 5483 784CHP2 126 7185 126 1312 3698 5482 784CHP2 127 7197 126 1311 3699 5485 5482 784CHP2 127 7197 127 1313 3699 5485 5484 784CHP2 128 7219 128 1914 3760 5486 784CHP2 129 7226 129 1915 3701 5487 784CHP2 139 7226 130 1916 3702 5488 784CHP2 131 7234 1310 1916 3702 5488 784CHP2 131 7234 1312 1918 3704 5490 784CHP2 131 7235 1313 1917 3703 5489 784CHP2 131 7235 134 1920 3706 5491 784CHP2 131 7235 134 1920 3706 5492 784CHP2 135 7247 135 1921 3707 5493 784CHP2 135 7247 136 1922 3708 5494 784CHP2 137 7262 137 1921 3705 5495 784CHP2 137 7262 137 1921 3705 5495 784CHP2 137 7262 137 1921 3705 5495 784CHP2 137 7262 139 1392 3705 5495 784CHP2 137 7262 139 1392 3705 5495 784CHP2 137 7262 139 1392 3713 5495 784CHP2 137 7262 139 1392 3713 5495 784CHP2 137 7262 139 1392 3713 5495 784CHP2 141 7282 141 1327 3713 5495 784CHP2 141 7282 141 1327 3713 5495 784CHP2 141 7282 141 1327 3713 5500 784CHP2 144 7293 144 1930 3716 5500 784CHP2 144 7293 144 1930 3716 5500 784CHP2 148 7312 149	I		sequence		SEQ ID NO: in	09/488,725
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133			L		_	
134				l		
135						
136		L			1	
137						
138						
139	L				l 	L
140	L					
141	140				_	L
142	141					
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154 1940 3726 5512 784CIP2_155 7333 155 1941 3727 5513 784CIP2_156 7350 156 1942 3728 5514 784CIP2_157 7352 157 1943 3729 5515 784CIP2_158 7364 158 1944 3730 5516 784CIP2_159 7403 159 1945 3731 5517 784CIP2_160 7431 160 1946 3732 5518 784CIP2_161 7441 161 1947 3733 5519 784CIP2_162 7453 162 1948 3734 5520 784CIP2_163 7467 163 1949 3735 5521 784CIP2_164 7471 164 1950 3736 5522 784CIP2_165 7493 165 1951 3737 5523 784CIP2_165 7502 166 1952 3738 5524 784CIP2_167 7514						7330
155 1941 3727 5513 784CIP2_156 7350 156 1942 3728 5514 784CIP2_157 7352 157 1943 3729 5515 784CIP2_158 7364 158 1944 3730 5516 784CIP2_159 7403 159 1945 3731 5517 784CIP2_160 7431 160 1946 3732 5518 784CIP2_161 7441 161 1947 3733 5519 784CIP2_162 7453 162 1948 3734 5520 784CIP2_163 7467 163 1949 3735 5521 784CIP2_164 7471 164 1950 3736 5522 784CIP2_165 7493 165 1951 3737 5523 784CIP2_165 7493 165 1951 3737 5523 784CIP2_166 7502 166 1952 3738 5524 784CIP2_167 7511	1					
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169 1955 3741 5527 784CIP2_170 7541 170 1956 3742 5528 784CIP2_171 7570 171 1957 3743 5529 784CIP2_172 7578 172 1958 3744 5530 784CIP2_173 7583 173 1959 3745 5531 784CIP2_174 7592 174 1960 3746 5532 784CIP2_175 7601 175 1961 3747 5533 784CIP2_176 7602 176 1962 3748 5534 784CIP2_177 7608 177 1963 3749 5535 784CIP2_178 7615 178 1964 3750 5536 784CIP2_179 7617 179 1965 3751 5537 784CIP2_181 7624 180 1966 3752 5538 784CIP2_182 7626 181 1967 3753 5539 784CIP2_184 7640	168					
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173 1959 3745 5531 784CIP2_174 7592 174 1960 3746 5532 784CIP2_175 7601 175 1961 3747 5533 784CIP2_176 7602 176 1962 3748 5534 784CIP2_177 7608 177 1963 3749 5535 784CIP2_178 7615 178 1964 3750 5536 784CIP2_179 7617 179 1965 3751 5537 784CIP2_181 7624 180 1966 3752 5538 784CIP2_182 7626 181 1967 3753 5539 784CIP2_183 7640 182 1968 3754 5540 784CIP2_184 7641		1958	3744			
174 1960 3746 5532 784CIP2_175 7601 175 1961 3747 5533 784CIP2_176 7602 176 1962 3748 5534 784CIP2_177 7608 177 1963 3749 5535 784CIP2_178 7615 178 1964 3750 5536 784CIP2_179 7617 179 1965 3751 5537 784CIP2_181 7624 180 1966 3752 5538 784CIP2_182 7626 181 1967 3753 5539 784CIP2_183 7640 182 1968 3754 5540 784CIP2_184 7641		1	3745	5531	784CIP2_174	7592
176 1962 3748 5534 784CIP2_177 7608 177 1963 3749 5535 784CIP2_178 7615 178 1964 3750 5536 784CIP2_179 7617 179 1965 3751 5537 784CIP2_181 7624 180 1966 3752 5538 784CIP2_182 7626 181 1967 3753 5539 784CIP2_183 7640 182 1968 3754 5540 784CIP2_184 7641			3746	5532		
177 1963 3749 5535 784CIP2_178 7615 178 1964 3750 5536 784CIP2_179 7617 179 1965 3751 5537 784CIP2_181 7624 180 1966 3752 5538 784CIP2_182 7626 181 1967 3753 5539 784CIP2_183 7640 182 1968 3754 5540 784CIP2_184 7641	L	1961	3747	5533		
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179 1965 3751 5537 784CIP2_181 7624 180 1966 3752 5538 784CIP2_182 7626 181 1967 3753 5539 784CIP2_183 7640 182 1968 3754 5540 784CIP2_184 7641	L 1		3749	5535	784CIP2_178	7615
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nucleotide	length	sequence	peptide	SEQ ID NO: in	0.5.5.8.
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185	1971	3757	5543	784CIP2 187	7642
186	1972	3758	5544	784CIP2 188	7649
187	1973	3759	5545	784CIP2 189	7656
188	1974	3760	5546	784CIP2_189	7657
189	1975	3761	5547	784CIP2 191	7657
190	1976	3762	5548	784CIP2_191	
191	1977	3763	5549	784CIP2 193	7662 7668
192	1978	3764	5550	784CIP2_193	
193	1979	3765	5551	784CIP2_194 784CIP2_195	7673
194	1980	3766	5552		7690
195	1981	3767	5553		7700
196	1982	3768	5554	784CIP2_197	7709
197	1983	3769	5555	784CIP2_198	7736
198	1984	3770		784CIP2_199	7737
199	1985	3771	5556	784CIP2_200	7744
200	1986	3771	5557	784CIP2_201	7771
200	1986		5558	784CIP2_202	7786
201	1987	3773	5559	784CIP2_203	7791
202	1988	3774	5560	784CIP2_204	7797
203	1989	3775	5561	784CIP2_205	7806
205	1990	3776	5562	784CIP2_206	7812
206		3777	5563	784CIP2_207	7812
206	1992	3778	5564	784CIP2_208	7818
207	1993	3779	5565	784CIP2_209	7822
209	1994	3780	5566	784CIP2_210	7827
210	1995	3781	5567	784CIP2_211	7830
210	1996	3782	5568	784CIP2_212	7835
211	1997	3783	5569	784CIP2_214	7840
212	1998	3784	5570	784CIP2_215	7858
	1999	3785	5571	784CIP2_216	7858
214	2000	3786	5572	784CIP2_217	7861
215	2001	3787	5573	784CIP2_218	7866
216 217	2002	3788	5574	784CIP2_219	7868
	2003	3789	5575	784CIP2_220	7896
218	2004	3790	5576	784CIP2_221	7898
219	2005	3791	5577	784CIP2_222	7900
220	2006	3792	557B	784CIP2_223	7906
221	2007	3793	5579	784CIP2_224	7908
222	2008	3794	5580	784CIP2_225	7909
223	2009	3795	5581	784CIP2_226	7917
224	2010	3796	5582	784CIP2_227	7932
225	2011	3797	5583	784CIP2_228	7940
226	2012	3798	5584	784CIP2_229	7940
227	2013	3799	5585	784CIP2_230	7984
228	2014	3800	5586	784CIP2_231	7984
229	2015	3801	5587	784CIP2_232	8001
230	2016	3802	5588	784CIP2_233	8021
231	2017	3803	5589	784CIP2_234	8029
232	2018	3804	5590	784CIP2_235	8033
233	2019	3805	5591	784CIP2_236	8040
234	2020	3806	5592	784CIP2_237	8052
235	2021	3807	5593	784CIP2_238	8096
236	2022	3808	5594	784CIP2_239	8096
237	2023	3809	5595	784CIP2_240	8113
238	2024	3810	5596	784CIP2_241	8126
239	2025	3811	5597	784CIP2 242	8132
240	2026	3812	5598	784CIP2 243	8137
241	2027	3813	5599	784CIP2 244	8137
242	2028	3814	5600	784CIP2 245	8159
243	2029	3815	5601	784CIP2 246	8159
244	2030	3816	5602	784CIP2 247	8161
245	2031	3817	5603	784CIP2 248	8176

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length	full-	nucleotide	of contig	corresponding	U.S.S.N.
nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
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247 248	2033	3819	5605	784CIP2_250	8200
248	2034	3820	5606	784CIP2_251	8212
250	2035	3821	5607	784CIP2_252	8220
251	2036	3822	5608 5609	784CIP2_253	8238
252	2037	3824	5610	784CIP2_254 784CIP2_255	8254
253	2039	3825	5611	784CIP2_255 784CIP2_256	8255 8288
254	2040	3826	5612	784CIP2_256 784CIP2_257	8288
255	2041	3827	5613	784CIP2_257	8329
256	2042	3828	5614	784CIP2_238	8362
257	2043	3829	5615	784CIP2 260	8429
258	2044	3830	5616	784CIP2 261	8436
259	2045	3831	5617	784CIP2 262	8448
260	2046	3832	5618	784CIP2 263	8472
261	2047	3833	5619	784CIP2 264	8502
262	2048	3834	5620	784CIP2 265	8504
263	2049	3835	5621	784CIP2_266	8507
264	2050	3836	5622	784CIP2_268	8509
265	2051	3837	5623	784CIP2_269	8515
266	2052	3838	5624	784CIP2_270	8519
267	2053	3839	5625	784CIP2_271	8530
268	2054	3840	5626	784CIP2_272	8532
269	2055	3841	5627	784CIP2_273	8532
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271	2057	3843	5629	784CIP2_275	8541
272 273	2058 2059	3844	5630	784CIP2_276	8543
274	2060	3845 3846	5631 5632	784CIP2_277	8593
275	2061	3847	5633	784CIP2_278 784CIP2_279	8595
276	2062	3848	5634	784CIP2_2/9	8615 8620
277	2063	3849	5635	784CIP2_280	8621
278	2064	3850	5636	784CIP2 282	8623
279	2065	3851	5637	784CIP2 283	8625
280	2066	3852	5638	784CIP2 284	8628
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286	2072	3858	5644	784CIP2_290	8634
287	2073	3859	5645	784CIP2_291	8635
288	2074	3860	5646	784CIP2_292	8636
289 290	2075	3861	5647	784CIP2_293	8659
290	2076 2077	3862	5648	784CIP2_294	8660
292	2077	3863 3864	5649 5650	784CIP2_295	8667
293	2079	3865	5651	784CIP2_296 784CIP2_297	8667
294	2080	3866	5652	784CIP2_297 784CIP2_298	8685
295	2081	3867	5653	784CIP2_298 784CIP2_299	8805 8896
296	2082	3868	5654	784CIP2_299 784CIP2_300	8978
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298	2084	3870	5656	784CIP2_302	9048
299	2085	3871	5657	784CIP2 303	9116
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310	2096	3882	5668	784CIP2_313	9632
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312	2098	3884	5670	784CIP2_315	9664
313	2098	3885	5671	784CIP2_316	9691
314	2100	3886	5672	784CIP2_317	9700
315	2100	3887	5673	784CIP2_318	9716
316	2102	3888	5674	784CIP2_319	9721
317	2103	3889	5675	784CIP2 321	9870
318	2104	3890	5676	784CIP2 322	9887
319	2105	3891	5677	784CIP2_323	9923
320	2105	3892	5678	784CIP2_323	9938
321	2107	3893	5679	784CIP2 325	9964
322	2108	3894	5680	784CIP2_325	10007
323	2109	3895	5681	784CIP2 327	10007
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325	2111	3897	5683	784CIP2 329	10156
326	2112	3898	5684	784CIP2 330	10276
327	2113	3899	5685	784CIP2 331	10283
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329	2115	3901	5687	784CIP2B 2	167
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331	2117	3903	5689	784CIP2B 4	210
332	2118	3904	5690	784CIP2B 5	225
333	2119	3905	5691	784CIP2B 6	226
334	2120	3906	5692	784CIP2B 7	264
335	2121	3907	5693	784CIP2B 8	268
336	2122	3908	5694	784CIP2B_9	293
337	2123	3909	5695	784CIP2B_10	293
338	2124	3910	5696	784CIP2B_11	293
339	2125	3911	5697	784CIP2B_12	302
340	2126	3912	5698	784CIP2B_13	311
341	2127	3913	5699	784CIP2B_14	352
342	2128	3914	5700	784CIP2B_15	358
343	2129	3915	5701	784CIP2B_16	368
344	2130	3916	5702	784CIP2B_17	393
345	2131	3917	5703	784CIP2B_18	477
346	2132	3918	5704	784CIP2B_19	508
347	2133	3919	5705	784CIP2B_20	508
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349	2135	3921	5707	784CIP2B_22	578
350	2136	3922	5708	784CIP2B_23	588
351	2137	3923	5709	784CIP2B_24	591
352	2138	3924	5710	784CIP2B_25	593
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357	2143	3929	5715	784CIP2B_30	692
358	2144	3930	5716	784CIP2B_31	753
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360	2146	3932	5718	784CIP2B_33	787
361	2147	3933	5719	784CIP2B_34	833
362	2148	3934	5720	784CIP2B_35	838
363	2149	3935	5721	784CIP2B_36	870
364	2150	3936	5722	784CIP2B_37	891
365 366	2151	3937	5723	784CIP2B_38	891
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367 368	2153 2154	3939 3940	5725 5726	784CIP2B_40 784CIP2B 41	924 932

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373	2159	3945 3946	5732	784CIP2B_48	1023
374	2160	3946	5733	784CIP2B 48	1104
376	2161	3948	5734	784CIP2B 49	1114
377	2163	3949	5735	784CIP2B 50	1144
378	2164	3950	5736	784CIP2B 51	1262
379	2165	3951	5737	784CIP2B 52	1318
380	2166	3952	5738	784CIP2B 53	1319
381	2167	3953	5739	784CIP2B 54	1328
382	2168	3954	5740	784CIP2B_55	1436
383	2169	3955	5741	784CIP2B_56	1464
384	2170	3956	5742	784CIP2B_57	1584
385	2171	3957	5743	784CIP2B_58	1617
386	2172	3958	5744	784CIP2B_59	1724
387	2173	3959	5745	784CIP2B_60	1728
388	2174	3960	5746	784CIP2B_61	1772
389	2175	3961	5747	784CIP2B_62	1809
390	2176	3962	5748	784CIP2B_63	1868
391	2177	3963	5749	784CIP2B_64	1898
392	2178	3964	5750	784CIP2B_65 784CIP2B_66	1926 1965
393	2179	3965 3966	5751 5752	784CIP2B_66	1967
394	2180	3966	5753	784CIP2B 68	1995
396	2181	3968	5754	784CIP2B_69	2005.
396	2183	3969	5755	784CIP2B 70	2027
398	2184	3970	5756	784CIP2B 71	2055
399	2185	3971	. 5757	784CIP2B 72	2103
400	2186	3972	5758	784CIP2B 73	2106
401	2187	3973	5759	784CIP2B_74	2166
402	2188	3974	5760	784CIP2B_75	2175
403	2189	3975	5761	784CIP2B_76	2176
404	2190	3976	5762	784CIP2B_78	2236
405	2191	3977	5763	784CIP2B_79	2250
406	2192	3978	5764	784CIP2B_80	2300
407	2193	3979	5765	784CIP2B_81	2323
408	2194	3980	5766	784CIP2B_82	2340
409	2195	3981	5767	784CIP2B_83	2371
410	2196	3982	5768	784CIP2B_84 784CIP2B 85	2399 2411
411	2197	3983 3984	5769 5770	784CIP2B 86	2411
412		 	5771	784CIP2B_87	2430
413	2199	3985	5772	784CIP2B 88	2439
415	2200	3987	5773	784CIP2B 89	2447
416	2202	3988	5774	784CIP2B 90	2461
417	2203	3989	5775	784CIP2B_91	2487
418	2204	3990	5776	784CIP2B_92	2492
419	2205	3991	5777	784CIP2B_93	2512
420	2206	3992	5778	784CIP2B_94	2564
421	2207	3993	5779	784CIP2B_95	2678
422	2208	3994	5780	784CIP2B_96	2816
423	2209	3995	5781	784CIP2B_97	2818
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426	2212	3998	5784	784CIP2B_100	3137
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428	2214	4000	5786	784CIP2B_102	3160
429	2215	4001	5787	784CIP2B_103	3323 3360
430	2216	4002	5788 5789	784CIP2B_104 784CIP2B 105	3360
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nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
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	sequence			application	
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434	2220	4006	5792	784CIP2B_108	3442
435	2221	4007	5793	784CIP2B_109	3442
436	2222	4008	5794	784CIP2B_110	3444
437	2223	4009	5795	784CIP2B_111	3855
438	2224	4010	5796	784CIP2B_112	3863
439	2225	4011	5797	784CIP2B_113	4090
440	2226	4012	5798	784CIP2B_114	4105
441	2227	4013	5799	784CIP2B_115	4142
442	2228	4014	5800	784CIP2B_116	4142
443	2229	4015	5801	784CIP2B_117	4149
444	2230	4016	5802 5803	784CIP2B_118 784CIP2B 119	4196 4202
445	2231	4017	l		4274
446	2232	4018	5804 5805	784CIP2B_120 784CIP2B 121	4304
447	2233	4019	5805	784CIP2B_121 784CIP2B_122	4304
448	2234	4020	5806	784CIP2B_122 784CIP2B_123	4311
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451	2236	4022	5809	784CIP2B_124	4323
452	2238	4024	5810	784CIP2B 126	4332
453	2239	4025	5811	784CIP2B 127	4488
454	2240	4026	5812	784CIP2B 128	4588
455	2241	4027	5813	784CIP2B 129	5569
456	2242	4028	5814	784CIP2B 130	5573
457	2243	4029	5815	784CIP2B 131	5577
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459	2245	4031	5817	784CIP2B 133	5582
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465	2251	4037	5823	784CIP2B_139	5594
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468	2254	4040	5826	784CIP2B_142	5602
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470	2256	4042	5828	784CIP2B_144	5608
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473	2259	4045	5831	784CIP2B_147	5622
474	2260	4046	5832	784CIP2B_148	5623
475	2261	4047	5833	784CIP2B_149	5624
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477	2263	4049	5835	784CIP2B_151	5627
478	2264	4050	5836	784CIP2B_152	5628
479	. 2265	4051	5837	784CIP2B_153	5630
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482	2268	4054	5840	784CIP2B_156	5641
483	2269	4055	5841	784CIP2B_157	5643
484	2270	4056	5842	784CIP2B_158	5647
485	2271	4057	5843	784CIP2B_159	5649
486	2272	4058	5844	784CIP2B_160	5658
487	2273	4059	5845	784CIP2B_161	5659
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489	2275	4061	5847	784CIP2B_163	5672
490	2276	4062	5848	784CIP2B_164	5674
491	2277	4063	5849	784CIP2B_165	5678 5680
492	2278	4064	5850	784CIP2B_166	5684
493	2279	4065	5851	784CIP2B_167	7004

Of full- No. of full- Incledidge Incleded Inc	SEQ ID NO:	SEO ID	SEQ ID NO:	T CBO #5	Tall Time	
Length calculation calcu		_		SEQ ID	Priority	SEQ ID
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495 2281 4067 5853 784CIPZB 168 5686 496 2282 4068 5854 784CIPZB 167 5698 497 2283 4069 5855 784CIPZB 170 5698 498 2284 4070 5855 784CIPZB 171 5712 499 2285 4071 5857 784CIPZB 171 5712 500 2286 4072 5858 784CIPZB 174 5720 501 2287 4073 5855 784CIPZB 174 5720 501 2287 4073 5855 784CIPZB 174 5720 501 2287 4073 5855 784CIPZB 176 5730 502 2288 4074 5860 784CIPZB 176 5730 503 2289 4075 5861 784CIPZB 176 5730 504 2290 4076 5862 784CIPZB 178 5734 504 2290 4076 5862 784CIPZB 178 5734 505 2292 4078 5864 784CIPZB 178 5734 507 2293 4079 5863 784CIPZB 178 5734 508 2294 4080 5865 784CIPZB 180 5744 508 2295 4081 5867 784CIPZB 181 5744 508 2295 4081 5867 784CIPZB 181 5745 510 2296 4082 5868 784CIPZB 183 5749 511 2297 4081 5869 784CIPZB 183 5749 512 2298 4084 5870 784CIPZB 185 5750 513 2299 4086 5870 784CIPZB 185 5750 514 2300 4086 5871 784CIPZB 187 5761 515 2301 4087 5873 784CIPZB 187 5761 516 2302 4088 5873 784CIPZB 187 5761 517 2303 4089 5873 784CIPZB 189 5762 518 2301 4087 5873 784CIPZB 189 5762 519 2305 4091 5877 784CIPZB 199 5784 519 2305 4091 5877 784CIPZB 199 5784 520 2306 4092 5878 784CIPZB 199 5784 521 2307 4093 5879 784CIPZB 199 5784 522 2308 4094 5880 784CIPZB 199 5887 522 2308 4094 5880 784CIPZB 199 5784 523 2301 4096 5882 784CIPZB 199 5883 524 2311 4097 5883 784CIPZB 199 5883 525 2312 4098 5887 784CIPZB 199 5883 526 2312 4098 5881 784CIPZB 200 5883 526 2312 4098 5882 784CIPZB 201 5883 526 2312 4098 5881 784CIPZB 201 5883 527 2313 4095 5881 784CIPZB 201 5883 528	494		4066	5053	application	
496						
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Solid 2290						5730
Soc Soc				1	784CIP2B_177	5734
Social State				1	784CIP2B_178	5738
SOT 2293			4077	5863	784CIP2B 179	5739
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617	2403	4189	5975	784CIP2B 294	6149

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nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
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619	2405	4191	5977	784CIP2B_296	6159
620 621	2406	4192	5978	784CIP2B_297	6164
622	2407	4193	5979	784CIP2B_298	6167
623	2408	4194 4195	5980	784CIP2B_299	6172
624	2410		5981	784CIP2B_300	6173
625	2410	4196 4197	5982 5983	784CIP2B_301	6190
626	2412	4198	5984	784CIP2B_302	6194
627	2413	4199	5985	784CIP2B_303	6196
628	2414	4200	5986	784CIP2B_304 784CIP2B_305	6197
629	2415	4201	5987	784CIP2B 305	6198
630	2416	4202	5988	784CIP2B_308	6198
631	2417	4203	5989	784CIP2B_308	6214
632	2418	4204	5990	784CIP2B 310	6215 6219
633	2419	4205	5991	784CIP2B 311	6226
634	2420	4206	5992	784CIP2B 312	6229
635	2421	4207	5993	784CIP2B 313	6234
636	2422	4208	5994	784CIP2B 314	6237
637	2423	4209	5995	784CIP2B 315	6238
638	2424	4210	5996	784CIP2B 316	6239
639	2425	4211	5997	784CIP2B 317	6239
640	2426	4212	5998	784CIP2B 318	6239
641	2427	4213	5999	784CIP2B 319	6240
642	2428	4214	6000	784CIP2B_320	6244
643	2429	4215	6001	784CIP2B_321	6245
644	2430	4216	6002	784CIP2B_322	6250
645	2431	4217	6003	784CIP2B_323	6252
646	2432	4218	6004	784CIP2B_324	6252
647	2433	4219	6005	784CIP2B_325	6256
648 649	2434	4220	6006	784CIP2B_326	6260
650	2435 2436	4221	6007	784CIP2B_327	6261
651	2436	4222	6008	784CIP2B_328	6264
652	2438	4223 4224	6009	784CIP2B_329	6265
653	2439	4225	6010 6011	784CIP2B_330	6266
654	2440	4226	6012	784CIP2B_331 784CIP2B_332	6270
655	2441	4227	6013	784CIP2B_332	6271
656	2442	4228	6014	784CIP2B 334	627 4 6276
657	2443	4229	6015	784CIP2B_335	6281
658	2444	4230	6016	784CIP2B 337	6281
659	2445	4231	6017	784CIP2B 338	6288
660	2446	4232	6018	784CIP2B 339	6292
661	2447	4233	6019	784CIP2B_340	6294
662	2448	4234	6020	784CIP2B 343	6312
663	2449	4235	6021	784CIP2B 344	6312
664	2450	4236	6022	784CIP2B_345	6312
665	2451	4237	6023	784CIP2B_346	6322
666	2452	4238	6024	784CIP2B_347	6324
667	2453	4239	6025	784CIP2B 349	6329
668	2454	4240	6026	784CIP2B_350	6331
669	2455	4241	6027	784CIP2B_351	6333
670	2456	4242	6028	784CIP2B_352	6334
671	2457	4243	6029	784CIP2B_353	6337
672	2458	4244	6030	784CIP2B_354	6339
673 674	2459	4245	6031	784CIP2B_355	6346
675	2460	4246	6032	784CIP2B_356	6348
676	2461	4247	6033	784CIP2B_357	6348
677	2462	4248	6034	784CIP2B_358	6350
678	2463	4249	6035	784CIP2B_359	6351
679	2465	4250 4251	6036	784CIP2B_360	6355
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682	2468	4254	6040	784CIP2B 364	6371
683	2469	4255	6041	784CIP2B 365	6376
684	2470	4256	6042	784CIP2B 366	6379
685	2471	4257	6043	784CIP2B 367	6380
686	2472	4258	6044	784CIP2B 368	6381
687	2473	4259	6045	784CIP2B_369	6392
688	2474	4260	6046	784CIP2B_370	6395
689	2475	4261	6047	784CIP2B_371	6397
690	2476	4262	6048	784CIP2B_372	6400
691	2477	4263	6049	784CIP2B_373	6401
692	2478	4264	6050	784CIP2B_374	6411
693	2479	4265	6051	784CIP2B_375	6411
694	2480	4266	6052	784CIP2B_376	6411
695	2481	4267	6053	784CIP2B_377	6416
696	2482	4268	6054	784CIP2B_378	6418
697	2483	4269	6055	784CIP2B_379	. 6422
698	2484	4270	6056·	784CIP2B_380	6423
700	2485	4271	6057	784CIP2B_381	6426
700	2486	4272	6058	784CIP2B_382	6427
702	2487	4273	6059	784CIP2B_383	6428
702	2488 2489	4274	6060	784CIP2B_384	6429
703	2489	4275	6061	784CIP2B_385	6430
705	2490	4276	6062	784CIP2B_386	6432
706	2491	4277 4278	6063	784CIP2B_387	6432
707	2492	4278	6064 6065	784CIP2B_388	6438
708	2494	4279	6066	784CIP2B_389	6441
709	2495	4281	6067	784CIP2B_390	6446
710	2496	4282	6067	784CIP2B_391	6454
711	2497	4283	6069	784CIP2B_392 784CIP2B 394	6459
712	2498	4284	6070	784CIP2B_394 784CIP2B_395	6461
713	2499	4285	6071	784CIP2B_395	6468
714	2500	4286	6072	784CIP2B 396	6487
715	2501	4287	6073	784CIP2B 398	6491
716	2502	4288	6074	784CIP2B 399	6506
717	2503	4289	6075	784CIP2B 401	6514
718	2504	4290	6076	784CIP2B 402	6519
719	2505	4291	6077	784CIP2B 403	6521
720	2506	4292	6078	784CIP2B 404	6532
721	2507	4293	6079	784CIP2B 405	6536
722	2508	4294	6080	784CIP2B 406	6543
723	2509	4295	6081	784CIP2B 407	6544
724	2510	4296	6082	784CIP2B 408	6548
725	2511	4297	6083	784CIP2B 409	6551
726	2512	4298	6084	784CIP2B 410	6551
727	2513	4299	6085	784CIP2B_411	6552
728	2514	4300	6086	784CIP2B_412	6554
729	2515	4301	6087	784CIP2B 413	6556
730	2516	4302	6088	784CIP2B 414	6560
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732	2518	4304	6090	784CIP2B_416	6564
733	2519	4305	6091	784CIP2B_417	6567
734	2520	4306	6092	784CIP2B 418	6573
735	2521	4307	6093	784CIP2B 419	6575
736	2522	4308	6094	784CIP2B 420	6577
737	2523	4309	6095	784CIP2B 421	6593
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739	2525	4311	6097	784CIP2B_423	6599
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744	2530	4316	6102	784CIP2B_428	6631
745	2531	4317	6103	784CIP2B_429	6632
746	2532	4318	6104	784CIP2B_430	6633
747	2533	4319	6105	784CIP2B_431	6634
748	2534	4320	6106	784CIP2B_432	6638
749	2535	4321	6107	784CIP2B_433	6641
750	2536	4322	6108	784CIP2B_434	6644
751	2537	4323	6109	784CIP2B_435	6646
752	2538	4324	6110	784CIP2B_436	6648
753	2539	4325	6111	784CIP2B_437	6652
754	2540	4326	6112	784CIP2B_438	6654
755	2541	4327	6113	784CIP2B_439	6657
756	2542	4328	6114	784CIP2B_440	6658
757	2543	4329	6115	784CIP2B_441	6663
758	2544	4330	6116	784CIP2B_442	6664
759	2545	4331	6117	784CIP2B_443	6668
760	2546	4332	6118	784CIP2B_444	6669
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763	2549	4335	6121	784CIP2B_447	6687
764	2550	4336	6122	784CIP2B_448 784CIP2B_449	6689
765	2551	4337	6123	784CIP2B_449	6698
766	2552	4338	6125	784CIP2B_450	6699
767	2553	4339	6126	784CIP2B 451	6705
768	2554	4340	6127	784CIP2B 452	6711
769	2555	4341	6128	784CIP2B 453	6713
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772	2557 2558	4344	6130	784CIP2B_455	6725
773	2559	4345	6131	784CIP2B 457	6726
774	2560	4346	6132	784CIP2B_437	6727
775	2561	4346	6133	784CIP2B_458	6730
776	2562	4348	6134	784CIP2B 460	6730
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782	2568	4354	6140	784CIP2B 466	6751
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785	2571	4357	6143	784CIP2B 469	6761
786	2572	4358	6144	784CIP2B_470	6765
787	2573	4359	6145	784CIP2B_471	6768
788	2574	4360	6146	784CIP2B 472	6773
789	2575	4361	6147	784CIP2B_473	6776
790	2576	4362	6148	784CIP2B_474	6796
791	2577	4363	6149	784CIP2B_475	6798
792	.2578	4364	6150	784CIP2B 476	6823
793	2579	4365	6151	784CIP2B 477	6825
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795	2581	4367	6153	784CIP2B 479	6839
796	2582	4368	6154	784CIP2B 480	6844
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798	2584	4370	6156	784CIP2B 483	6854
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799	2585	4371	6157	784CIP2B 484) 605/
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SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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808	2594	4380	6166	784CIP2B_493	6894
809	2595	4381	6167	784CIP2B_494	6901
810	2596	4382	6168	784CIP2B_495	6904
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812	2598	4384	6170	784CIP2B_497	6914
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814	2600	4386	6172	784CIP2B_499	6923
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816	2602	4388	6174	784CIP2B_501	6931
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830	2616	4402	6188	784CIP2B_515	6996
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837		4408	6194	784CIP2B_521	7025
838	2623	4409	6195	784CIP2B_522	7050
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852	2638	4424	6210	784CIP2B_536 784CIP2B_537	7104
853	2639	4425	6212	784CIP2B_537	7105
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855	2641	4427	6213	784CIP2B_539	7109
856	2642	4428	6214	784CIP2B_540	7119
857	2643	4429	6215	784CIP2B 542	7119
858	2644	4430	6216	784CIP2B_542 784CIP2B_543	
859	2645	4431	6217	784CIP2B 544	7121 7126
860	2646	4432	6218	784CIP2B 544 784CIP2B 545	
861	2647	4433	6219		7127
862	2648	4434	6220		7130
863	2649	4435	6221		7131
864	2650	4436	6222	784CIP2B_548 784CIP2B_549	7144
865	2651	4437	6223	784CIP2B 550	7163
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SEO ID NO:	SEO ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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nucleotide	length	sequence	peptide	SEQ ID NO: in	09/488,725
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869	2655	4441	6227	784CIP2B_554	7190
870	2656	4442	6228	784CIP2B_555	7191
871	2657	4443	6229	784CIP2B_556	7203
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878	2664	4450	6236	784CIP2B_563	7230
879	2665	4451	6237	784CIP2B_564	7237
880	2666	4452	6238	784CIP2B_565	7240
881	2667	4453	6239	784CIP2B_566	7245
882	2668	4454	6240	784CIP2B_567	7250
883	2669	4455	6241	784CIP2B_568 784CIP2B_569	7251 7255
884	2670	4456	6242		7255
885	2671	4457	6243		7265
886	2672	4458	6244	784CIP2B_571 784CIP2B_572	7268
887	2673	4459	6245	784CIP2B_572	7275
888	2674	4460	6246	784CIP2B 573	7279
889	2675	4461	6248	784CIP2B 575	72 83
890	2676	4462	6248	784CIP2B_575	7283
891	2677	4463	6250	784CIP2B_577	7287
892	2678 2679	4464	6251	784CIP2B_377	7301
893	2680	4466	6252	784CIP2B_578	7308
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896	2682	4468	6254	784CIP2B 581	7309
897	2683	4469	6255	784CIP2B 582	7319
898	2684	4470	6256	784CIP2B 583	7320
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901	2687	4473	6259	784CIP2B 586	7334
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906	2692	4478	6264	784CIP2B 591	7363
907	2693	4479	6265	784CIP2B_592	7363
908	2694	4480	6266	784CIP2B_593	7365
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911	2697	4483	6269	784CIP2B_596	7372
912	2698	4484	6270	784CIP2B_599	7375
913	2699	4485	6271	784CIP2B_600	7381
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920	2706	4492	6278	784CIP2B_607	7399
921	2707	4493	6279	784CIP2B_608	7405
922	2708	4494	6280	784CIP2B_609	7406
923	2709	4495	6281	784CIP2B_610	7406
924	2710	4496	6282	784CIP2B_611	7409
	2711	4497	6283	784CIP2B 612	7410
925	2711	1 332,		· · · · · · · -	
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SEQ ID NO:	SEQ ID	SEQ ID NO:	SEQ ID	Priority	SEQ ID
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1181	2967	4753	6539	784CIP2B_870	8236
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1246	3032	4818	6604	784CIP2B 936	8419
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1248	3034	4820	6606	784CIP2B 938	8430
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1257	3043	4829	6615	784CIP2B 947	8451
1258	3044	4830	6616	784CIP2B 948	
1259	3045	4831	6617	784CIP2B_948	8452
1260	3046	4832	6618	784CIP2B_949	8460
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1262	3048	4834	6620	784CIP2B 952	
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1264	3050	4836	6622	784CIP2B_953	8465
1265	3051	4837	6623	784CIP2B_955	8467
1266	3052	4838	6624	784CIP2B 956	8470 8471
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1269	3055	4841	6627	784CIP2B 959	8475
1270	3056	4842	6628	784CIP2B_959	
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1274	3060	4846	6632	784CIP2B_963	8482 8486
1275	3061	4847	6633	784CIP2B 965	
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1277	3063	4849	6635		8492
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1285	3071		6642	784CIP2B_974	8531
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1287	3073	4858	6644	784CIP2B_976	8542
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	sequence			application	
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1308	3094	4880	6666	784CIP2B 998	8665
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1312	3098	4884	6670	784CIP2B_1002	8692
1313	3099	4885	6671	784CIP2B_1003	8706
1314	3100	4886	6672	784CIP2B_1004	8716
1315	3101	4887	6673	784CIP2B_1005	8719
1316	3102	4888	6674	784CIP2B_1006	8743
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1324	3110	4896	6682	784CIP2B_1013	8842
1325	3111	4897	6683	784CIP2B 1015	8842
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1327	3113	4899	6685	784CIP2B 1017	8871
1328	3114	4900	6686	784CIP2B 1018	8921
1329	3115	4901	6687	784CIP2B 1019	8927
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1331	3117	4903	6689	784CIP2B_1021	8994
1332	3118	4904	6690	784CIP2B_1022	9023
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1334	3120	4906	6692	784CIP2B_1024	9058
1335	3121	4907	6693	784CIP2B_1025	9058
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1338	3123	4910	6695	784CIP2B 1027 784CIP2B 1028	9079 9082
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1343	3129	4915	6701	784CIP2B_1033	9105
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1347	3133	4919	6705	784CIP2B_1037	9174
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1356	3141 3142	4927 4928	6713 6714	784CIP2B_1045	9379
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1359	3145	4931	6717	784CIP2B_1048	9500
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1374	3160	4946	6732	784CIP2B 1064	9646
1375	3161	4947	6733	784CIP2B 1065	9747
1376	3162	4948	6734	784CIP2B 1066	9773
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1378	3164	4950	6736	784CIP2B 1068	9801
1379	3165	4951	6737	784CIP2B 1069	9811
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1382	3168	4954	6740	784CIP2B 1072	9854
1383	3169	4955	6741	784CIP2B 1073	9864
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1385	3171	4957	6743	784CIP2B 1075	9871
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1413	3199	4985	6772	784CIP2C 1	33
1414	3200	4986	6773	784CIP2C_2	271
1415	3201	4987	l	784CIP2C_2 784CIP2C_3	848
1416	3202	4988	6774	784CIP2C 4	849
1417	3203	4989	6775		
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1419	3205	4991	6777	784CIP2C_6	953
1420	3206	4992	6778	784CIP2C_7	980
1421	3207	4993	6779	784CIP2C_8	1595
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1431	3217	5003	6789	784CIP2C 18	2905
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1440	3226	5012	6798	784CIP2C 27	2993
1441	3227	5013	6799	784CIP2C 28	2993
1442	3228	5014	6800	784CIP2C 29	3017
1443	3229	5015	6801	784CIP2C 30	3046
1444	3230	5016	6802	784CIP2C 31	3050
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1446	3232	5018	6804	784CIP2C 33	3359
1447	3233	5019	6805	784CIP2C 34	3432
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1449	3235	5021	6807	784CIP2C 36	3439
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1472	3258	5044	6830	784CIP2C 61	3553
1473	3259	5045	6831	784CIP2C_62	3564
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1476	3262	5048	6834	784CIP2C 65	3573
1477	3263	5049	6835	784CIP2C 66	3574
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1479	3265	5051	6837	784CIP2C 68	3615
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1515		4	I			<u> </u>
1616		1	1	· · · · · · · · · · · · · · · · · · ·		
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1653 3439 5225 7011 784CIP2D 1 746 1654 3440 5226 7012 784CIP2D 2 3558 1655 3441 5227 7013 784CIP2D 3 3558 1656 3442 5228 7014 784CIP2D 4 3633 1657 3443 5229 7015 784CIP2D 5 3658 1658 3444 5230 7016 784CIP2D 6 3732 1659 3445 5231 7017 784CIP2D 7 4004 1660 3446 5232 7018 784CIP2D 8 4700 1661 3447 5233 7019 784CIP2D 9 4703 1662 3448 5234 7020 784CIP2D 10 4774 1663 3449 5235 7021 784CIP2D 11 4894 1664 3450 5236 7022 784CIP2D 11 4894 1665 3451 5237 7023 784CIP2D 12 4918 1665 3451 5237 7023 784CIP2D 13 5159 1666 3452 5238 7024 784CIP2D 14 7443 1667 3453 5239 7025 784CIP2D 15 8673 1668 3454 5240 7026 784CIP2D 16 8679 1669 3455 5241 7027 784CIP2D 16 8679 1669 3455 5242 7028 784CIP2D 17 8727) · · · · · · · · · · · · · · · · · · ·
1654 3440 5226 7012 784CIP2D_2 3558 1655 3441 5227 7013 784CIP2D_3 3558 1656 3442 5228 7014 784CIP2D_4 3633 1657 3443 5229 7015 784CIP2D_5 3658 1658 3444 5230 7016 784CIP2D_6 3732 1659 3445 5231 7017 784CIP2D_7 4004 1660 3446 5232 7018 784CIP2D_7 4004 1661 3447 5233 7019 784CIP2D_9 4703 1662 3448 5234 7020 784CIP2D_9 4703 1663 3449 5235 7021 784CIP2D_11 4894 1664 3450 5236 7022 784CIP2D_12 4918 1665 3451 5237 7023 784CIP2D_13 5159 1666 3452 5238 7024 784CIP2D_14 7443					_	
1655 3441 5227 7013 784CIP2D 3 3558 1656 3442 5228 7014 784CIP2D 4 3633 1657 3443 5229 7015 784CIP2D 5 3658 1658 3444 5230 7016 784CIP2D 6 3732 1659 3445 5231 7017 784CIP2D 7 4004 1660 3446 5232 7018 784CIP2D 8 4700 1661 3447 5233 7019 784CIP2D 9 4703 1662 3448 5234 7020 784CIP2D 10 4774 1663 3449 5235 7021 784CIP2D 11 4894 1664 3450 5236 7022 784CIP2D 12 4918 1665 3451 5237 7023 784CIP2D 13 5159 1666 3452 5238 7024 784CIP2D 14 7443 1667 3453 5239 7025 784CIP2D 15 8673 <td></td> <td></td> <td></td> <td></td> <td></td> <td>L</td>						L
1656 3442 5228 7014 784CIP2D_4 3633 1657 3443 5229 7015 784CIP2D_5 3658 1658 3444 5230 7016 784CIP2D_6 3732 1659 3445 5231 7017 784CIP2D_7 4004 1660 3446 5232 7018 784CIP2D_8 4700 1661 3447 5233 7019 784CIP2D_9 4703 1662 3448 5234 7020 784CIP2D_10 4774 1663 3449 5235 7021 784CIP2D_11 4894 1664 3450 5236 7022 784CIP2D_12 4918 1665 3451 5237 7023 784CIP2D_13 5159 1666 3452 5238 7024 784CIP2D_14 7443 1667 3453 5239 7025 784CIP2D_15 8673 1668 3454 5240 7026 784CIP2D_16 8679 </td <td></td> <td></td> <td></td> <td></td> <td>4</td> <td>L</td>					4	L
1657 3443 5229 7015 784CIP2D_5 3658 1658 3444 5230 7016 784CIP2D_6 3732 1659 3445 5231 7017 784CIP2D_7 4004 1660 3446 5232 7018 784CIP2D_8 4700 1661 3447 5233 7019 784CIP2D_9 4703 1662 3448 5234 7020 784CIP2D_10 4774 1663 3449 5235 7021 784CIP2D_11 4894 1664 3450 5236 7022 784CIP2D_12 4918 1665 3451 5237 7023 784CIP2D_13 5159 1666 3452 5238 7024 784CIP2D_14 7443 1667 3453 5239 7025 784CIP2D_15 8673 1668 3454 5240 7026 784CIP2D_16 8679 1669 3455 5241 7027 784CIP2D_18 8734 <					<u> </u>	
1658 3444 5230 7016 784CIP2D_6 3732 1659 3445 5231 7017 784CIP2D_7 4004 1660 3446 5232 7018 784CIP2D_8 4700 1661 3447 5233 7019 784CIP2D_9 4703 1662 3448 5234 7020 784CIP2D_10 4774 1663 3449 5235 7021 784CIP2D_11 4894 1664 3450 5236 7022 784CIP2D_12 4918 1665 3451 5237 7023 784CIP2D_13 5159 1666 3452 5238 7024 784CIP2D_14 7443 1667 3453 5239 7025 784CIP2D_15 8673 1668 3454 5240 7026 784CIP2D_16 8679 1669 3455 5241 7027 784CIP2D_17 8727 1670 3456 5242 7028 784CIP2D_18 8734					<u> </u>	
1659 3445 5231 7017 784CIP2D_7 4004 1660 3446 5232 7018 784CIP2D_8 4700 1661 3447 5233 7019 784CIP2D_9 4703 1662 3448 5234 7020 784CIP2D_10 4774 1663 3449 5235 7021 784CIP2D_11 4894 1664 3450 5236 7022 784CIP2D_12 4918 1665 3451 5237 7023 784CIP2D_13 5159 1666 3452 5238 7024 784CIP2D_14 7443 1667 3453 5239 7025 784CIP2D_15 8673 1668 3454 5240 7026 784CIP2D_16 8679 1669 3455 5241 7027 784CIP2D_17 8727 1670 3456 5242 7028 784CIP2D_18 8734			I			1
1660 3446 5232 7018 784CIP2D_8 4700 1661 3447 5233 7019 784CIP2D_9 4703 1662 3448 5234 7020 784CIP2D_10 4774 1663 3449 5235 7021 784CIP2D_11 4894 1664 3450 5236 7022 784CIP2D_12 4918 1665 3451 5237 7023 784CIP2D_13 5159 1666 3452 5238 7024 784CIP2D_14 7443 1667 3453 5239 7025 784CIP2D_15 8673 1668 3454 5240 7026 784CIP2D_16 8679 1669 3455 5241 7027 784CIP2D_17 8727 1670 3456 5242 7028 784CIP2D_18 8734		l	5231			4004
1661 3447 5233 7019 784CIP2D_9 4703 1662 3448 5234 7020 784CIP2D_10 4774 1663 3449 5235 7021 784CIP2D_11 4894 1664 3450 5236 7022 784CIP2D_12 4918 1665 3451 5237 7023 784CIP2D_13 5159 1666 3452 5238 7024 784CIP2D_14 7443 1667 3453 5239 7025 784CIP2D_15 8673 1668 3454 5240 7026 784CIP2D_16 8679 1669 3455 5241 7027 784CIP2D_17 8727 1670 3456 5242 7028 784CIP2D_18 8734	L			1		4700
1663 3449 5235 7021 784CIP2D 11 4894 1664 3450 5236 7022 784CIP2D 12 4918 1665 3451 5237 7023 784CIP2D 13 5159 1666 3452 5238 7024 784CIP2D 14 7443 1667 3453 5239 7025 784CIP2D 15 8673 1668 3454 5240 7026 784CIP2D 16 8679 1669 3455 5241 7027 784CIP2D 17 8727 1670 3456 5242 7028 784CIP2D 18 8734		3447	5233	7019	784CIP2D_9	4703
1664 3450 . 5236 7022 784CIP2D_12 4918 1665 3451 5237 7023 784CIP2D_13 5159 1666 3452 5238 7024 784CIP2D_14 7443 1667 3453 5239 7025 784CIP2D_15 8673 1668 3454 5240 7026 784CIP2D_16 8679 1669 3455 5241 7027 784CIP2D_17 8727 1670 3456 5242 7028 784CIP2D_18 8734	1662	3448	5234	7020	784CIP2D_10	4774
1665 3451 5237 7023 784CIP2D 13 5159 1666 3452 5238 7024 784CIP2D 14 7443 1667 3453 5239 7025 784CIP2D 15 8673 1668 3454 5240 7026 784CIP2D 16 8679 1669 3455 5241 7027 784CIP2D 17 8727 1670 3456 5242 7028 784CIP2D 18 8734	1663	3449	5235	7021	784CIP2D_11	4894
1666 3452 5238 7024 784CIP2D 14 7443 1667 3453 5239 7025 784CIP2D 15 8673 1668 3454 5240 7026 784CIP2D 16 8679 1669 3455 5241 7027 784CIP2D 17 8727 1670 3456 5242 7028 784CIP2D 18 8734	1664	3450	- 5236	7022	784CIP2D_12	4918
1667 3453 5239 7025 784CIP2D 15 8673 1668 3454 5240 7026 784CIP2D 16 8679 1669 3455 5241 7027 784CIP2D 17 8727 1670 3456 5242 7028 784CIP2D 18 8734	1665	3451	5237	7023	784CIP2D_13	5159
1668 3454 5240 7026 784CIP2D 16 8679 1669 3455 5241 7027 784CIP2D 17 8727 1670 3456 5242 7028 784CIP2D 18 8734	1666	3452	5238	7024	784CIP2D_14	7443
1669 3455 5241 7027 784CIP2D 17 8727 1670 3456 5242 7028 784CIP2D 18 8734	1667	3453	5239	7025	784CIP2D_15	L
1670 3456 5242 7028 784CIP2D 18 8734	1668	3454	5240	7026	784CIP2D_16	
	1669	3455	5241			L
1671 3457 5243 7029 784CIP2D_19 8756			l .	1		1
	1671	3457	5243	7029	784CIP2D_19	8756

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1673	3459	5245	7031	784CIP2D 21	8844
1674	3460	5246	7032	784CIP2D 22	8846
1675	3461	5247	7033	784CIP2D 23	8912
1676	3462	5248	7034	784CIP2D 24	8918
1677	3463	5249	7035	784CIP2D 25	8918
1678	3464	5250	7036	784CIP2D 26	8941
1679	3465	5251	7037	784CIP2D 27	8941
1680	3466	5252	7038	784CIP2D 28	8951
1681	3467	5253	7039	784CIP2D 29	8951
1682	3468	5254	7040	784CIP2D 30	9007
1683	3469	5255	7041	784CIP2D 31	9012
1684	3470	5256	7042	784CIP2D 32	9013
1685	3471	5257	7043	784CIP2D 33	9025
1686	3472	5258	7044	784CIP2D 34	9053
1687	3473	5259	7045	784CIP2D 35	9054
1688	3474	5260	7046	784CIP2D 36	9054
1689	3475	5261	7047	784CIP2D 37	9113
1690	3476	5262	7048	784CIP2D 38	9113
1691	3477	5263	7049	784CIP2D_38	9152
1692	3478	5264	7050	784CIP2D 40	9152
1693	3479	5265	7051	784CIP2D_40	9211
1694	3480	5266	7052	784CIP2D 42	9223
1695	3481	5267	7053	784CIP2D_42 784CIP2D_43	9223
1696	3482	5268	7054	784CIP2D_43	9231
1697	3483	5269	7055	784CIP2D_44	9236
1698	3484	5270	7056	784CIP2D 46	9236
1699	3485	5271	7057	784CIP2D_46	9303
1700	3486	5272	7058	784CIP2D 47	9309
1701	3487	5273	7059	784CIP2D_48	9314
1702	3488	5274	7060	784CIP2D 50	9326
1703	3489	5275	7061	784CIP2D_50	9339
1704	3490	5276	7062	784CIP2D 52	9348
1705	3491	5277	7063	784CIP2D_52	9376
1706	3492	5278	7064	784CIP2D 54	9382
1707	3493	5279	7065	784CIP2D 55	9407
1708	3494	5280	7066	784CIP2D_55	9414
1709	3495	5281	7067	784CIP2D_56	9439
1710	3496	5282	7068	784CIP2D 58	9485
1711	3497	5283	7069	784CIP2D 59	9493
1712	3498	5284	7070	784CIP2D_59	9501
1713	3499	5285	7071	784CIP2D_60	9526
1714	3500	5286	7072	784CIP2D_61	9526
1715	3501	5287	7072	784CIP2D_62 784CIP2D_63	
1716	3502	5288	7074	784CIP2D 64	9551 9557
1717	3503	5289	7075	784CIP2D_64	9568
1718	3504	5290	7076	784CIP2D_65	
1719	3505	5291	7077	784CIP2D_66	9588
1720	3506	5292	7078	784CIP2D_67	9597
1721	3507	5293	7079	784CIP2D_68 784CIP2D_69	9615
1722	3508	5294	7079		9628
1723	3509	5295		784CIP2D_70	9649
1724	3510	5295	7081	784CIP2D_71	9652
1725	3510		7082	784CIP2D_72	9660
1726	3511	5297	7083	784CIP2D_73	9662
1727	3512	5298	7084	784CIP2D_74	9725
1727		5299	7085	784CIP2D_75	9746
	3514	5300	7086	784CIP2D_76	9777
1729	3515	5301	7087	784CIP2D_77	9787
1730	3516	5302	7088	784CIP2D_78	9790
7777	7 5 2 2				
1731	3517	5303	7089	784CIP2D_79	9842
1731 1732 1733	3517 3518 3519	5303 5304 5305	7089 7090 7091	784CIP2D_79 784CIP2D_80 784CIP2D_81	9842 9842 9848

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1735	3521	5307	7093	784CIP2D 83	10010
1736	3522	5308	7094	784CIP2D 84	10010
1737	3523	5309	7095	784CIP2D 85	_l
1738	3524	5310	7096		10052
1739	3525	5311	7097		10057
1740	3526	5311	1	784CIP2D_87	10085
	1	I	7098	784CIP2D_89	10139
1741	3527	5313	7099	784CIP2D_90	10142
1742	3528	5314	7100	784CIP2D_92	10165
1743	3529	5315	7101	784CIP2D_93	10173
1744	3530	5316	7102	784CIP2D_94	10173
1745	3531	5317	7103	784CIP2D_95	10273
1746	3532	5318	7104	784CIP2E_1	3121
1747	3533	5319	7105	784CIP2E 2	3628
1748	3534	5320	7106	784CIP2E 4	3673
1749	3535	5321	7107	784CIP2E 5	4018
1750	3536	5322	7108	784CIP2E 6	4467
1751	3537	5323	7109	784CIP2E 7	4865
1752	3538	5324	7110	784CIP2E 8	4916
1753	3539	5325	7111	784CIP2E 9	4923
1754	3540	5326	7112	784CIP2E 10	4926
1755	3541	5327	7113	784CIP2E 11	4962
1756	3542	5328	7114	784CIP2B 12	4963
1757	3543	5329	7115	784CIP2B 13	4964
1758	3544	5330	7116	784CIP2E 14	4988
1759	3545	5331	7117	784CIP2E 15	5835
1760	3546	5332	7118	784CIP2E 16	7682
1761	3547	5333	7119	784CIP2E_18	7682
1762	3548	5334	7120	784CIP2E 18	7699
1763	3549	5335	7121	784CIP2E_18	I
1764	3550	5336	7121		7707
1765	3551	5337		784CIP2E_20	7707
1766	3552	5338	7123	784CIP2E_21	7752
1767	3553		7124	784CIP2E_22	8357
		5339	7125	784CIP2E_23	9065
1768	3554	5340	7126	784CIP2E_24	9324
L	3555	5341	7127	784CIP2F_1	2976
1770	3556	5342	7128	784CIP2F_2	3559
1771	3557	5343	7129	784CIP2F_3	4021
1772	3558	5344	7130	784CIP2F_4	4474
1773	3559	5345	7131	784CIP2F_5	4566
1774	3560	5346	7132	784CIP2F_6	4705
1775	3561	5347	7133	784CIP2F_7	4707
1776	3562	5348	7134	784CIP2F_8	4712
1777	3563	5349	7135	784CIP2F_9	5008
1778	3564	5350	7136	784CIP2F_10	5009
1779	3565	5351	7137	784CIP2F_11	5015
1780	3566	5352	7138	784CIP2F 12	5015
1781	3567	5353	7139	784CIP2F 13	7724
1782	3568	5354	7140	784CIP2F 14	7725
1783	3569	5355	7141	784CIP2F 15	8828
1784	3570	5356	7142	784CIP2F 16	8830
1785	3571	5357	7143	784CIP2F 17	9739
1786	3572	5358	7144	784CIP2F 18	9896
			/ 4 7 7	104C1F2F_10	7070

TRADOCS:1416247.1(%C\$7011.DOC)

TABLE 7

IA	BLE 7		
SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
140.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
J	corresponding	to first	L=Leucine; M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	1	sequence	
	sequence		\=possible nucleotide insertion)
5359	337	1131	AHLSARLSALILDEVAILPAPONLSVLSTNMKHLLMWSPVIAPG
Ì	į.	1	ETVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDVTDDITA
	}	1	TVPYNLRVRATLGSQTS/CLEHP/VSIPLIETQPSLPDL/RMEI
1	Į.	ļ	TKDGFHLVIELEDLGPOFEFLVAYWRREPGAEEHVKMVRSGGIP
	1	ĺ	
	}	1	VHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVEVQGEAIPL
}	1	1	VLALFAFVGFMLILVVVPLFVWKMGRLLQ/YLLLPRGGSSQTPW
1		{	KITOF
5360	2	1115	PRVRSSGGQEDPASQQWARPRFTQPSKMRRRVIARPVGSSVRLK
3360	1 2	1 1113	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
į.		į	CVASGHPRPDITWMKDDQALTRPEAAEPRKKKWTLSLKNLRPED
ļ.		1	SGKYTCRVSNRAGAINATYKVDVIQRTRSKPVLTGTHPVNTTVD
	1		FGGTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKF
	ļ	1	VVLPTGDVWSRPDGSYLNKLLITRARQDDAGNYICLGANTMGYS
1	ł	i	FRSAFLTVLPDPKPPGPPVASSSSATSLPWPVVIGIPAGAVFIL
1]	1	
		1	GTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLPSL
l		1	AALSAGPGVGLCEEHGSPAAPQHLLGPGPVAGPKLYPKLYTGHS
		1	TPHTYTHPPPSCQLNSSHS
5361	3	925	HEGSISSANILLDDOFOPKLTDFAMAHFRSHLEHQSCTINMTSS
3301		1	SSKHLWYMPEEYIRQGKLSIKTDVYSFGIVIMEVLTGCRVVLDD
		1	
	i		PKHIQLRDLLRELMEKRGLDSCLSFLDKKVPPCPRNFSAKLFCL
	}	ł	AGRCAATRAKLRPSMDEVLNTLESTQASLYFAEDPPTSLKSFRC
			PSPLFLENVPSIPVEDDESQNNNLLPSDEGLRIDRMTQKTPFEC
			SOSEVMFLSLDKKPESKRNEEACNMPSSSCEESWFPKYIVPSOD
	ì	ì	LRPYKVNIDPSSEAPGHSCRSRPVESSCSSKFSWDEYEQYKKE
	 	4879	SCOVEGCTRTYNSSOSIGKHMKTAHPDQYAAFKMQRKSKKGQKA
5362	2	4879	
	1	1	NNLNTPNNGKFVYFLPSPVNSSNPFFTSQTKANGNPACSAQLQH
1	i		VSPPIFPAHLASVSTPLLSSMESVINPNITSQDKNEQGGMLCSQ
İ			MENLPSTALPAQMEDLTKTVLPLNIDRGSDPFLSLPAESSSIDL
1		1	FPSPADSGTNSVFSQLENNTNHYSSQLEGNTNSSFLKGGNGENA
	i		VFPSQVNVANNFSSTNAQQSAPEKVKKDRGRGQTGKERKPKHNK
1 .			
}	1	1	RAKWPAIIRDGKFICSRCYRAFTNPRSLGGHLSKRSYCKPLDGA
1	1	}	EIAQBLLQSNGQPSLLASMILSTNAVNLQQPQQSTFNPEACFKD
1	· ·		PSFLQLLAENRSPAFLPNTFPRSGVTNFNTSVSQEGSEIIIQAL
1		ļ	ETAGIPSTFEGAEMLSHVSTGCVSDASQVNATVMPNPTVPPLLH
1	1	1	TVCHPNTLLTNQNRTSNSKTSSIEECSSLPVFPTNDLLLKTVEN
			· · · · · · · · · · · · · · · · · · ·
	1		GLCSSSFPNSGGPSQNFTSNSSRVSVISGPQNTRSSHLNKKGNS
	1		ASKRRKKVAPPLIAPNASQNLVTSDLTTMGLIAKSVEIPTTNLH
ļ	1	1	SNVIPTCEPQSLVENLTQKLNNVNNQLFMTDVKENFKTSLESHT
ì			VLAPLTLKTENGDSQMMALNSCTTSVNSDLQISBDNVIQNFEKT
	}		LEIIKTAMNSQILEVKSGSQGAGETSQNAQINYNIQLPSVNTVQ
}		1	NNKLPDSSP\FSSFISVMPTESNIPQSE\VSHKEDQIQEILEGL
1	}		QKLKLENDLSTPASQCVLINTSVTLTPTPVKSTADITVIQPVSE
j	1		MINIQFNDKVNKPFVCQNQGCNYSAMTKDALFKHYGKIHQYTPE
ļ		1	MILEIKKNQLKFAPFKCVVPTCTKTFTRNSNLRAHCQLVHHFTT
1		1	EEMVKLKIKRPYGRKSOSENVPASRSTOVKKOLAMTEENKKESO
1		j	PALELRAETONTHSNVAVIPEKOLIEKKSPDKTESSLOVITVTS
1		1	1
1			EQCNTNALTNTQTKGRKIRRHKKEKEEKKRKKPVSQSLEFPTRY
1			SPYRPYRCVHQGCFAAFTIQQNLILHYQAVHKSDLPAFSAEVEE
I			ESEAGKESEETETKQTLKEFRCQVSDCSRIFQAITGLIQHYMKL
1		1	HEMTPEEIESMTASVDVGKPPCDQLECKSSFTTYLNYVVHLEAD
1			HGIGLRASKTEEDGVYKCDCEGCDRIYATRSNLLRHIFNKHNDK
1			1
I			HKAHLIRPRRLTPGQENMSSKANQEKSKSKHRGTKHSRCGKEGI
1		ļ	KMPKTKRKKKNNLENKNAKIVQIEENKPYSLKRGKHVYSIKARN
1			DALSECTSRFVTQYPCMIKGCTSVVTSESNIIRHYKCHKLSKAF
1		1	TSOHRNLLIVFKRCCNSQVKETSEQEGAKNDVKDSDTCVSESND
I			NSRTTATVSQKEVEKNE*DEMDELTELFITKLINEDSTSVETQA
			· 1
1			NTSSNVSNDFQEDNLCQSERQKASNLKRVNKEKNVSQNKKRKVE
1		1	KAEPASAAELSSVRKEEETAVAIQTIEEHPASFDWSSFKPMGFE
1		}	VSFLKFLEESAVKQKKNTDKDHPNTGNKKGSHSNSRKNIDKTAV
1		İ	TSGNHVCPCKESETFVQFANPSQLQCSDNVKIVLDKNLKDCTEL
L	_1,		

SEQ P	redicted	Predicted end	Amino acid segment containing signal peptide
	eginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	ucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	ocation	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
II	o first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
I	mino acid	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid ·	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	***************************************	Codon, /=possible nucleotide deletion,
	mino acid	sequence	\=possible nucleotide insertion)
8	sequence		\=possible nucleotide insertion/
			VLKQLQEMKPTVSLKKLEVHSNDPDMSVMKDISIGKATGRGQY
5363	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
			PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
	ĺ		RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
	į		QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
			PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
			CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
1			CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
}			EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
]			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
ļ			DSGVVYSVGMQLA*K1QGMKQML/C1CLGMGV3CQETAV1Q11G
			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
1			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
Ļ			DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
1			DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1		1	DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
1			GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
			TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
j			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
1		ĺ	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
			SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
.			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
1		}	PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
İ			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
ļ			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
1			
			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
1			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1		(PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
		!	TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
1			LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
ļ			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
ì			GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
1			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
		1	SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
ł			APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
İ		1	YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
, l			ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
1		1	PRINCE AND A SACRAMAN
1			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
		1	ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
}		į	QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
		1	SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
		1	ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
		1	DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
		1	NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
) i		1	RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1		1	QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
1			SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
]			ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPCTSTSAT
			LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
1			DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
ļ l			DESCRIPTION OF THE PROPERTY OF THE CONTRACT OF THE PROPERTY OF
) 1			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
 			HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1			RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
, 1			ADREDSRE
5364	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
		i .	
1		1	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
ļ			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	location	to first	L=Leucine, M=Methionine, N=Asparagine,
1	corresponding	l	
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
ì			PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1	ł		CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
]	ļ	ĺ	CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
		ł	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
1	1		EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
1	1	ľ	DSGVVYSVGMQLA+KTQGNKQML\CTCLGNGVSCQETAVTQTYG
1			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
1			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
ļ			DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
Į.	1	1	DKOHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
1]	1	DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
	1		
Į	1	1	GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
1	1 .	1	TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
	1	}	GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
ŧ	1	1	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
İ	1	1	SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
	l .		VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
l			PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
1		1	ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGORLPLSRNTF\AEN
)			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
\ \			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
		İ	TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
ļ			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
			LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
}			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
			GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
ſ			\LRGROKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
			APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1		Î	YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
1			ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
ļ		ł	EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
			DVDSIKIAWESPOGOVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1			ELOGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1	1		OVTPTSLSAOWTPPNVOLTGYRVRVTPKEKTGPMKEINLAPDSS
1	1	}	SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
	1	1	_
			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
]	DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
1	1	1	NLRFLATTPNSLLVSWQPPRARITGYIIXYEKPGSPPREVVPRP
			RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
			QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
		1	SGQQPSVGQQMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGQE
		1	ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLQFRVPGTSTSAT
		1	LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNQPT
			DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
		1	SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
			HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
			RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
		İ	ADREDSRE
5365	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
1 3333		1	PPSWRRQPPGGIRRDFSRRLRREANLVATCLPVRASLPHRLNML
1			RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
İ			QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
			PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1			CTIANRCHEGGOSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
1	1		CYTANRCHEGGOSYKIGDTWRRPHEIGGIMLECVCLONGROEWI CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
L	<u></u>	<u> </u>	CKLTHDKCLDUMMO1914AQE1MEVLIAQUIMIAAACICTQRQQQK

SEQ	Predicted	Predicted end	Amino acid segment containing
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid F-Phonylal-1-1
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Trentonine, V=valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	bequence	Codon, /=possible nucleotide deletion,
	bequence		\=possible nucleotide insertion)
			ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
1		1	EWKCERHTSVOTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
1		}	DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
}			GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
1		ĺ	DNMKWCGTTQNYDADQKFGFCPMAAHEEICTTNEGVMYRIGDQW
		1	DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
			DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
-		Í	GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
i			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
-			PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
			SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
			PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
ļ			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
1			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
1			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
	1		ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
ļ			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
			TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
	·		LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
1			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
	[GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEOHESTP
1	ľ		\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
1			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1			APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSOMOVTDVODNS
			ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
1			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
ł .	}		ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
1 !			QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
			SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
1			ARVTDATETTITISWRTKTETITGFQVDAVPANGQTPIQRTIKP
1 1	1	i	DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
	Ì		NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
		İ	RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
	[ĺ	QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
1 1	1		SGOOPSVGOOMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGOE
	İ		ALSOTTISWAPFODTSEYIISCHPVGTDEEPLOFRVPGTSTSAT
			LTGLTRGATYNI IVEALKDOORHKVREEVVTVGNSVNEGLNOPT DDSCFDPYTVSHYAVGDEWERMSESGFKLLCQCLGFGSGHFRCD
1	ĺ	ĺ	SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
	i		HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
1			RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
j l	ľ		ADREDSRE
5366	8066	703	RLCCTGGGEGTPGASGKRGPAATTSLVLCIPSVPPPVPFPTLWP
			PPSWRRQPPGGIRDFSRRLRREANLVATCLPVRASLPHRLNML
		I	RGPGPGLLLLAVLCLGTAVPSTGASKSKRQAQQMVQPQSPVAVS
			QSKPGCYDNGKHYQINQQWERTYLGNALVCTCYGGSRGFNCESK
		1	PEAEETCFDKYTGNTYRVGDTYERPKDSMIWDCTCIGAGRGRIS
1	ł	ł	CTIANRCHEGGQSYKIGDTWRRPHETGGYMLECVCLGNGKGEWT
]		j	CKPIAEKCFDHAAGTSYVVGETWEKPYQGWMMVDCTCLGEGSGR
] [ļ	ITCTSRNRCNDQDTRTSYRIGDTWSKKDNRGNLLQCICTGNGRG
[EWKCERHTSVQTTSSGSGPFTDVRAAVYQPQPHPQPPPYGHCVT
			DSGVVYSVGMQLA*KTQGNKQML\CTCLGNGVSCQETAVTQTYG
		1	GNSNGEPCVLPFTYNGRTFYSCTTEGRQDGHLWCSTTSNYEQDQ
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
.NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	Lalouging M. Mathianian N. Ralysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ı	amino acid	ľ	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	1	sequence	Codon, /=possible nucleotide deletion,
 	sequence	ļ <u>. </u>	\=possible nucleotide insertion)
			KYSFCTDHTVLVQTRGGNSNGALCHFPFLYNNHNYTDCTSEGRR
			DNMKWCGTTQNYDADQKFGFCPMAAHEBICTTNEGVMYRIGDOW
1	1	,	DKQHDMGHMMRCTCVGNGRGEWTCIAYSQLRDQCIVDDITYNVN
			DTFHKRHEEGHMLNCTCFGQGRGRWKCDPVDQCQDSETGTFYQI
ſ			GDSWEKYVHGVRYQCYCYGRGIGEWHCQPLQTYPSSSGPVEVFI
Ì	:		TETPSQPNSHPIQWNAPQPSHISKYILRWRPKNSVGRWKEATIP
į			GHLNSYTIKGLKPGVVYEGQLISIQQYGHQEVTRFDFTTTSTST
	1	•	PVTSNT\VTGETTPFSPLVATSESVTEITASSFVVSWVSASDTV
1			SGFRVEYELSEEGDEPQYLVLPSTATSV\NIP\DLLPGRKYIVN
1			VYQISEDGEQSLILSTSQTTAPDAPPDPTVDQVDDTSIVVRWSR
}			PQAPITGYRIVYSPSVEGSSTELNLPETANSVTLSDLQPGVQYN
			ITIYAVEENQESTPVVIQQETTGTPRSDTVPSPRDLQFVEVTDV
			KVTIMWTPPESAVTGYRVDVIPVNLPGEHGQRLPLSRNTF\AEN
1			TGLSPGVTYYFKVFAVSHGRESKPLTAQQTTKL\DAPTNLQFVN
I			ETDSTVLVRWTPPRAQITGYRLTVGLTRRGQPRQYNVGPSVSKY
1			DI DNI ODNEDVENICI NA TRONOGORNA TOMOTO DEL PROGRESSIONE
			PLRNLQPASEYTVSLVAIKGNQESPKATGVFTTLQPGSSIPPYN
j			TEVTETTIVITWTPAPRIGFKLGVRPSQGGEAPREVTSDSGSIV
			VSGLTPGVEYVYTIQVLRDGQERDAP\IVNK\VVTPLSPPTNLH
ļ			LEANPDTGVLTVSWERSTTPDITGYRITTTPTNGQQGNSLEEVV
1			HADQSSCTF\DNLEVPGLEYNVSVYTVKDDKESVPISDTIIPAV
			PPPTDLRFTN/ILGPDTMRVTW\APPPSIDLTNFLVRYSPVKNE
			GRMLQSLSIFFLSDN\AVVLTNLLPGTEYVVSVSSVYEQHESTP
1 1			\LRGRQKTGLDSP\TGIDFS\DITA\NSFT\VHW\IAPRA/TPI
			TGYRIR\HHPEHF\SGRPREDR\VPHSRNSITLTNLTPGTEYVV
			SIVALNGREESPLLIGQQSTVSDVPRDLEVVAATPTSLLI\SWD
1 1			APAVTVRYYRITYGETGGNSPVQEFTVPGSKSTATISGLKPGVD
1			YTITVYAVTGRGDSPASSKPISINYRTEIDKPSQMQVTDVQDNS
1 1			ISVKWLPSSSPVTGYRVTTT\PKNGPG\PTKTKTAGPDQTEMTI
			EGLQPTVEYVVSVYAQNPSGESQPLVQTAVTNIDRPKGLAFTDV
			DVDSIKIAWESPQGQVSRYRVTYSSPEDGIHELFPAPDGEEDTA
1			ELQGLRPGSEYTVSVVALHDDMESQPLIGTQSTAIPAPTDLKFT
			QVTPTSLSAQWTPPNVQLTGYRVRVTPKEKTGPMKEINLAPDSS
		1	SVVVSGLMVATKYEVSVYALKDTLTSRPAQGVVTTLENVSPPRR
			ARVTDATETTITISWRTKTETITGFQVDAVPANGOTPIORTIKP
			DVRSYTITGLQPGTDYKIYLYTLNDNARSSPVVIDASTAIDAPS
			NLRFLATTPNSLLVSWQPPRARITGYIIKYEKPGSPPREVVPRP
1			RPGVTEATITGLEPGTEYTIYVIALKNNQKSEPLIGRKKTDELP
1 (j		QLVTLPHPNLHGPEILDVPSTVQKTPFVTHPGYDTGNGIQLPGT
			SGOOPSVGOOMIFEEHGFRRTTPPTTATPIRHRPRPYPPNVGOE
1			ALSQTTISWAPFQDTSEYIISCHPVGTDEEPLOFRVPGTSTSAT
1			LTGLTRGATYNIIVEALKDQQRHKVREEVVTVGNSVNEGLNOPT
1			DDSCFDPYTVSHYAVGDEWERMSESGFKLLCOCLGFGSGHFRCD
			SSRWCHDNGVNYKIGEKWDRQGENGQMMSCTCLGNGKGEFKCDP
			HEATCYDDGKTYHVGEQWQKEYLGAICSCTCFGGQRGWRCDNCR
		1	RPGGEPSPEGTTGQSYNQYSQRYHQRTNTNVNCPIECFMPLDVQ
1 1			ADREDSRE
5367	235	3591	KKILNMLCKKNIVIEYLADILYEYLYGFCFSGIKKYLIIHVLRL
1		J	ILELWMTRLLLEKSVSLQTQYLLLIVKILSWFPGKEMRHHLQIM
			EVMMRKQDS/RIVGNGSEQQLQKELADVLMDPPMDDQPGEKELV
		{	KRSQLDGEGDGPLSNQLSASSTINPVPLVGLQKPEMSLPVKPGQ
		ĺ	GDSEASSPFTPVADEDSVVFSKLTYLGCASVNAPRSEVEALRMM
			SILRSQCQISLDVTLSVPNVSEGIVRLLDPQTNTEIANYPIYKI
}	1	}	TECABGROCADE A EMECIANY OF EDSTAIN COST OF COS
	1		LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FERSANOTEL CARRA POTENCIA FRANCE I LYSEATA FRANCE I
]			LYSFATAFRRSAKQTPLSATAAPQTPDSDIFTFSVSLEIKEDDG
1	1	ļ	KGYFSAVPKDKDRQCFKLRQGIDKKIVIYVQQTTNKELAIERCF
1	ĺ		GLLLSPGKDVRNSDMHLLDLBSMGKSSDGKSYVITGSWNPKSPH
1			FQVVNEETPKDKVLFMTTAVDLVITEVQEPVRFLLETKVRVCSP
1			NERLFWPFSKRSTTENFFLKLKQIKQRERKNNTDTLYEVVCLES
1			ESERERRKTTASPSVRLPQSGSQSSVIPSPPEDDEREDNDEPLL
1 1	1	1	SGSGDVSKECAEKILETWGELLSKWHLNLNVRPKQLSSLVRNGV
			PEALRGEVWQLLAGCHNNDHLVEKYRILITKESPQDSAITRDIN

CEO	Drodietod	Predicted end	Amino acid segment containing signal nontide
SEQ	Predicted		Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
			RTFPAHDYFKDTGGDGQDSLYKICKAYSVYDEEIGYCOGOSFLA
ł	1		AVLLLHMPEEQAFSVLVKIMFDYGLRELFKONFEDLHCKFYOLE
İ	1	1	RLMQEYIPDLYNHFLDISLEAHMYASQWFLTLFTAKFPLYMVFH
1	1	ł	IIDLLLCEGISVIFNVALGLLKTSKDDLLLTDFEGALKFFRVQL
			PKRYRSEENAKKLMELACNMKISQKKLKKYEKEYHTMREQQAQQ
1	1	<u> </u>	EDPIERFERENRRLQEANMRLEQENDDLAHELVTSKIALRKDLD
1	1	Ì	NAEEKADALNKELLMTKQKLIDAEEEKRRLEEESAHLKKMCRRE
1	1	İ	
ĺ	[LDKAESEIKKNSSIIGDYKQICSQLSERLEKQQTANKVEIEKIR
ł	İ	!	QKVDDCERCREFFNKEGRVKGISSTKEVLDEDTDEEKETLKNQL
1	i .		REMELELAQTKL\QLVEAECKIQD\LEHPF*GLPFNE\VQAA\K
i		ĺ	KTWFNRTLSSIKTATGVQGKETC
F260	 	2014	L
5368	573	2014	GAAAGAADPRRGSLGGRTMLDFAIFAVTFLLALVGAVLYLYPAS
1			RQAAGIPGITPTEEKDGNLPDIVNSGSLHEFLVNLHERYGPVVS
1	1	1	FWFGRRLVVSLGTVDVLKQHINPNKTLD/LF*NHAEVIIKVSIW
1	į.		WWQCE+KP\QRKKLYENGVTDSLKSNFALLLKLPEELLDKWLSY
1	[PETOH\VPLSQHMLGFAMKSVTOMVMGSTFEDDOEVIRFOKNHG
1			TVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERK
ļ	1		
	ì		GRNFSQHIFIDSLVQGNLNDQQILEDSMIFSLASCIITAKLCTW
1	İ	1	AIWFLTTSEEVQKKLYEEINQVFGNGPVTPEKIEQLRYCQHVLC
	ţ		ETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVLQDP
}	1	1	NTWPSPHKFDPDRFDDELVMKTFSSLGFSGTQECPELRFAYMVT
1	1	ſ	TVLLSVLVKRLHLLSVEGQVIETKYELVTSSREEAWITVSKRY
5369	1	6622	PRSLCFSLWAEAAVLADGGLRRRRRLLRGTMSASFVPNGASLED
3305	,	0022	1
		l .	CHCNLFCLADLTGIKWKKYVWQGPTSAPILFPVTEEDPILSSFS
	1	l	RCLKADVLG/VWRRDQRPERRE\L*IFWGGEDP\VLLTLFTMTY
			QKKKMECGRMDFPMNAVLCFSKAVHNLLERCLMNRNFVRIGKWF
1	1	i	VKPYEKDEKPINKSEHLSCSFTFFLHGDSNVCTSVEINOHOPVY
1	ł	ſ	LLSEEHITLAQQSNSPFQVILCPFGLNGTLTGQAFKMSDSATKK
]	į.	J	LIGEWKQFYPISCCLKEMSEEKQEDMDWEDDSLAAVEVLVAGVR
ļ	l .	ł	
1	1	1	MIYPACFVLVPQSDIPTPSPVGSTHCSSSCLGVHQVPASTRDPA
]	J	MSSVTLTPPTSPEEVQTVDPQSVQKWVKFSSVSDGFNSDSTSHH
1			GGKIPRKLANHVVDRVWQECNMNRAQNKRKYSASSGGLCEEATA
1	1	1	AKVASWDFVEATQRTNCSCLRHKNLKSRNAGQQGQAPSLGQQQQ
			ILPKHKTNEKQEKSEKPQKRPLTPFHHRVSVSDDVGMD\ADS\A
			SQRLV\ISAP\DSQ\VRFSNIR\TNDVAK\TPQMHGTEMANSPQ
	(1	PPPLSP\HPCDVVDEGVTKTPSTPQSQHFYQMPTPDPLVPSKPM
1	İ	1	
			EDRIDSLSQSFPPQYQEAVEPTVYVGTAVNLEEDEANIAWKYYK
1 .	1		FPKKKDVEFLPPQLPSDKFKDDPVGPFGQESVTSVTELMVQCKK
1	1		PLKVSDELVQQYQIKNQCLSAIASDAEQEPKIDPYAFVEGDEEF
1		ļ	LFPDKKDRONSEREAGKKHKVEDGTSSVTVLSHEEDAMSLFSPS
1		1	IKQDAPRPTSHARPPSTSLIYDSDLAVSYTDLDNLFNSDEDELT
1	1		PGSKRSANGSDDKASCKRSKTGNLDPLSCISTADLHKMYPTPPS
1			LEQHIMGFSPMNMNNKEYGSMDTTPGGTVLEGNSSSIGAQFKIE
1	1	[VDEGFCSPKPSEIKDFSYVYKPENCQILVGCSMFAPLKTLPSQY
1		i	LPLIKLPEECIYRQSWTVGKLELLSSGPSMPFIKEGDGSNMDQE
I			YGTAYTPQTHTSCGMPPSSAPPSNSGAGILPSPSTPRFPTPRTP
1		1	RTPRTPRGAGGPASAOGSVKYENSDLYSPASTPSTCRPLNSVEP
1			
1			ATVPSIPEAHSLYVNLILSESVMNLFKDCNSDSCCICVCNMNIK
1			GADVGVYIPDPTQEAQYRCTCGFSAVMNRKFGNNSGLFFEDELD
1	Į.	}	IIGRNTDCGKEAEKRFEALRATSAEHVNGGLKESEKLSDDLILL
1]		LQDQCTNLFSPFGAADQDPFPKSGVISNWVRVEERDCCNDCYLA
1			LEHGRQFMDNMSGGKVDEALVKSSCLHPWSKRNDVSMQCSQDIL
I			
}		ļ	RMLLSLQPVLQDAIQKKRTVRPWGVQGPLTWQQFHKMAGRGSYG
		İ	TDESPEPLPIPTFLLGYDYDYLVLSPFALPYWERLMLEPYGSQR
			DIAYVVLCPENEALLNGAKSFFRDLTAIYESCRLGQHRPVSRLL
			TDGIMRVGSTASKKLSEKLVAEWFSQAADGNNEAFSKLKLYAQV
1			CRYDLGPYLASLPLDSSLLSQPNLVAPTSQSLITPPQMTNTGNA
1		ĺ	NTPSATLASAASSTMTVTSGVAISTSVATANSTLTTASTSSSSS
Į	ļ		
1.			SNLNSGVSSNKLPSFPPFGSMNSNAAGSMSTQANTVQSGQLGGQ
1			QTSALQTAGISGESSSLPTQPHPDVSESTMDRDKVGIPTDGDSH
L			AVTYPPAIVVYIIDPFTYENTDESTNSSSVWTLGLLRCFLEMVQ
			*_

SEQ Predicted Predicted end Amino acid segment containing sign	al peptide
ID beginning nucleotide (A=Alanine, C=Cysteine, D=Aspartic	
NO: nucleotide location Glutamic Acid, F=Phenylalanine, G	
location corresponding H=Histidine, I=Isoleucine, K=Lysin	
corresponding to first L=Leucine, M=Methionine, N=Asparas	
to first amino acid P=Proline, Q=Glutamine, R=Arginine	
amino acid residue of S=Serine, T=Threonine, V=Valine,	
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknow	vn. *=Stop
amino acid sequence Codon, /=possible nucleotide delet	
sequence \=possible nucleotide insertion)	
TLPPHIKSTVSVQIIPCQYLLQPVKHEDREIYPC	HLKSLAFSAF
TQCRRPLPTSTNVKTLTGFGPGLAMETALRSPD	•
FILAPVKDKOTELGETFGEAGOKYNVLFVGYCLS	
TDLYGELLETCIINIDVPNRARRKKSSARKFGL	
OMSSLPWRVVIGRLGRIGHGELKDWSCLLSRRNI	_
CRMCGISAADSPSILSACLVAMEPQGSFVIMPD	-
TTLNMQTSQLNTPQDTSCTHILVFPTSASVQVAS	
AFNPNNDGADGMGIFDLLDTGDDLDPDIINILP	
GSHYPHGGDAGKGQSTDRLLSTEPHEEVPNILQ	
AKAGPLPDWFWSACPQAQYQCPLFLKASLHLHVI	-
KHSHPLDSNQTSDVLRFVLEQYNALSWLTCDPA	-
FVVLNQLYNFIMNML	QDIRECTI III
5370 1226 716 RWSRKLELRRAAQATESRPPQSQEMHPPTGKEVI	IAL KRI PDCAN
ANDVETVOOLLEDGADPCAADDKGRTALHFASCI	
DHGADPNQRDGLGNTPLHLAACTNHVPVITTLLI	
AGRTPLHLAKSKLNILQEGHAQCLKAVR/HGGE	
APRAT*AARCSGVFPSPSRWLGSAPWSRSSCTI	
AVRPLSSAAOGSAPSSSSCCTVSTSLALABSLSI	
GCISWL	inderent vo
5371 1331 167 IAAMLWKLLLRSQSCRLCSFRKMRSPPKYRPFLJ	20XGTTVTTDKOC
SKENTRTVEKLYKCSVDIRKIRR*KDGYF*RMI	
LQELGADETAVASILERCPEAIVCSPTAVNTQRI	
ELIKLIEOFPESFTIKDQENQKLNVOFFQELGI	
AAPNVFHNPVEKNKQMVRILQESYLDVGGSEAN	
NPFILLNSPTAIKETLEFLQEQGFTSFEILQLLS	
PRSIQNSISFSKNAFKCTDHDLKQLVLKCPALLY	
QGLLREGISIAQIRETPMVLELTPQIVQYRIRKI	
HLANLNGSKKEFEANFGKIQAKKVRPLFNPVAPI	
5372 51 857 SPGAQFLWAAPDMPDPLFSAVQGKDEILHKALCI	
PLRLLILLFVTELSGAHNTTVFQGVAGQSLQVSG	
RKAWCRQLGEKGPCQRVVSTHNLWLLSFLRRWNG	
GTLTITLRNLQPHDAGLYQCQSLHGSEADTLRX	
HRDAGDLWFPG\DLRASRMPMWSTASPGASWKE	
SWPASFSSRF*QPAPSGLQPGMDRSQGHIHPVN	
KLCOG	
5373 2814 346 VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSP	POPMATYATAS
QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPK:	_
TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKI	
ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSP(
KTSTTGSILNLNLDRSKAEMDLKELSESVQQQS	-
IRSRFOLNLDKTIESCKAOLGINEISEDVYTAV	-
DSSDSEYISDDEQKS*GTSQEDTEDKEGCQMDKI	
TNPVEIKEELKSTSPASEKADPGAVKDKASPEPI	
PHP I KDKLKGKDETDSPTVHLGLDSDSE\NBLV	
GRKNKKEPKEPSPKODVVGKTPPSTTVGSHSPPI	
TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQI	
AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQS	
STLVSSVNGDLPIGTASADVAADIAKYTSKL\MI	
YNDLSKN\TTWKAOLAEDSOGLRIEIEKLOWLHO	
LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQ	
ANFKKEAIFYCCWNTSYCDYPCO\QAHWPEH\MI	
\OBADAE\VNTETLNKSSOGSSSSTOSAPSETAS	
EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSI	. '
DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGT	
5374 2814 346 VKKTKSIFNSAMQEMEVYVENIRRKFGVFNYSPI	
53/4 2814 346 VKKTKSIFNSAMQEMEVIVENIKRKRGVFNISPI QMLLDPTNPSAGTAKIDKQEKVKLNFDMTASPKI	· ·
TGRRISLSDMPRSPMSTNSSVHTGSDVEQDAEKI	
TGRKISLSUMPKSPMSTNSSVHTGSUVEQUAENI ESMDFLDKSTASPASTKTGQAGSLSGSPKPFSP(
KTSTTGSILNINDRSKAEMDLKELSESVQQQS	
VISITESTIMENTAL NUMBERS SOUND VISITESTIMENTAL NUMBERS SOUN	TAETITOLVUG
TOCOPOLNIC DEPT CONTRACTOR OF	
IRSRFQLNLDKTIESCKAQLGINEISEDVYTAVI DSSDSEYISDDEQKS+GTSQEDTEDKEGCQMDKI	CHSDSEDSEKS

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	[(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	L=Leucine, m=methionine, m=msparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	Bequence		TNPVEIKEELKSTSPASEKADPGAVKDKASPEPEKDFSGKAKPS
	1		PHPIKDKLKGKDETDSPTVHLGLDSDSE\NELVIDLGEDHSGRE
	1	1	GRKNKKEPKEPSPKQDVVGKTPPSTTVGSHSPPETPVLTRSSAQ
	\	İ	
		ſ	TSAAGATATTSTSSTVTVTAPAPAATGSPVKKQRPLLPKE\TAP
	!	ì	AVQRSCGTSSTVQQKEITQSPSTSTITLVTSTQSSPLVTSSGSM
	1	1	STLVSSVNGDLPIGTASADVAADIAKYTSKL\MDAIKGTM\TEI
		i	YNDLSKN/TTWKAQLAEDSQGLRIEIEKLQWLHQQEL/SEMKHN
		1	LELTMAEMRQSWEQERDRLIAEVKKQLELEKQQAVDETKKKQWC
		1	ANFKKEAIFYCCWNTSYCDYPCQ\QAHWPBH\MKSCTQSATAPQ
	1		\QEADAE\VNTETLNKSSQGSSSSTQSAPSETASA\SKEKETSA
		1	EKSKESGSTLDLSGSRETPSSILLGSNQGSDHSR\SNKSSWSSS
			DEKRGS\TRSDHN/TPSTQHGRSLLPGKESRAGTPFLGTSK
		 	HIFLAEEEPMLERRCRGPLAMGPAQPRLLSGPSQESPQTLGKES
5375	2907	1116	RGLRQQGTSVA\QSGAQAPGRAHRCAHCRRHFPGWVA\LWLHTR
			KGLKUQGISVA\QSGAQAPGKARKCARCKKRIPGWVA\DWDRIK
			RCQA/RGLPLPCPECGRRFRHAPFLALHRQVHAAATPDWGFACH
		Į.	LCGQSFRGWVALVLHLRAHSAAKAGPFACPKMARDAFWRRKAAS
			SSILRRCHPSRPRGPRPFICGNCGRSILPTWDQ/LKVAHKRVHV
	Į.		SRRP*ERGPPAKVFWGPRPRGPPTGDTPPGPGGDAVDRPF\QCA
	}		CCGKRFRHK\PNLIRSHAACTSGERPHQ/CSRECG\KRFTNKPY
	- L		LTS\HRRITHTARQPYPCKECGRRFRHKPNLLSHSKIHKRSEGS
		1	AQAAPGPGSPQLPAGPQESAAEPTPAVPLKPAQEPPPGAPPEHP
	1	1	ODPIEAPPSLYSCODCGRSFRLERFLRAHQRQHTGERPFTCAEC
			GKNFGKKTHLVAHSRVHSGERPFRLARKCGRRFLPRASQSGGRN
	}	ł	SAEPNAPRFGPFVCPDCGKAFRHKPYLAAHRPIATPAEKPYVCP
	1	}	DCRKAFSQKSNL\VSHRRIHTGERPYACPDCDRSFSQKSNLITH
	1	1	
	ļ	_	RKSHIRDGAFCCAICGQTFDDEERLLAHQKKHDV
5376	4504	591	VSTFSLCLWPAGGGGRGRVSNMAQSKRHVYSRTPSGSRMSAEAS
	Į.		ARPLRVGSRVEVIGKGHRGTVAYVGATLFATGKWVGVILDEAKG
	}	4	KNDGTVQGRKYFTCDEGHGIFVRQSQIQVFEDGADTTSPETPDS
	ì		SASKVLKREGTDTTAKTSKLRGLKPKKAPTARKTTTRRPKPTRP
		Į.	ASTGVAGASSSLGPSGSASAGELSSSEPSTPAQTPLAAPIIPTP
ļ	}	ļ	VLTSPGAVPPLPSPSKEEEGLRAQVRDLEEKLETLRLKRAEDKA
	•	ļ	KLKELEKHKIQLEQVQEWKSKMQEQQADLQRRLKEARKBAKEAL
(i	<u> </u>	EAKERYMEEMADTADAIEMATLDKEMAEERAESLQQEVEALKER
)	1		VDELTTDLEILKAEIEEKGSDGAASSYQLKQLEEQNARLKDALV
l			RMRDLSSSEKQEHVK\LQKLMEKKNQELEVVRQQRERLQEELSQ
1	1		AESTIDELKEQVDAALGAEEMVEMLTDRNLNLEEKVRELRETVG
[l		
İ			DLEAMNEMNDELQENARETELELREQLDMAGARVREAQKRVEAA
1			QETVADYQQTIKKYRQLTAHLQDVNRELTNQQEASVERQQQPPP
1			ETFDFKIKFAETKAHAKAIEMELRQMEVAQANRHMSLLTAFMPD
1			SFLRPGGDHDCVLVLLLMPRLICKAELIRKQAQEKFELSENCSE
1			RPGLRGAAGEQLSFAAIGLVY\SLMPAAGHRYHRY*CHALSQCR
l		1	LD\VYKKVGSLYPEMSAHERSLDFLIELLHKDQLDETVNVEPLT
		1	KAIKYYOHLYSIHLAEQPEDCTMQLADHIKFTQSALDCMSVEVG
ĺ		1	RLRAFLOGGOEATDIALLLRDLETSCS\DIRQFCKKIRRRMPGT
ł		1	DAPGIPAALAFGPQVSDTLLDCRKHLTWVVAVLQEVAAAAAQLI
ì	Ĭ	}	APLAENEGLLVAALEELAFKASEQIYGTPSSSPYECLRQSCNIL
		Ì	ISTMNK/LVTAMQEGEYDAERPPSKPPP/VELRAAALRAEITDA
1		1	EGLGLKLEDRETVIKELKKSLKIKGEELSEANVRLTLLEKKLDS
Į.		j	EGLGLKLEDRETVIKELKKSLKIKGEELISEAKVKDIDLEAKODS AAKDADERIEKVQTRLEETQALLRKKEKEFEETMDALQADIDQL
1		1	AAKUADEKIERVQIKBEBIQADEKAREKETEEIRDADQADIDQB
ł	1		EAEKAELKQRLNSQSKRTIEGLRGPPPSGIATLVSGIAGEEQQR
1			GAIPGQAPGSVPGPGLVKDSPLLLQQISAMRLHISQLQHENSIL
	1		KGAQMKASLASLPPLHVAKLSHEGPGSELPAGALYRKTSQLLET
	1		LNQLSTHTHVVDITRTSPAAKSPSAQLMEQVAQLKSLSDTVEKL
1	j		KDEVLKETVSQRPGATVPTDFATFPSSAFLRAKEEQQDDTVYMG
1			KVTFSCAAGFGORHRLVLTQEQLHQLHSRLIS
F227	762	1106	DVPCKRVLPAEAQEKGQLTLSCGESGEEG\F*YHEVRQAEGES*
5377	/02	1100	/WFGPNVRLVHTQLKTKKPSGTLKAKFYLHTGSTKFAARISCTK
1	1	ļ	
1	1	1	SS*WPGYDGWWGGQYIFIFRGMRWEBQP
		_	THE PARTY DOLD DOLD DOLD DOLD DE MODERNE LE LE LE LE LE LE LE LE LE LE LE LE LE
5378	2009	664	QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	1	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Gittamic Acid, rarhenylatanine, Gadiyethe,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	1	Bequesto	\=possible nucleotide insertion)
	sequence	 	SFSFRNSKQTYSGVPIIAANMDTVGTFBMAKVLCKS*VPGSFWD
ļ	i	İ	VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
,	į.	ļ	VPQMGCVF BI IKUF I BKWKIBDBS VBDFAS I BVABKI SHI IAVI
1		Į.	KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
l		1	QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
1	Ì	I €	EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
I	(HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
}	1	l	ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
	1		PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
}	1	1	VNPIFSEAC
L			QASGTTLRPLPDLPQLKRREATSRNRALKPRGRLVLMTSCLPAL
5379	2009	664	RFIATPRLSAMPHIDNDVKLDFKDVLLRPKRSTLKSRSEVDLTR
	1		RETATPRESAMPHIUNDVREDERDVERERRSIERSEVDEIR
1		1	SFSFRNSKQTYSGVPIIAANMDTVGTFEMAKVLCKS*VPGSFWD
1			VPQMGCVFLIYKLFTLKWKMLLLSVLLPASILVAEKFSLFTAVH
1		1	KHYSLVQWQEFAGQNPDCLEHLAASSGTGSSDFEQLEQILEAIP
]		}	QVKYICLDVANGYSEHFVEFVKDVRKRFPQHTIMAGNVVTGEMV
		1	EELILSGADIIKVGIGPGSVCTTRKKTGVGYPQLSAVMECADAA
	1		HGLKGHIISDGGCSCPGDVAKAFGAGADFVMLGGMLAGHSESGG
1			ELIERDGKKYKLFYGMSS*I\AM\KKYAGGVAEYRASEGKTVEV
1			PFKGDVEHTIRDILGGIRSTCTYVGAAKLKELSRRTTFIRVTQQ
ł	1		
			VNPIFSEAC PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
5380	2	2050	PSKAGGAERGKAAAAKSPGGSAAGWECPSVDDEAGACTMSSCVS
	1		SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
1	1		SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
1	1	1	SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
ŀ	}	1 .	RLPRRPTVESHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
1	i	1	YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
{			RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV
		Į	F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
ì	1	1	H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
1	ļ	\	FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
1	ļ	i	CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
1		1	CLHSKIKSQALEFPDQPDIAEDDKDBIIRMEDAWFESKIVVFEI
1		1	KLHPWVTRHGAEPLPSEDENCTLVEVTEERVENSVKHIPSLATV
}			ILVKTMIRKRSFGNPFEGSRRBERSLSAPGNLLTKKPTRECESL
1		ł	SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR
ì	1	1	*PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
1	ı		PDLVGAPGSHFCFLNIALLRYNSHTM
5381	2	2050	PSRAGGAERGRAAAARSPGGSAAGWECPSVLDEAGACTMSSCVS
1 2201	1		SQPSSNRAAPQDELGGRGSSSSESQKPCEALRGLSSLSIHLGME
1	1		SFIVVTECEPGCAVDLGLARDRPLEADGQEVPLDTSGSQARPHL
	'		SGRKLSLQERSQGGLAAGGSLDMNGRCICPSLPYSPVSSPQSSP
1	Į.		RLPRRPTVBSHHVSITGMQDCVQLNQYTLKDEIGKGSYGVVKLA
.]			KREKKETAROUNAST TOMOCAONACT TRANSTONOS TOAAMIN
1	\	1	YNENDNTYYAMKVLSKKKLIRQAAFPRRPPPRGTRPAPGGCIQP
1			RGPI\EQVYQEIA\ILKKLDHPNVV\KLVEVL\DDPNEDHLYMV
j .	}		F\ELVNQGPVMEVPTLKPLSEDQARFYFQDLIKGIEYLHYQKII
1			H\RDIKPSNLLVGEDGHIKIADFGVSNEFKGSDALLSNTVGTPA
1	Į.		FMAPESLSETRKIFSGKALDVWAMGVTLYCFVFG*CPFMDERIM
ļ	1		CLHSKIKSQALEFPDQPDIAEDLKDLITRMLDKNPESRIVVPEI
			KLHPWVTRHGAEPLPSEDENCTLVEVTEEEVENSVKHIPSLATV
1			ILVKTMIRKRSFGNPFEGSRREERSLSAPGNLLTKKPTRECESL
			SELKT*KISPLPACCKVT*EFPHPSGCRPSCWQPPFLHTHSQPR
		1	PEDVI KIRANACCKAI - ELAMARCKAR CAMALEL DELI CACCAI
		1	*PEPPRTDEALCPYETGRTCWAPLLQVLWWVGTPLPFPLSTSWL
1		}	PDLVGAPGSHFCFLNIALLRYNSHTM.
5382	1536	203	GARGSQQDAPALQEABVRGPERAQPARGRMTKARLFRLWLVLGS
		l	VFMILLIIVYWDSAGAAHFYLHTSFSRPHTGPPLPTPGPDRDRE
			LTADSDVDEFLDKFLSAGVKQSDLPRKETEQPPAPGSMBESVRG
			YDWSPRDARRSPDQGRQQAERRSVLRGFCANSSLAFPTKERPFD
)	}	1	DIPNSELSHLIVDDRHGAIYCYVPKVACTNWKRVMIVLSGSLLH
		1	RGAPYRDPLRIPREHVHNASAHLTFNKFWRRYGKLSRHLMKVKL
1	}		KKYTKFLFVRDPFVRLISAFRSKFELENEEF/*PQVRRAHAAAV
		1	KKIIATEFVKDYFVKLISAFKSKTSLENGEF/-FUVKAKAKAK
	}		RQPHQPARLGARGLPRWPQ\VSFANFIQYLLDPHTEKLAPFNEH
1		.1	WRQVYRLCHPCQIDYDFVGKLETLDEDAAQLLQLLQVDLAAPLP

	·		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1 10:	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence	L	\=possible nucleotide insertion)
ł –			PELPGTGPPSSWEEDWFAKIPLAWRQQLYKLYEADFVLFGYPKP
- 5365			ENLLRD
5383	45	5250	VERLLGCRNSKRTWRMLISKNMPWRRLQGISFGMYSAEELKKLS
	1		VKSITNPRYLDSLGNPSANGLYDLALGPADSKEVCSTCVQDFSN
ĺ			CSGHLGHIELPLTVYNPLLFDKLYLLLRGSCLNCHMLTCPRAVI
			HLLLCQLRVLEVGALQAVYELERILSRFLEENADPSASEIREEL
1		1	EQYTTEIVQNNLLGSQGAHVKNVCESKSKLIALFWKAHMNAKRC PHCKTGRSVVRKEHNSKLTITFPAMVHRTAGQKDSEPLGIEEAQ
}		Ì	IGKRGYLTPTSAREHLSALWKNEGFFLNYLFSGMDDDGMESRFN
			PSVFFLDPLVVPPSRSRPVSRLGDQMFTNGQTVNLQAVMKDVVL
		1	IRKLLALMAQEQKLPEEVATPTTDEEKDSLIAIDRSPLSTLPGQ
ĺ			SLIDKLYNIWIRLQSHVNIVFDSEMDKLMMDKYPGIRQILEKKE
			GLFRKHMMGKRVDYAARSVICPDMYINTNEIGIPMVFATKLTYP
[QPVTPWNVQELRQAVINGPNVHPGASMVINEDGSRTALSAVDMT
			QREAVAKQLLTPATGAPKPQGTKIVCRHVKNGDILLLNRQPTLH
			RPSIQAHRARILPEEKVLRLHYANCKAYNADFDGDEMNAHFPQS
		ļ	ELGRAEAYVLACTDQQYLVPKDGQPLAGLIQDHMVSGASMTTRG
			CFFTREHYMELVYRGLTDKVGRVKLLSPSILKPFPLWTGKQVVS TLLINIIPEDHIPLNLSGKAKITGKAWVKETPRSVPGFNPDSMC
1			ESQVIIREGELLCGVLDKAHYGSSAYGLVHCCYEIYGGETSGKV
1 1			LTCLARLFTAYLQLYRGFTLGVEDILVKPKADVKRQRIIEESTH
i l		l	CGPQAVRAALNLPEAASYDEVRGKWQDAHLGKDQRDFNMIDLKF
1			KEEVNHYSNBINKACMPFGLHRQFPENTLQLMVQSGAKGSTVNT
] }			MQISCLLGQIELEGRSTPLMASGKSLPCFEPYEFTPRAGGFVTG
			RFLTGIKPPEFFFHCMAGREGLVDTAVKTSRSGYLORCIIKHLE
			GLVVQYDLTVRDSDGSVVQFLYGEDGLDIPKTQFLQPKQFPFLA
			SNYEVIMKSQHLHEVLSRADPKKALHHFRAIKKWQSKHPNTLLR
			RGAFLSYSQKIQEAVKALKLESENRNGR/RPWDS/G/RMLRMWY
			ELDEESRRKYQKKAAACPDPSLSVWRPDIYFASVSETFETKVDD
į l			YSQEWAAQTEKSYEKSELSLDRLRTLLQL\KWQRSLCEPGEAVG
1			LLAAQSIGEPSTQMTLNTFHFAGRGEMNVTLGIPRLREILMVAS ANIKTPMMSVPVLNTKKALKRVKSLKKQLTRVCLGEVLQKIDVQ
			ESFCMEEKQNKFQVYQLRFQFLPHAYYQQEKCLRPEDILRFMET
			RFFKLLMESIKKKNNKASAFRNVNTRRATQRDLDNAGELGRSRG
[[ĺ		EQEGDEEEEGHIVDAEABEGDADASDAKRKEKQEEEVDYESEEE
1			EEREGEENDDEDMQEERNPHREGARKTQEQDEEVGL/GH*GGPV
			PSRPPDAAPETHPQPGAPGA\EAMERRVQAVREIHPFIDDYQYD
}]		TEESLWCQVTVKLPLMKINFDMSSLVVSLAHGAVIYATKGITRC
			LLNETTNNKNEKELVLNTEGINLPELFKYAEVLDLRRLYSNDIH
		ļ	AIANTYGIEAALRVIEKEIKDVFAVYGIAVDPRHLSLVADYMCF
			EGVYKPLNRFGIRSNSSPLQQMTFETSFQFLKQATMLGSHDELR
5384	196	886	SPSACLVVGKVVRGGTGLFELKQPLR QSCGQRLPTVL*L*GPPGSCPCILSLF\PGRPHALPEIRPYINI
		000	TILKGDKGDPGPMGLPGYMGREGPQGEPGPQGSKGDKGEMGSPG
			APCQKRFFAFSVGRKTALHSGEDFQTLLFERVFVNLDGCFDMAT
			GQFAAPLRGIYFFSLNVHSWNYKETYVHIMHNQKEAVILYAQPS
			ERSIMQSQSVMLDLAYGDRVWVRLFKRQRENAIYSNDFDTYITF
			SGHLIKAEDD
5385	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM
			SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
			VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
			SDGERKAYVRLAPDYDALVVATKIGIT
5386	326	799	LMVPRTKKEAPAPPKAEAKAKAL\KAKKAVLKDVHSHKKNKIHM
			SPTFRRPKTL*LRRQPKYPWKSTPRRNKLDHHVIIKFPLTTE*A
1		ļ	VKKIENNSLLVFTVDVKANKHQIKQAVKK/LCDIDVAKVNTLIQ
5387			SDGERKAYVRLAPDYDALVVATKIGIT
2301	2	2117	FVVAASGGCWFVLGERRAGSLLSASYGTFAMPGMVLFGRRWAIA
		. [SDDLVFPGFFELVVRVLWWIGILTLYLMHRGKLDCAGGALLSSY
!		· i	LIVLMILLAVVICTVSAIMCVSMRGTICNPGPRKSMSKLLYIRL
}			ALFFPEMVWASI.CXXLITIX DOMODOMADIO FEROMERIO CONTENTO L
j	ļ	j	ALFFPEMVWASLGAAWVADGVQCDRTVVNGIIATVVVSWIIIAA TVVSIIIVFDPLGGKMAPYSSAGPSHLDSHDSSQLLNGLKTAAT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	1	1	
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Deque	\=possible nucleotide insertion)
 	Bequence		SVWETRIKLLCCCIGKDDHTRVAFSSTAELFSTYFSDTDLVPSD
	1	1	
]	1	ŀ	IAAGLALLHQQQDNIRNNQEPAQVVCHAPGSSQEADLDAELKNC
l	1		HHYMQFAAAAYGWPLYIYRNPLTGLCRIGGDCCRSKNPQTMT/M
			VGGDQLQL/CTSAPILHTHRAAVQGLHPRQLPWTRFTELPFLVA
1	ļ.	}	LDHRKESVVVAVRGTMSLQDVLTDLSAESEVLDVECEVQDRLAH
ļ	i	-	KGISQAARYVYQRLINDGILSQAFSIAPEYRLVIVGHSLGGGAA
1	ľ .	ţ	ALLATMVRAAYPQVRCYAFSPPRGLWSKALQEYSQSFIVSLVLG
ļ	}	}	KDVIPRLSVTNLEDLKRRILRVVAHCNKPKYKILLHGLWYELFG
1	1		
1		1	GNPNNLPTELDGGDQEVLTQPLLGEQSLLTRWSPAYSFSSDSPL
Į		1	DSSPKYPPLYPPGRIIHLQEEGASGRFGCCSAAHYSAKWSHEAE
		1	FSKILIGPKMLTDHMPDILMRALDSVVSDRAACVSCPAQGVSSV
1	1	1	DVA
5388	1569	753	TADGGAGGGGRRQAGVRRHYLYPFTGGYRRRAACQAERPAARS
l		1	KDTDLAAYOKGNLGVOLRNMAOETNHSOVPMLCSTGCGFYGNPR
[1	TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST
}	1	1	SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
1		1	DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
	1		TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
l			ILEHLQTKN
5389	1569	753	TADGGAGGGGRRQAGVRRHYLYPFTGGYRRRAACQAERPAARS
ľ		1	KDTDLAAYQKGNLGVQLRNMAQETNHSQVPMLCSTGCGFYGNPR
į.	1	ł	TNGMCSVCYKEHLQRQNSSNGRISPPVQCTDGSVPEAQSALDST
	1	ļ	SSSMQPSPVSNQSLLSESVASSQLDSTSVDKAVPETEDVQASVS
1	1		DTAQQPSEEQSKSLE\NRNKKRIAVSCAGRKWDLLGLNAGVEMF
	I		TVVYTVTQMYTIALTITKQMLKNFVFQQEFKSFGSFHQQLLEYK
		1	
	<u></u>		ILEHLQTKN
5390	217	1332	EDPRKLMEDKMWSECEGPEMSLVCLTDFQAHAREQLSKSTRDFI
ļ	ļ	i	EGGADDSITRDDNIAAFKRIRLRPRYLRDVSEVDTRTTIQGEEI
		1	SAPICIAPTGFHCLVWPDGEMSTARAAQAA\GICYITSTFASCS
l	i	ļ	LEDIVIAAPEGLRWFQLYVHPDLQLNKQLIQRVESLGFKALVIT
]	Į.	1	LDTPVCGNRRHDIRNQLRRNLTLTDLQSPKKGNAIPYFQMTPIS
1			TSLCWNDLSWFQSITRLPIILKGILTKEDAELAVKHNVQGIIVS
ļ			NHGGRQLDEVLASIDALTEVVAAVKGKIEVYLDGGVRTGNDVLK
1.	i	·	ALALGAKCIFLGDAILWALASKGEHGVKEVLNILTNEFHTSMA\
j	1	J	LTGCRSVAEINRNLVOFSRL
5391	ļ		1
5391	1	1292	VKKAAGRSRGPPTAGGQRCEEAPGTVMERRLGVRAWVKENRGSF
			QPPVCNKLMHQEQLKVMFVGGPNTRKDYHIEEGEEVFYQLEGDM
			VLRVLEQGKHRDVVIRQGEIFLLPARVPHSPQRFANTVGLVVER
[1	RRLETELDGLRYYVGDTMDVLFEKWFYCKDLGTQLAPIIQEFFS
	Į	1 .	SEQYRTGKPIPDQLLKEPPFPLSTRSIMEPMSLDAWLDSHHREL
1 .		1	QAGTPLSLFGDTYETQVIAYGQGSSEGLRQNVDVWLWQLEGSSV
			VTMGGRRLSLGPWMDSLLVLSWGPSY\AW\ERTQGSVALSVT\Q
1			DPACKKSPWGEPSCHGLKAATGVPSTLEVPSLPNNSPSPHYLSV
			YCRCVPHRPAHCCHPPSCPSQPRCHAPGRAAAPHLLWQTQPTAL
1			PVLPGGLPPAPLLPIPLSLOTOCSTSTPRRPSIKAS
F222	 	 	<u> </u>
5392	ı	1623	IRGSNAQKVVGASGSGGAGPQPDPAGPGGVPALAAAVLGACEPR
		,	CAAPCPLPALSRCRGAGSRGSRGGRGAAGSGDAAAAAEWIRKGS
			FIHKPAHGWLHPDARVLGPGVSYVVRYMGCIEVLRSMRSLDFNT
			RTQVTREAINRLHEAVPGVRGSWKKKAPNKALASVLGKSNLRFA
1			GMSISIHISTDGLSLSVPATRQVIANHHMPSISFASGGDTDMTD
1			YVAYVAKDPINQRACHILECCEGL\AQSIISTVGQAFELRFKQY
1			LHSPPKVALPPERLAGPEESAWGDEEDSLEHNYYNSIPGKEPPL
			GGLVDSRLALTQPCALTALDQGPSPSLRDACSLPWDVGSTGTAP
			_
İ			PGDGYVQADARGPPDHEEHLYVNTQGLDAPEPEDSPKKDLFDMR
1	j		PFEDALKLHECSVAAGVTAAPLPLEDQWPSPPTRRAPVAPTEEQ
1			LRQEPWYHGRMSRRAAERMLRADGDFLVRDSVTNPGQYVLTGMH
1	İ		AGQPKHLLLVDPEGVVRTKDVLFESISHLIDHHLQNGQPIVAAE
		<u>L</u>	SELHLRGVVSREP
5393	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
İ _			PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG
			· · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
i			
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
1			\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
\			LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
1	1		SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
Į			QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
1		1	STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
[ļ	RAPTDDDKNIYLTLPPNDHVNSNN
5394	2	982	GGDSAGMTMETQMSQNVCPRNLWLLQPLTVLLLLASADSQAAAP
	ļ		PKAVLKLEPPWINVLQ\EDSVTLTCQGAPQP/ERSDSIQWFHNG
1			\NLIPTHTQPS\YRFKANNN\DSGEYTCQTGQTSL\SDPVHLTV
1			LSEWLVLQTPHLEFQEGETIMLRCHS\WRDKP\LVKVTFFQNGK
<u> </u>	İ	J	SQKFSHLDPTFSIPQANHSHSGDYHCTGNIGYTLFSSKPVTITV
1		1	QVPSMGSSSPMGIIVAVVIATAVAAIVAAVVALIYCRKKRISAN
1	}	1	STDPVKAAQFEPPGRQMIAIRKRQLEETNNDYETADGGYMTLNP
			RAPTDDDKNIYLTLPPNDHVNSNN
5395	2325		RASDAKNOEGLLNTRRKSTDSVPISKSTLSRSLSLOASDFDGAS
2372	3135	531	
		1	SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
		1	KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
			LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
]	l		RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
1			SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
	İ	1	PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL
ŀ		}	PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
	1		ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
ſ		ĺ	TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
Į.	1	1	YPOPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPOD
			DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
[Î	ALVNTAAKNOHPVPRGLAPNOESHLOVPEKSSOKELEAMGLGTP
ł			SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
ł		İ	PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
ſ		1	PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
1			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
l		}	\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
1			YOALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
1	1	4	CRV\DALERTLEQKNKEIBELTKICDELIAKMGKS
5396	3135	531	RASDAKNOEGLLNTRRKSTDSVPISKSTLSRSLSLOASDFDGAS
			SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKOTTK
ł		İ	KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
			LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
1 .			RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
			SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
			PRSPAEPNDIPIAKGTYTFDIDKWDDPNFNPFSSTSKMOESPKL
			PQQSYNFDPDTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
			1
1.		1	ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
1		[TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
		1	YPQPSDLSTFVNETKFSSPTEELDYRNSYEIEYMEKIGSSLPQD
	}	1	DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFRETE
		1	ALVNTAAKNOHPVPRGLAPNOESHLOVPEKSSOKELEAMGLGTP
			SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
			PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
]	PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
			YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLINSVEK
		Ī	\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
1			YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
			CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
5397	3135	531	RASDAKNQEGLLNTRRKSTDSVPISKSTLSRSLSLQASDFDGAS
	1]	SSGNPEAVALAPDAYSTGSSSASSTLKRTKKPRPPSLKKKQTTK
		\	KPTETPPVKETQQEPDEESLVPSGENLASETKTESAKTEGPSPA
		1	LLEETPLEPAAGPKAACPLDSESVEGVVPPASGGGRVQNSPPVG
			RKTLPLTTAPEAGEVTPSDSGGQEDSPAKGHSVRLEFDYSEDKS
1		1	,
1	1		SWDNQQENPPPTKKIGKKPVAKMPLRRPKMKKTPEKLDNTPASP
	1	l	PRSPAEPNDIPLAKGTYTFDIDKWDDPNFNPFSSTSKMQESPKL

	T 57 - 4-	Tipungs 2 3	Aming gold germant containing
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	1		
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
	- Sodanise		POOSYNFOPOTCDESVDPFKTSSKTPSSPSKSPASFEIPASAME
	İ		
	1	J	ANGVDGDGLNKPAKKKKTPLKTDTFRVKKSPKRSPLSDPPSQDP
			TPAATPETPPVISAVVHATDEEKLAVTNQKWTCMTVDLEADKQD
		1	YPQPSDLSTFVNETXFSSPTEELDYRNSYEIEYMEKIGSSLPQD
	1		DDAPKKQALYLMFDTSQESPVKSSPVRMSESPTPCSGSSFEETE
	ì		ALVNTAAKNOHPVPRGLAPNOESHLQVPEKSSOKELEAMGLGTP
	\		SEAIEITAPEGSFASADALLSRLAHPVSLCGALDYLEPDLAEKN
	!	1	
		1	PPLFAQKLQREAAHPTDVSISKTALYSRIGTAEVEKPAGLLFQQ
	1	[PDLDSALQIARAEIITKEREVSEWKDKYEESRREVMEMRKIVAE
	1	1	YEKTIAQMIEDEQREKSVS\HQTVQQLVLEKEQA\LADLNSVEK
		1	\SLADLFRRYEKMKEVLEGFRKNEEVLKRCAQEYLSRVKKEEQR
	i		YQALKVHA\EEKLDRANAE\IAQVRGKAQQEQAAHQASLAERSS
			CRV\DALERTLEQKNKEIEELTKICDELIAKMGKS
	 	 	
5398	56	5426	SGEVCRMESNFNQEGVPRPSYVFSADPIARPSEINFDGIKLDLS
	İ		HEFSLVAPNTEANSFESKDYLQVCLRIRPFTQSEKELESEGCVH
	1		ILDSQTVVLKEPQCILGRLSEKSSG\QM\AQKFSFFPGFLGPAT
	1		TQKEFFQGCIMHP\VKDLLKGQSRLIFTYGLTNSGKTYTFQGTE
			ENIRILPRTLNVLFDSLQERLYTKMNLKPHRSRBYLRLSSEQEK
	1		EEIASKSALLROIKEVTVHNDSDDTLYGSLTNSLNISEFEESIK
	1		
	1		DYEQANLNMANSIKFSVWVSFFEIYNEYIYDLFVPVSSKFQKRK
	1	(MLRLSQDVKGYSFIKDLQWIQVSDSKEAYRLLKLGIKHQSVAFT
	1		KLNNASSRSHSIFTVKILQIEDSEMSRVIRVSELSLCDLAGSER
			TMKTONEGERLRETGNINTSLLTLGKCINVLKNSEKSKFQQHVP
	ļ		FRESKLTHYF/QSFFNGKGKICMIVNISQCYLAYDETLNVLKFS
	1		AIAOKVCVPDTLNSSQEKLFGPVKSSQDVSLDSNSNSKILNVKR
	ł	1	ATISWENSLEDLMEDEDLVEELENAEETED/VGETKLLDEDLDK
			TLEENKAFISHEEKRKLLDLIEDLKKKLINEKKEKLTLEFKIRE
		1	EVTQEFTQYWAQREADFKETLLQEREILEENAERRLAIFKDLVG
			KCDTREBAAKDICATKVETEEATACLELKFNQIKAELAKTKGEL
			IKTKEELKKRENESDSLIQELETSNKKIITQNQRIKELINIIDQ
		1	KEDTINEFONLKSHMENTFKCNDKADTSSLIINNKLICNETVEV
	Į.	i	PKDSKSKICSERKRVNENELQQDEPPAKKGSIHVSSAITEDQKK
		į.	SEEVRPNIABIEDIRVLQENNEGLRAFLLTIENELKNEKEEKAE
			LNKQIVHFQQELSLSEKKNLTLSKEVQQIQSNYDIAIAELHVQK
			SKNQEQEEKIMKLSNEIETATRSITNNVSQIKLMHTKIDELRTL
		}	DSVSQISNIDLLNLRDLSNGSBEDNLPNTQLDLLGNDYLVSKQV
	l .		KEYRIQEPNRENSFHSSIEAIWEECKEIVKASSKKSHQIEELEQ
}			QIEKLQAEVKGYKDENNRLKEKEHKNQDDLLKEKETLIQQLKEE
	1	İ	LQEKNVTLDVQIQHVVEGKRALSELTQGVTCYKAKIKELETILE
Ì	j		TQKVERSHSAKLEQDILEKESIILKLERNLKEFQEHLQDSVKNT
			KDLNVKELKLKEEITQLTNNLQDMKHLLQLKEEEEETNRQETEK
Ì	1		LKEELSASSARTQN\LNADLQRKEEDYADLKEKLTDAKKQIKQV
			QKEVSVMRDEDKLLRIKINELEKKKNQCSQELDMKQR\TIQQLK
l	}		EOLINOKVEEAIQOYERACKDLNVKEKIIEDMRMTLEEQEQTQV
			EQDQVL\BAKLEEVERLATELDRWRVKCNDLETKNNQRSNKEHE
		-	NNTDVLGKLTNLQDELQESEQKYNADRKKWLEEKMMLITQAKEA
]	J		
1	!		ENIRNKEMKKYAEDRERFFKQQNEMEILTAQLTEKDSDLQKWRE
1	1		ERDQLVAALEIQLKALISSNVQKDNEIEQLKRIISETSKIETQI
	ļ		MDIKPKRISSADPDKLQTEPLSTSFEISRNKIEDGSVVLDSCEV
ł	į.		STENDQSTRFPKPELEIQFTPLQPNKMAVKHPGCTTPVTVKIPK
l		1	ARKRKSNEMEEDLVKCENKKNATPRTNLKFPISDDRNSSVKKEQ
(1		
	1	}	KVAIRPSSKKTYSLRSQASIIGVNLATKKKEGTLQKFGDFLQHS
	i	1	PSILQSKAKKIIETMSSSKLSNVBASKENVSQPKRAKRKLYTSE
1		1.	ISSPIDISGQVILMDQKMKESDHQIIKRRLRTKTAK
5399	705	230	GPRMAKFLSQDQINEYKECFSLYDKQQRGKIKATDLMVAMRCLG
			ASPTPGEVQRHLQTHGIDGNGELDFSTFLTIMHMQIKQEDPKKE
1			ILLAMLMVDKEKKGYVMASDLRSKLTSLGEKLTHKEV\DDLFRE
1	Į	1	
ı		1	\ADIEPNGKVKYDEFIHKITSYLDGTY
5400	931	248	SHCSSGMEIPPTNYPASRAALVAQNYINYQQGTPHRVFEVQKVK
5400	931	248	

SEC	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nuclcotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
			FGNVSPEMTLVLHLAWVACGYIIWQNSTEDTWYKMVKIOTVKOV
		ì	QRNDDFIELDYTILLHNIASQEIIPWQMQVLWHPQYGTKVKHNS
			RLPKEVQLE
5401	3	1360	TGWSYGPTTSLAFLAPRDFPFPPKLLIHPQAVVRLSCGAGSMGS
			QAAAEWRNWASWEGSSSLSGCSMGCFKDDRIVFWTWMFSTYFME
			KWAPRODDMLFYVRRKLAYSGSESGADGRKAAEPEVEVEVYRRD
			SKKLPGLGDPDIDWEESVCLNLILQKLDYMVTCAVCTRADGGDI
			HIHKKKSQQVFASPSKHPMDSKGEESKISYPNIFFMIDSF\BE\
1			VFSDMTVGKGEMVCVELVASDKTNTFQGVIFQGSIRYEALKKVY
1			DNRVSVAARMAQK\MSFGFSKYSNMEF\VR\MKGPQGKGHAEMA
			VSRVSTGDTSPCGTEEDSSPASPMHERVTSFSTPPTPERNNRPA
		1	FFSPSLKRKVPRNRIAEMKKSHSANDSEEFFREDDGGADLHNAT
[NLRSRSLSGTGRSLVGSWLKLNRADGNFLLYAHLTYVTLPLHRI
			LTDILEVRQKPILMT
5402	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
1			PGADILNSYAGLACVEEPNDMITESSLDVAEEEIIDDDDDDDTL
1		}	TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS
1			PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEQ
1			PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
			ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
1			MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE
1			DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
-			PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
1			RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
1			MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
			VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
Ì			ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS
1		}	QVAMKONELLEPNSF
5403	3445	1563	GECFIMAAVVQQNDLVFEFASNVMEDERQLGDPAIFPAVIVEHV
			PGADILNSYAGLACVEBPNDMITESSLDVAREEIIDDDDDDDITL
,			TVEASCHDGDETIETIEAAEALLNMDSPGPMLDEKRINNNIFSS
			PEDDMVVAPVTHVSVTLDGIPEVMETQQVQEKYADSPGASSPEO
1			PKRKKGRKTKPPRPDSPATTPNISVKKKNKDGKGNTIYLWEFLL
	ł] 	ALLQDKATCPKYIKWTQREKGIFKLVDSKPVSRLWRKHKNKP\D
Ì			MNYEPMGRALRYYYQRGILAKVEGQRLVYQFKEMPKDLIYINDE
	1		DPSSSIESSDPSLSSSATSNRNQTSRSRVSSSPGVKGGATTVLK
			PGNSKAAKPKDPVEVAQPSEVLRTVQPTQSPYPTQLFRTVHVVQ
			PVQAVPEGEAARTSTMQDETLNSSVQSIR\TIQAPTQVPVVVSP
			RNQQ\LHTVTLQTVPLTTVIASTDPSAGTGSQKFILQAIPSSQP
1	1		MTVLKENVMLQSQKAGSPPSIVLGPARV\QQVLTSNVQTICNGT
1	1		VSV\ASSPSFS\ATAPVVTLFLLGSSQLVAHPPGTVITSVIKTQ
			ETKTLTQEVEKKESEDHLKENTEKTEQQPQPYVMVVSSSNGFTS
F404	100		QVAMKQNELLEPNSF
5404	187	1111	LPVTLIFAKMKTLQSTLLLLLLVPLIKPAPPTQQDSRIIYDYGT
			DNFEESIFSQDYEDKYLDGKNIKEKETVIIPNEKSLQLQKDEAI
			TPLPPKKENDEMPTCLLCVCLSGSVYCEEVDIDAVPPLPKESAY
1	1		LYARPNKIKKLT\AKDFADIPNLRRLDFTGNLIEDIEDGTFSKL
[SLVEELSLAENQLLKLPVLPPKLTLFNAKYNKIKSRGIKANAFK KINNITTELYLDUNALESUDINLDESIDVINLAENDINE
			KLNNLTFLYLDHNALESVPLNLPESLRVIHLQFNNIASITDDTF CKANDTSYIRDRIEEIRLEGNPIVLGKHPNSFICLKRLPIGSYF
5405	2199	1220	QNSRSLHMDPQNQHGSGSSLVVIQQPSLDSRPRLDYEREIQPTA
		1220	ILSLDQIKAIRGSNEYTEGPSVVKRPAPRTAPRQEKHERTHEII
			PINVNNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGS
-			NSSASSEQGLLGRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGS
1	1		LKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLACNRQCLCSAE
			SMVEYGTCMCL\VKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSR
}			YLCMGAMSLFLPCLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNS
	1		NTVYCKLESCPSRGQGKPS
5406	279	2732	RWRTYNVEGPLTFMDVAIEFCLEEWQCLDTAQQNLYRNVMLENY
		ь <u>. </u>	The state of the s

Predicted Predicted Predicted en Indicating Predicted Indicating Indi			Predicted end	Amino acid segment containing signal peptide
MO: location corresponding to first amino acid residue of amino acid residue of amino acid sequence and corresponding to first amino acid sequence and corresponding to first amino acid sequence and corresponding to first amino acid sequence and corresponding to first amino acid sequence and corresponding to the correspondi				
corresponding to first amino acid amino acid residue of amino acid amino acid amino acid amino acid sequence se	ID	beginning	nucleotide	
corresponding to first amino acid amino acid residue of amino acid amino acid amino acid amino acid sequence se	NO-	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid sequence sequ		1		
to first amino acid residue of amino acid amino acid amino acid amino acid sequence ### Tryptophan, Y=Tyrosine, X=Unknown. *=Stop Codon, /=possible nucleotide deletion, V=possible nucleotide deletion, V=possible nucleotide deletion, N=possible nucleotid		1		
amino acid mino acid sequence where the property of the control of amino acid sequence where the control of the control of amino acid sequence where the control of the con		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
amino acid mino acid sequence where the property of the control of amino acid sequence where the control of the control of amino acid sequence where the control of the con	Į.	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
menidue of amino acid sequence whityptophan, Y-Tyrosine, X-Unknown, **Stop Codon, /*possible nucleotide deletion, /*possible nucleotide deletion, /*possible nucleotide deletion, /*possible nucleotide deletion, /*possible nucleotide deletion, /*possible nucleotide insertion) RIUFER(S) INAUSERUE (THE GREEN PEREMENVAKPPVMC SHPTODEW PSGNILDE POKATLER YNNCEKISVILKEH) VERVER (THE COMMENT OF THE STOP SHE SHE SHE SHE SHE SHE SHE SHE SHE SHE	1			
amino acid sequence Codon, /=possible nucleotide deletion, -possible nucleotide insertion -possible nucleotide insertion SHIPTEG/IINOSKPDLTCLEGEESHREPMRIEWVAKEPOWC SHIPTOGPEPBORIND POPKATLERY NACERINVHLAKENHSVDB CKVERRGYNGFROCLEATOSKITLEDKCVKAPHKFSNDRHKIS CKVERRGYNGFROCLEATOSKITLEDKCVKAPHKFSNDRHKIS HTEKLIPCEGGGARYSCHILDHKUITUTEKPYTCCECKGGKAP NCPSILTHKIRINGEKPYTCEBCKVYMWSSRITHKKHYTCE KINCEGGRAPHKSSILTHKIITUTEKPYTCCEGKGYKAP KINCEGGRAPHKSSILTHKIITUTEKPYTCCEGGKYMSSRITHKKHYTCE CECGGARYOFSILTHKRIHTAGEKPYTCEGGKYMSSRITHKK KNYTRYKLYKCEGCGARPKSSILTHKKHIHTGEKPYTCEGGKYMSSRITHKK KNYTRYKLYKCEGCGARPKSSILTHKKHHTGEKPYTCEGGKAPKNSSRITHKK KNYTRYKLYKCEGCGARPKSSILTHKKHHTGEKPYTCEGGKAPKNSSRITHKK KNYTRYKLYKCEGCGARPKSSILTHKKHHTGEKPYTCEEGGKAPKNSSRITHKK KNYTRYKLYKCEGCGARPKSSILTHKKHHTGEKPYTCEEGGKAPKNSSRITHKK KNYTRYKLYKCEGCGARPKSSTLTHKKHHTGEKPYTCEEGGKAPKNSSRITHKKHTGEKPYTCEEGGKAPKNSSRITHKKHHTGEKPYTCEEGGKAPKNSSRITHKKHHTGEKPYTCEEGGKAPKNSSRITHKKHHTGEKPYTCEEGGKAPKNSSRITHKKHTGEKPYTCEEGGKAPKNSSRITHKKHTGEKPYTCEEGGKAPKNSSRITHKKHTGEKPYTCEEGGKAPKNSSRITHKKHTGEKPYTCEEGGKAPKNSSRITHKKHTGEKPYTCEEGGKAPKNSSRITHKKHTGEKPYTCEEGGKAPKNSSRITHKKHTGEKPYTCEEGGKAPKNSSRITHKKHTGEKPYTCEEGGKAPKNSSRITHKKHTGEKPYTCEEGGKAPKNSSRITHKKHTGEKPYTCEEGGKAPKNSSRITHKKHTGEKPYTCEEGGKAPKNSSRITHKKHTGEKPYTCEEGGKAPKNSSRITHKKHTTEKKOPTTCEEGGKAPKNSSRITHKKHTTEKKOPTTCETTEKTKTTEKTAPKTCEEGGKAPKNSSRITHKKHTTTEKKOPTTCETTEKTKTTEKTAPKTCEEGGKAPKNSSRITHKKHTTTTCKTTTTTKKTTTTTKTTTTTTKTTTTTTTTT	i			
Sequence N=possible nucleotide insertion		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence N=possible nucleotide insertion	}	amino acid	semience	Codon. /=possible nucleotide deletion,
RILUPEG/ITAUSKPOLITCLEGEKEDMEPMERIEWAKPEPUNG SHPTODF PEPGHILD POKATLERY NICKERHINHLIKANKEPUNG CKVURRGYNOFFOCLE PATOSKI FLIDKCVAFHKFSINSHKI SI CKVURRGYNOFFOCLE PATOSKI FLIDKCVAFHKFSINSHKI SI THEKKI-FKCKEGOSF CHIGSHLOAJKIL LITHVAYINC KOK GGGAF NCPSI LITHKER INTGEKPYTCEBCGKVFMSSSRITTHKKHTTOSKOYT KLYKCKEGOKAFNISS ILTHKKI HITGEKFYKCKEGAFAROSS KINTSHKKI-HIDGKCYKCEBCCKAFFMSSKI-THKKHTHOSKOYT CECGGAROFOSIL THKKH INTGEKFYKCKEGGAFSSS SINT THKEHITTEKFYKCBECOKAFFMSSKI-THKKHHTOSKOYT KREHITTEKFYKCBECOKAFFMSSKI-THKKHHTOSKOYTHKK KNYTTYKI-JKCBECOKAFFMSSKI-THKKHHTOSKOYTHKK KNYTTYKI-JKCBECOKAFFMSSLITTHKKHHTOSKOYTHKK KNYTTYKI-JKCBECOKAFFMSSLITTHKKHHTEKFKYKCBECOKAF PKASKKI-TBKH,TTTEKFYKYCEBCOKAFFMSSRITTHKK KNYTTYKI-JKCBECOKAFFMSSLITTHKKHHTEKFKYKCBECOKAFF SENDITTHKKHTHOSKOYTKCBECOKAFFMSSLITTHKKHHTOSKOYTHKRHTO GEKTYKCBECOKAFFNSSLITTHKKHHTOSKOYTKCBECOKAFFNSSLITTHKKHHTOSKOYTKCBECOKAFFNSSLITTHKKHHTOSKOYTKCBECOKAFFNSSLITTHKKHTOSKOYTKCBECOKAFFNSSLITTHKKHHTOSKOYTKCBECOKAFFNSSLITTHKKHTOSKOYTKCBECOKAFFNSSLITTHKTOSKOYTKCBECOKAFFNSSLITTHKKHTOSKOYTKCBECOKAFFNSSLITTHKKTAFTNOSKOYTKCBECOKAFFNSSLITTHKKHTOSKOYTKCBECOKAFFNSSLITTHKKTAFTNOSKOYTKCB	1	1	bequence	· · · ·
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KCGKARNCPSILTHKINRINTGEKPYKCEGGKVPMWSSLITHKK HYNYRYKLYKEGKGKA AFKWSKLTEHKITHTGKPYKCEGCKARNHESILTKHKRIHTG GEKPYKCEGCKARNHESILTKKKHRIHTGKPYKCEGCKARNES SSNITHKKIHTGGKPYKCEGCKARNHESILTKKKHRIHT GEKPYKCEGCKARNESTILTKKKIHTGKPYKCEGCKARNES SSNITHKKHITGKPYKCEGCKARNESTILTKKKIHTGKPYKCEGCKARNES LSTRKIHTGKRYKPKCEKCKARNESNILTHKKIHTGKPYKCEGCKARNESNILTH KRITCHKLYPEDVYLLTHTOTTSNIK 5407 3 659 RPRRGSSCTGMIAGMILKRARPRYCKEKCKARNYSNITTH NKIHTGKLYVPEDVYLTHTOTTSNIK KRIMIGFITEDKKKMIGSNAKDRGMYCKSSONKSYRILTH KRIGMIGFITEDKKKMIGSNAKDRGMYCKSSONKSYRILTY KRIMIGFITEDKKKMIGSNAKDRGMYCKSSONKSYRILTY KRIMIGFITEDKKKMIGSNAKDRGMYCKSSONKSYRILTY KRIMIGFITEDKKKMIGSNAKDRGMYCKSSONKSYRILTY KRIMIGFITEDKKKMIGSNAKDRGMYCKSSONKSYRILTY KRIMIGFITEDKKKMIGSNAKDRGMYCKSSONKSYRILTY KRIMIGFITEDKKKMIGSNAKDRGMYCKSSONKSYRILTY KRIMIGFITEDKKKMIGSNAKDRGMYCKSSONKSYRILTY KRIMIGFITEDKKKMIGSNAKDRGMYCKSSONKSYRILTY KRIMIGFITEDKKKMIGSNAKDRGMYCKSSONKSYRILTY KRIMIGFITEDKYRMIGFITENTSTIPLOMPTICATOMPT KRIMIGFITEDKYRMIGSRAMPYTOPLOMPT KRIMIGFITENTSTIPLOMPTICATOMPT KRIMIGFITENTSTIPLOMPT KRIMIGFITENTSTIPLOMPT GSNATCHTORY SARGTCHPCAQOPMBEGVUQERFSGSEFWGGGGEFTLEKKENP GSNATCHPCAQOPMBEGVUQERFSGSEFWGGGGEFLEARTHPP REPUBLING MPFHYDPERSCWYRAT SQEDQLATCWQARHGE VENNINSWEBERFITANSKI DEHKVPTERGISLALGNTCFM NSSICCUSNTOPLTOYFTSGRHIYELINTHPIGMKGIMAKCYGD LVQLMSGTGONVAPLKKEMPTAKYAP FROPCOQDSGELLAFT. LDGILBIDLMRVHEKPYVELKDSGRPDBEVAARABADHHLRARRS IVVLPHEGLISAGVKKTCGHISVRPDPFHYLSJELPLDMDSYMHI EITVIKLDGTTPVYGCIRLNMDEKYTGLKKQLSDLCGLASEQIL LLABVHSSNIKNFPQDNGKVRLSVSGPLCAFEIPVYSPSIJASSP TUTDFSSSSSTRIMEPTLITNSDLPPHI FINMFMPTTVVPCOTEK NETMWONHFSSLPDSPFTGYSILANTHROMPMTTVPCOTEK NETMWONHFSSLPDSPFTGYSILANTHROMPMTTVPCOTEK NETMWONHFSSLPDSPFTGYSILANTHROMPMTTVPCOTEK NETMWONHFSSLPDSPFTGYSILANTHROMPMTTVPCOTEK NETMWONHFSSLPDSPFTGYSILANTHROMPMTTVPCOTEK NETMWONHFSSLPDSPFTGYSILANTHROMPMTTVPCOTEK NETMWONHFSSLPDSPFTGYSILANTHROMPMTTVPCOTEK NETMWONHFSSLPDSPFTGYSILANTHROMPMTTVPCOTEK NETMWONHFSSLPDSPFTGYSILANTHROMPMTTAKARSPLOSPRIANTHROMPT LLABVHSSNIKHPONGRAMAKTOND PELLIHLINGTGGFTCHARTSPLEPELDBALDANTHROMPT NASHOLOVATORPONGRAMAKTOND NASHOLOV	{		ĺ	1
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NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQBLWSGTQKNVAPLKLRNTIANYAPRFNGQQDSQELLAFIL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAMDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLPLPMDSYMHL EITVIKLDGTTPYRYGLRLMNDEKYTGLKKQLSDLCGLNSEQIL LAEVHGSNIKNFPQDNQKVRLSVSGPLCAFEIPVPVSPISASSP TQTDFSSSPSTNEMFTLTTNGDLPPPIFIPNOMPNTVVPCGTEK NFTNGMVNGHMPSLPDSPPTGYIIAVHRKMMETELYFLSSQKNR PSLFGMPLIVPCTVHTRKKDLYDAWIQVSRLASPLPPGEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAMCPWXFFCRGCKLTCGE DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHBSVEQSRRAQ VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRPQFVNGRWIKSQKLVKFPRESFDPSA FLUPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSKSGTSCPSSKNSSPNSSPRTLGRS KGRLPPQIGSKNKLSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHERACGNGCGNGYSNGQLG NHSEEDSTDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYSQCGIDYAQFLPK TDGKKMADTSSMBEDFSDY\EKYCVLQ 5409 2745 6128 QSSKGTCHPOAQQPWDEGWQEAPSQSEPWGQSQEPFTMPQRLP HARQHTPLPLGSADYRRVVSVRPQSPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGYPSLALAQGGPQGSNFFLENKSMP RLPTDLDIGGPWFFHYDFERSCWVRAISQEDQLATCWQAEHCGE VENKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM NSSIQCVSNTOPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELMSGTQKNNAPLKLRWTIARYAPRFNGFQQQDSQELLAPL LGGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAMDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVILLDGTTPVRYGLGRLNKKQLSDLCGLNSEQIL	ļ	1	1	RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE
NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQBLWSGTQKNVAPLKLRNTIANYAPRFNGQQDSQELLAFIL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAMDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLPLPMDSYMHL EITVIKLDGTTPYRYGLRLMNDEKYTGLKKQLSDLCGLNSEQIL LAEVHGSNIKNFPQDNQKVRLSVSGPLCAFEIPVPVSPISASSP TQTDFSSSPSTNEMFTLTTNGDLPPPIFIPNOMPNTVVPCGTEK NFTNGMVNGHMPSLPDSPPTGYIIAVHRKMMETELYFLSSQKNR PSLFGMPLIVPCTVHTRKKDLYDAWIQVSRLASPLPPGEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAMCPWXFFCRGCKLTCGE DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHBSVEQSRRAQ VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRPQFVNGRWIKSQKLVKFPRESFDPSA FLUPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSKSGTSCPSSKNSSPNSSPRTLGRS KGRLPPQIGSKNKLSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHERACGNGCGNGYSNGQLG NHSEEDSTDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYSQCGIDYAQFLPK TDGKKMADTSSMBEDFSDY\EKYCVLQ 5409 2745 6128 QSSKGTCHPOAQQPWDEGWQEAPSQSEPWGQSQEPFTMPQRLP HARQHTPLPLGSADYRRVVSVRPQSPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGYPSLALAQGGPQGSNFFLENKSMP RLPTDLDIGGPWFFHYDFERSCWVRAISQEDQLATCWQAEHCGE VENKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM NSSIQCVSNTOPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELMSGTQKNNAPLKLRWTIARYAPRFNGFQQQDSQELLAPL LGGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAMDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVILLDGTTPVRYGLGRLNKKQLSDLCGLNSEQIL	İ	1	1	VONVOMENDERMERTANISSKT DOHKVOTEKGATGI.SNI GNTCFM
LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLMRVHEKPYVELKDSDGRPWEVAAEAMDHHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL LABVHGSNIKNFPQDNQKVRLUSVGFLCAFEITVPVSPJSASSP TQTDFSSSPSTNEMFTLTTNGDLPPPIFIPNOMPNTVVPCGTEK NFTNGMVNGHMSLPDSPPTGYIIAVHRKMMRTELYFLSSQKNR PSLFGMPLIVPCTVHTRKKDLYDAWNIQVSRLASPLPPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHBSVEGSRRAQ VSPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHHLKRFQFVNGRNIKSQKIVKFPRESFDPSAFLVPRDP ALCQHKPLTPQGGBLSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGGICELADALSRGH VLGGSQPELVTPQDHEVALANGFJVEHBRACGNGCOMGYSNGQLG NHSEEDSTDDQRBDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYRQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ 6128 GSKGTCHPDAQQDWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPGPPAOFQRFICSASPPWASRF STPCPGGAVREDTJPVGTQGYPSLALAQGGPGGSNFFLENKSMP RLPTDLDIGGPWFFHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIARYAPRFNGFQQDSGGLLAFL LGGLHEDLNRVHRKPYVELKDSDGRPDWEVAAEAMDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMLL EITVIKLDGTTPVRYGJGRLNKRDLSPLGLNSDCLANSSMIL	į.	1	1	
LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDFFKFLSJPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLOGLNSEQIL LAEVHGSNIKNFPQDNQKVRLSVSGFLCAFEIPVPVSPISASSP TQTDFSSSPSTNEMFTLTTNGDLPRPIFIPMSMTVVPCGTEK NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMRTELYFLSSQKNR PSLFGMPLIVPCTVHTRKKDLVDAVWIQVSRLASFPLPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIHLKRPQFVNGRWIKSGKIVKFPRESFPDSAFLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSKSGTSCPSSKNSSPNSSPNTLGRS KGRLRLDQIGSKNKLSSSKENLDASKENGAQQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIRPIYNLYAISCHSGILCGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMBEDFESDY\EKYCVLQ 5409 2745 6128 QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDFKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYVTYGTGGVPSLALAQGGPQGSWRFLENKSMP RLPTDLDIGGPWFPHYDFGRSCWVRAISQEDOLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM NSSIQCVSNTOPLTGYFIGGRHLYLELNRTNPIGMKGHMAKCYGD LVQELMSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAPL LGGLHEDLNRVHEKPYVELKGSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYFGLSLNMDBKYTGLKKQLSDLCGLNSEQIL	}	1	1	NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMRGHMARCYGD
IVVDLFHGQLRSQVKCKTCGHISVRPDFFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLMSEQIL LAEVHGSNIKNFPQDNQKVRLSVSGPLCAFEIPVPVSPISASSP TQTDFSSSPSTNEMFTLTTNGDLPRPIFIFIDMGMPNTVVPCGTEK NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR PSLFGMPLIVPCTYHTRKKDLYDAVWIQVSRLASFLPPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE DRAFIONAYIAVDWHPTALHLRYQTSQERVVDEHESVEGSRRAQ VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRPOFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQCIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ 5409 2745 6128 GGSKGTCHPQAQOPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGVRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDPERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFIGGRHJYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAPL LDGLHEDLNRVHEKPYVELKGSDGRPDWEVAARAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYFGLEKNGLSDLGGLNSEQIL	1		1	LVQBLWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL
IVVDLFHGQLRSQVKCKTCGHISVRPDFFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLMSEQIL LAEVHGSNIKNFPQDNQKVRLSVSGPLCAFEIPVPVSPISASSP TQTDFSSSPSTNEMFTLTTNGDLPRPIFIFIDMGMPNTVVPCGTEK NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR PSLFGMPLIVPCTYHTRKKDLYDAVWIQVSRLASFLPPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE DRAFIONAYIAVDWHPTALHLRYQTSQERVVDEHESVEGSRRAQ VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRPOFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQCIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ 5409 2745 6128 GGSKGTCHPQAQOPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGVRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDPERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFIGGRHJYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAPL LDGLHEDLNRVHEKPYVELKGSDGRPDWEVAARAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYFGLEKNGLSDLGGLNSEQIL			1	LOCILHEDI NEVHEKEYVEL KOSOGREDWEVAAEAWDNHI RENRS
EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL LABVHGSNIKNFPQDNQKVRLSVGGFLCAFEIPVPVSPISASSP TQTDFSSSPSTNEMFTLTTNGDLPPPIFIPNGMPNTVVPCGTEK NFTNGMVNGHMPSLPDSPTTGYIIAVHRKMMRTELYFLSSQKNR PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH AQDCDDSMGYQYFFTLRVVQKDGMSCAWCPWYRFCRGCKLDCGE DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEGSRRAQ VEPINLDSCLRAFTSEEBLGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRPQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ 5409 2745 6128 QGSKGTCHPQAQQPMDEGWQEAPSQSPEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSADAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAOFDRICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGFWFPHYDFRSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTOPLTGYFISGRHLVELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRPNGFQQQDSQELLAPL LDGLHEDLINRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPPNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRCHISVRFDPPPFLSLPLPMDSYMHL	1	1		
LAEVHGSNIKNFPQDNQKVRLSVSGPLCAFEIPVPVSPISASSP TQTDFSSSPSTNEMFTLTTNGDLPRPIFIPNCMPNTTVPCGTEK NFTNGMVNGMMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR PSLFGMPLIVPCTVHTRKKDLYDAVHIQVSRLASPLPPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKLDCGE DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRPGFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSNDEDFESDY\EKYCVLQ GSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTDLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWAGHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRRLYELMRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDFPNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDBKYTGLKKQDSDLCCLNSEQIL	1	1	1	
LAEVHGSNIKNFPQDNQKVRLSVSGPLCAFEIPVPVSPISASSP TQTDFSSSPSTNEMFTLTTNGDLPRPIFIPNCMPNTTVPCGTEK NFTNGMVNGMMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR PSLFGMPLIVPCTVHTRKKDLYDAVHIQVSRLASPLPPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKLDCGE DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRPGFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSNDEDFESDY\EKYCVLQ GSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTDLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWAGHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRRLYELMRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDFPNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDBKYTGLKKQDSDLCCLNSEQIL	1		ŀ	EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL
TQTDFSSSPSTNEMFTLTTMGDLPRPIFIPNGMPNTVVPCGTEK NFTNGMVNGHMPSLPDSPTGYIIAVHRKMMETELYFLSSQKNR PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASHH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKLDCGE DRAFIGNAYIANDWHPTALHLRYOTSGERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRROFVNGRWIKSQKIVKPPRESFDPSAFLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKEHPDEIDTDSAYILFYEQQGIDYAQFTLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ 5409 2745 6128 GCSKGTCHPQAQOPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFORPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELMSGTQKNVAPLKLRWTIAKYAPRFNGFQQODSQELLAFL LDGLHEDLNRVHEKPYVELKDSGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPPNFLSLPLPUNDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1 .	1	I	LAEVHGSNIKNFPODNOKVRLSVSGFLCAFEIPVPVSPISASSP
NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPI.PPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE DRAFIGMAYIAVDWHPTALHLRYQTSQERVVDEHBSVEQSRRAQ VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRPQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSNDEDFFSDY\EKYCVLQ GGSKGTCHPQAQQPWDEGWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFRSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAXYAPRFNGFQQODSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPPNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1	1	1	
PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE DRAFIGNAYIAVDWHPTALHHLRYOTSGERVVDEHESVEQSRRAQ VEPINLDSCLRAFTSEELGENEMYYCSKCKTHCLATKKLDLWR LPPILIIHLKRFQFVMGRWIKSQKIVKFPRESFDPSAFLVPRDP ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ 5409 2745 6128 QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQPPLCSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHGGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQBLLAFL LDGLHEDLNRVHEKPYVELKDSGRPDWEVAAEAMDNHLRRNS IVVDLFHGQLRSQVKCKTCGHISVRFDPPNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRINMDEKYTGLKKQLSDLCGLNSEQIL	1	1	1	
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ALCQHKPLTPQGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCYSNGQLG NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ 5409 2745 6128 QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDSGELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVABEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1		1	l e e e e e e e e e e e e e e e e e e e
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PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK TDGKKMADTSSMDEDFESDY\EKYCVLQ 5409 2745 6128 QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRPNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1	I	J	1
TDGKKMADTSSMDEDFESDY\EKYCVLQ 5409 2745 6128 QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHGGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1	1	1	NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
TDGKKMADTSSMDEDFESDY\EKYCVLQ 5409 2745 6128 QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHGGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1	1	1	PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEOOGIDYAOFLPK
5409 2745 6128 QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGHTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	1	1	1	
HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL				I TORVEWN I SOUTHER EDNI / EVICANA
HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	L			
APRPVPASRGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRPDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	5409	2745	6128	QGSKGTCHPQAQQPWDEGVWQEAPSQSEPWGQSQEPPTMPQRLP
STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQDDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	5409	2745	6128	
RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYBLNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQODSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDBKYTGLKKQLSDLCGLNSEQIL	5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL
RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYBLNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQODSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDBKYTGLKKQLSDLCGLNSEQIL	5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF
VRNKDMSWPEEMSFIANSSKIDRHKVPTEKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQODSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF
NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP
LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE
LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM
LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM
IVVDLFHGQLRSQVKCKTCGHISVRFDPFNFLSLPLPMDSYMHL EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD
EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRPNGFQQQDSQELLAFL
EITVIKLDGTTPVRYGLRLNMDEKYTGLKKQLSDLCGLNSEQIL	5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS
LAEVHGSNI KNFPODNOKVRLSVSGFLCAFEIPVPVSPISASSP	5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS
LAEVHGSNIKNFPODNOKVRLSVSGFLCAFEIPVPVSPISASSP	5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPFBKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNRTNPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFMGFQQQDSQBLLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPPNFLSLPLPMDSYMHL
	5409	2745	6128	HARQHTPLPLGSADYRRVVSVRPQGPHRDPKDSRDAAKREQGSL APRPVPASRGGKTLCKGYRQAPPGPPAQFQRPICSASPPWASRF STPCPGGAVREDTYPVGTQGVPSLALAQGGPQGSWRFLEWKSMP RLPTDLDIGGPWFPHYDFERSCWVRAISQEDQLATCWQAEHCGE VRNKDMSWPEEMSFIANSSKIDRHKVPTBKGATGLSNLGNTCFM NSSIQCVSNTQPLTQYFISGRHLYELNTPPIGMKGHMAKCYGD LVQELWSGTQKNVAPLKLRWTIAKYAPRFNGFQQQDSQELLAFL LDGLHEDLNRVHEKPYVELKDSDGRPDWEVAAEAWDNHLRRNRS IVVDLFHGQLRSQVKCKTCGHISVRFDPFMFLSLPLFMDSYMHL EITVIKLDGTTPVRYGLRLWNDEKYTGLKKQLSDLCGLNSEQIL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
,	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
] }	amino acid	sequence	Codon, /=possible nucleotide deletion,
	-	sequence	
i	sequence	<u> </u>	\=possible nucleotide insertion)
•			TOTOFSSSPSTNEMFTLTTNGDLPRPIFIPNGMPNTVVPCGTEK
}	·		NFTNGMVNGHMPSLPDSPFTGYIIAVHRKMMRTELYFLSSQKNR
ł		\ ·	PSLFGMPLIVPCTVHTRKKDLYDAVWIQVSRLASPLPPQEASNH
i i		į	AQDCDDSMGYQYPFTLRVVQKDGNSCAWCPWYRFCRGCKIDCGE
† !		1	DRAFIGNAYIAVDWHPTALHLRYQTSQERVVDEHESVEQSRRAQ
ì			VEPINLDSCLRAFTSEEELGENEMYYCSKCKTHCLATKKLDLWR
			LPPILITHLKRFQFVNGRWIKSQKIVKFPRESFDPSAFLVPRDP
l I		1	ALCOHKPLTPOGDELSEPRILAREVKKVDAQSSAGEEDVLLSKS
j }			PSSLSANIISSPKGSPSSSRKSGTSCPSSKNSSPNSSPRTLGRS
\ \	,	l .	Y ·
]			KGRLRLPQIGSKNKLSSSKENLDASKENGAGQICELADALSRGH
]]			VLGGSQPELVTPQDHEVALANGFLYEHEACGNGCGNGYSNGQLG
]	j		NHSEEDSTDDQREDTRIKPIYNLYAISCHSGILGGGHYVTYAKN
			PNCKWYCYNDSSCKELHPDEIDTDSAYILFYEQQGIDYAQFLPK
Į.			TDGKKMADTSSMDEDFESDY\EKYCVLQ
5410	2	710	LRFPGQARHVWLAARMQAPHKEHLYKLLVIGDLGVGKTSIIKRY
	_		VHONFSSHYRATIGVDFALKVLHWDPETVVRLQLWDIAGQERFG
Į į			NMTRVYYREAMGAFIVFDVTRPATFEAVAKWKNDLDSKLSLPNG
		l	KPVSVVLLANKCDQGKDVLMNNGLKMDQFCKEHGFVGWFETSAK
1			ENINIDEASRCLVKHILANECDLMESIEPDVVKPHLTSTKVASC
1		1	SG\CAKILVGTFAGVW
			· · · · · · · · · · · · · · · · · · ·
5411	1302	289	TGPAAAGRRKALGSFGKPSPVTGLRAARRRTRPSAPAAPSVGC
	ĺ		GKRRESDAGAGGERASVRTGSGRRGGRTMAGDSEQTLQNHQQPN
ļ		1	GGEPFLIGVSGGTASGKSSVCAKIVQLLGQNEVDYRQKQVVILS
		1	QDSFYRVLTSEQKAKALKGQFNFDHPDAFDNELILKTLKEITEG
)	}	l .	KTVQIPVYDFVSHSRKEETVTVYPADVVLFEGILAFYSQER/IR
1			DLFQMKLFVDTDADTRLSRRVLKDISERGRDLEQILSSSTLRFV
ļ.	i	1	KPA\FEEFCLPPK\KYADVIIPR\GADN\RVPINLIVQHIQ\DI
			LNGGPS\NRQTNGCLNGYTPSRKRQASESSSRPH
5412	3180	313	OGISNFFHKEANFWFEVSGYLISPLRSPFVDPALEWSLMASPWN
5412	3100	1 313	KMEGESSRFEIHTPVSDKKKKKCSIHKERPQKHSHEIFRDSSLV
i		1	NEOSOITRRKKRKKDFOHLISSPLKKSRICDETANATSTLKKRK
1			KRRYSALEVDERAGVTVVLVDKENINNTPKHFRKDVDVVCVDMS
			IEQKLPRK\PKTDKFQVLAKSH\AHKSEALHSKVREKKNKKHQR
			KAASWESQRA\RDTLPQSEFPTQEESWLSVGPGGEITELP\ASA
			HKNKSKKKKKSSNREYET\LAMPEGSQAGREAGTDMQESQPTV
			GLDDETPQLLGPTHKKKSKKKKKKKKSNHQEFESLAMPEGSQVGS
1			EVGADMQES\RPAVGLHGETAGIPAPAYKNKSKKKKKKSNHQEF
		1	EAVAMPESLESAYPEGSQVGSEVGTVEGSTALKGFKESNSTKKK
			SKKRKLTSVKRARVSGDDFSVPSKNSESTLFDSVEGDGAMMEEG
1		1	VKSRPRQKKTQACLASKHVQEAPRLEPANEEHNVETAEDSEIRY
1			LSADSGDADDSDADLGSAVKQLQEFIPNIKDRATSTIKRMYRDD
]		1	LERFKEFKAQGVAIKFGKFSVKENKQLEKNVEDFLALTGIESAD
1		1	KLLYTDRYPEEKSVITNLKRRYSFRLHIG\RNIARPWKLIYYRA
	1	1	KKMFDVNNYKGRYSEGDTEKLKMYHSLLGNDWKTIGEMVARRSL
l			SVALKFSOISSORNRGAWSKSETRKLIKAVEEVILKKMSPQBLK
1 '			
1			EVDSKLQENPESCLSIVREKLYKGISWVEVEAKVQTRNWMQCKS
1	1	1	KWTEILTKRMTNGRRIYYGMNALRAKVSLIERLYEINVEDTNEI
1			DWEDLASAIGDVPPSYVQTKFSRLKAVYVPFWQKKTFPEIIDYL
1			YETTLPLLKEKLEKMMEKKGTKIQTPAAPKQVFPFRDIFYYEDD
1	[SEGGGHRKRKRRPRRHAWFTPVIPVLWEAKAGWII
5413	3753	1304	RFPAGVAPRRAMANVSKKVSWSGRDRDDEEAAPLLRRTARPGGG
	1		TPLLNGAGPGAARQSPRSALFRVGHMSSVKLDDELLEP\DMDPP
1			HPFPKEIPHNEKLLSLKYESLDYDNSENQLFLEEERRINHTAFR
1			TVEIKRWVICALIGILTGLVACFIDIVVENLAGLKYRVIKGNID
1	1		KFTEKGGLSFSLLLWATLNAAFVLVGSVIVAFIEPVAAGSGIPQ
1			IKCFLNGVKIPHVVRLKTLVIKVSGVILSVVGGLAVGKEGPMIH
		1	
	i	1	SGSVIAAGISQGRSTSLKRDFKIFEYLRRDTEKRDFVSAGAAAG
			VSAAFGAPVGGVLFSLEEGASFWNQFLTWRIFFASMISTFTLNF
			VLSIYHGNMWDLSSPGLINFGRFDSEKMAYTIHEIPVFIAMGVV
			VLSIYHGNMWDLSSPGLINFGRFDSEKMAYTIHEIPVFIAMGVV GGVLGAVFNALNYWLTMFRIRYIHRPCLQVIEAVLVAAVTATVA
			VLSIYHGNMWDLSSPGLINFGRFDSEKMAYTIHEIPVFIAMGVV

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1 [corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P-Proline, Q-Glutamine, R-Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\≃possible nucleotide insertion)
			SVVSLFHDPPGSYNPLTLGLFTLVYFFLACWTYGLTVSAGVFIP
1			SLLIGAAWGRLFGISLSYLTGAAIWADPGKYALMGAAAOLGGIV
]]			RMTLSLTVIMMEATSNVTYGFPIMLVLMTAKIVGDVFIEGLYDM
1			HIQLQSVPFLHWEAPVTSHSLTAREVMSTPVTCLRRREKVGVIV
[[{	DVLSDTASNHNGFPVVEHADDTQPARLQGLILRSQLIVLLKHKV
į į			FVERSNLGLVQRRLRLKDFRDAYPRFPPIQSIHVSQDERECTMD
l i			LSEFMNPSPYTVPQEASLPRVPKLFRALGLRHLVVVDNRNQVVG
1			LVTRKDLARYRLGKRGLEELSLAQT
5414	2130	390	GVASAWDRALFSPLLSPTSRVFRTSPPRCVSTETGRRDRARVPS
}	2230		QWCSVLQGKLPVSGRTSLACVRSILLSPASSPRKVGIVGGTGAR
)			AGAAPRDHGRVRHRRPSSARRMTRTTGOCLAPRGCOGPRGTRSP
			RSPRSRTRRGCSASPACLP/CRSALIVAVLCYINLLNYMDRFTV
			AGVLPDIEOFFNIGDSSSGLIOTVFISSYMVLAPVFGYLGDRYN
		[RKYLMCGGIAFWSLVTLGSSFIPGEHFWLLLLTRGLVCVGEASY
		}	STIAPTLIADLFVADORSRMLSIFYFAIPVGSGLGYIAGSKVKD
			MAGDWHWALRVTPGLGVVAVLLLFLVVREPPRGAVERHSDLPPL
1 1			NPTSWWADLRALARNPSFVLSSLGFTAVAFVTGSLALWAPAFLL
		}	RSRVVLGETPPCLPGDSCSSSDSLIFGLITCLTGVLGVGLGVEI
1			SRRLRHSNPRADPLVCATGLLGSAPFLFLSLACARGSIVATYIF
] ;			IFIGETLLSMNWAIVADILLYVVIPTRRSTAEAFQIVLSHLLGD
1			AGSPYLIGLISDRLRRNWPPSFLSEFRALOFSLMLCAFVGALGG
i I			AAFLGTAHLH
5415	693	2986	IPPKTKLELQKH\LTTLT\NQEQATIFEEVQKLRPRNEQRENEL
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1			RLDMLKNKAKRSLTESLESILSRGNKARGLQBHSISVDLDSSLS
l i			STLSNTSKEPSVCEKEALPISESSFKLLGSSEDLSSDSESHLPE
1 1			EPAPLSPQQAFRRRANTLSHFPIECQEPPQPARGSPGVSQRKLM
1			RYHSVSTETPHERKDFESKANHLGDSGTPVKTRRHSWRQQIFL
			RVATPQKACDSSSRYEDYSELGELPPRSPLEPVCEDGPFGPPPE
1 1		}	EKKRTSRELRELWQKAILQQILLLRMEKENQKLQASENDLLNKR
1 1			LKLDYEEITPCLKEVTTVWEKMLSTPGRSKIKFDMEKMHSAVGQ
)			GVP\RHHRGEIWKFLAEQFHLKHQFPSKQQPKDVPYKELLKQLT
			SQQHAILIDLGRTFPTHPYFSAQLGAGQLSLYNILKAYSLLDQE
1 1			VGYCQGLSFVAGILLLHMSEEEAFKMLKFLMFDMGLRKQYRPDM
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			VLQEELIDSSPLSDNQRMDKLEKTNSSLRKQNLDLLEQLQVANG
			RIOSLEATIEKLLSSESKLKOAMLTLELERSALLOTVEELRRRS
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1 1			SYAPAAPTTSSMGSSIRHSPLSSGISTPVTNVSPMHLQHIRBQM
1			AIALKRLKELEEQVRTIPVIQVKISVLQEEKRQLVSQLKNQRAA
			SQINVCGVRKRSYSAGNASQLEQLSRARRSGGELYIDYEEEEME
			TVEQSTQRIKEFRQL\TADMQALEQKIQDSSCEASSELRENGEC RSVAVGAEENMNDIVVYHRGSRSCKDAAVGTLVEMRNCGVSVTE
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}			AMLGVMTEADKEIBLQQQTIBSLKEKIYRLEVQLRETTHDREMT
			KLKQELQAAGSRKKVDKATMAQPLVFSKVVEAVVQTRDQMVGSH
1			MDLVDTCVGTSVETNSVGISCQPECKNKVVGPELPMNWWIVKER
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GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR	5420	117	1733	
		<u> </u>	L	GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	I-louging M Mathierica W A
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
1	amino acid		P-Proline, Q-Glutamine, R-Arginine,
)		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ţ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ECIISTLLPATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
1	ì		LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS
1		1	LIHGLWNLVFLFSNLSLIFLMPFAYFFTESEGFAGSRKGVLGRV
1	1		YETVVMLMLLTLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
1		Į.	YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
1	Į.]	OL ACCUEED A LADDIC COMPANIE DA DISCULLA VANDE DE PER
			QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL
			LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
1		1	EAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGF
Ĭ)		YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
			TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
		İ	RAELIRAFGERE
5421	117	1733	NEAGGACPFKGGASGRLYLSPRLPRVSVAGCEERPLGWVWVLGG
	1		GGFLPARPPRAQRHLGFSHAEQSMEAPDYEVLSVREQLFHERIR
	1		ECIISTLLFATLYILCHIFLTRFKKPAEFTT\GMMKMPPSTRL/
			LLELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYYIQWLNGS
1	1	1	LIHGLWNLVPLFSNLSLIFLMPFAYFFTESBGFAGSRKGVLGRV
1			VETUMI MILTI WI CMUNIO OF TIMOTES TO THE SECOND OF THE SEC
1	1	1	YETVVMLMLITLLVLGMVWVASAIVDKNKANRESLYDFWEYYLP
j	1	ļ	YLYSCISFLGVLLLLVCTPLGLARMFSVTGKLLVKPRLLEDLEE
1]		QLYCSAFEEAALTRRICNPTSCWLPLDMELLHRQVLALQTQRVL
1	1		LEKRRKASAWQRNLGYPLAMLCLLVLTGLSVLIVAIHILELLID
1	!		EAAMPRGMQGTSLGQVSFSKLGSFGAVIQVVLIFYLMVSSVVGF
1	1		YSSPLFRSLRPRWHDTAMTQIIGNCVCLLVLSSALPVFSRTLGL
			TRFDLLGDFGRFNWLGNFYIVFLYNAAFAGLTTLCLVKTFTAAV
	L		RAELIRAFGERE
5422	3	1263	SCGESLPTWLAGASRPGIGRKGGAWGGRGGSSPAQVLLSPGPVF
			KAGCNWWHLSRDQAGVQRCDLGSSQPPPLGFKRFSCLSLPSSWD
1			YRSTVLCVSKMEADLSGFNIDAPRWDQRTFLGRVKHFLNITDPR
1			TVFVSERELDWAKVMVEKSRMGVVPPGTQVEQLLYAKKLYDSAF
			HPDTGEKMNVIGRMSFQLPGGMIITGFMLQFYRTMPAVIFWQWV
1	i		MOCENAL INVENDIA & COMCIDONAL GROUP MEMORY I PAGE
1	ļ		NQSFNALVNYTNRNAASPTSVRQMALSYFTATTTAVATAVGMNM
			LTKKAPPLVGRWVPFAAVAAANCVNIPMMRQQELIKGICVKDRN
1			ENEIGHSRRAAAIGITQVVISRITMSAPGMILLPVIMERLEKLH
ì			FMQKVKVL/SAPLQVMLSGCFLIFMVPVACGLFPQKCELPVSYL
			EPKLQDTIKAKYGELEPYVYFNKGL
5423	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ
			PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD
			ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE
]		EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG
		'	LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQERAEPRG
			GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
			GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKEYEDLLDYT
			YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
1			TNUSDNCDDARATAL DECCREBERT POWERS TO THE STATE OF THE STA
1			TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW
	}		SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL
1			RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
			LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
			PASFPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
	ſ		EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGOLPRK
1	i	İ	GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
1		ļ	SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
1			NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
1		ł	DKKPMAAMEHPCEGV
5424	3186	905	GVSMALGEEKAEAEASEDTKAQSYGRGSCRERELDIPGPMSGEQ
		,,,	PPRIMARGETTA PROGRAMMENT PROGR
1		l	PPRLEAEGGLISPVWGAEGIPAPTCWIGTDPGGPSRAHQPQASD
1			ANREPVAERSEPALSGLPPATMGSGDLLLSGESQVEKTKLSSSE
j !			EFPQTLSLPRTTICSGHDADTEDDPSLADLPQALDLSQQPHSSG
[LSCLSQWKSVLSPGSAAQPSSCSISASSTGSSLQGHQERAEPRG
			GSLAKVSSSLEPVVPQEPSSVVGLGPRPQWSPQPVFSGGDASGL
			GRRRLSFQAEYWACVLPDSLPPSPDRHSPLWNPNKBYEDLLDYT
1			YPLRPGPQLPKHLDSRVPADPVLQDSGVDLDSFSVSPASTLKSP
			TNVSPNCPPAEATALPFSGPREPSLKQWPSRVPQKQGGMGLASW

		1 5 37 3 3	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
i	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1			
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
)	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
<u> </u>	sequence	}	SQLASTPRAPGSRDARWERREPALRGAKDRLTIGKHLDMGSPQL
[-	_
ł	Į.	ł	RTRDRGWPSPRPEREKRTSQSARRPTCTESRWKSEEEVESDDEY
	ł	i	LALPARLTQVSSLVSYLGSISTLVTLPTGDIKGQSPLEVSDSDG
1			PASFPSSSSQSQLPPGAALQGSGDPEGQNPCFLRSFVRAHDSAG
1	1	1	EGSLGSSQALGVSSGLLKTRPSLPARLDRWPFSDPDVEGQLPRK
l	Į.	İ	GGEQGKESLVQC\VKTFC\CQLEELICWLYNV\ADVTDHGTPAR
1	i		
ĺ	1		SNLTSLK\SSLQLYRQFKKDIDEHQSLTESVLQKGEILLQCLLE
[1	NTPVLEDVLGRIAKQSGELESHADRLYDSILASLDMLAGCTLIP
l	1	ł	DKKPMAAMEHPCEGV
5425	1086	115	GFCPSPSLGHQPPRVLHPTMSMAVETFGFFMATVGLLMLGVTLP
-100			NSYWRVSTVHGNVITTNTIFENLWFSCATDSLGVYNCWEFPSML
1	1	1	
!	1		ALSGYIQACRALMITAILLGFLGLLLGIAGLRCTNIGGLELSRK
Ì			AKLAATAGAPH\ILPGICGMVAI\SWYAFNITR\DFSDPLYPGT
1		1	KYELGPALYLGWSASLISILGGLCLCSACCCGSDEDPAASARRP
1			YQAPVSVMPVATSDQEGDSSFGKYGRNALRVAALCRGPRCLPTA
	į.	1	PKKRGPGRGPFPYSNLRGRPRPVPVAPPRPRPRVLHSHGPSQAK
i	1		NCSWEVAYLPSEAGSLIF
5426	42	3435	ATSSQLGRADPPRGGTMERSPGEGPSPSPMDQPSAPSDPTDQP
5426	1 32	3435	· -
1	1	1	PAAHAKPDPGSGGQPAGPGAAGRALAVLTSFGRRLLVLIPVYLA
1	į	ſ	GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL
	i		TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
		1	LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
1	t	ì	KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
1	j	J	EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD
1	1	Ļ	
İ	ì	į	TMIMDSIAAPLVLPNRLLVPLVPDLQDVAQLRSPLPRGIIRIHL
	Į.	1	LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
		Į	POWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
İ	1		LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
			VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
	1	1	MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQBLDVQV
1	1	j	KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
	[· ·	1
ł	ì	1	KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
	1	<u> </u>	PCHTTPDSQFGTEHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
1			VKLKLAGRSFRSHVVREDLNPRWNEVFEVIVTSVPGQELEVEVF
1	1	1	DKDLDKDDFLGRCKVRLTTVLNSGFLDEWLTLEDVPSGRLHLRL
1		1	ERLTPRPTAABLEEVLQVNSLIQTQKSAELAAALLSIYMERAED
1	1		LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
}	1	1	RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
		1	
1	1	ĺ	SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
	}	1	GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE
		1	ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
1	1		KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
1 .			LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
E407	4	3435	ATSSOSLGRADPPRGGTMERSPGEGPSPSPMDOPSAPSDPTDOP
5427	42	3435	1
		1	PANHAKPDPGSGGQPAGPGAAGEALAVLTSFGRRLLVLIPVYLA
			GAVGLSVGFVLFGLALYLGWRRVRDEKERSLRAARQLLDDEEQL
		1	TAKTLYMSHRELPAWVSFPDVEKAEWLNKIVAQVWPFLGQYMEK
		1	LLAETVAPAVRGSNPHLQTFTFTRVELGEKPLRIIGVKVHPGQR
1		1	KEQILLDLNISYVGDVQIDVEVKKYFCKAGVKGMQLHGVLRVIL
	1	1	EPLIGDLPFVGAVSMFFIRRPTLDINWTGMTNLLDIPGLSSLSD
1			TMIMDSIAAFLVLPNRLLVPLVPDLODVAQLRSPLPRGIIRIHL
			,
1			LAARGLSSKDKYVKGLIEGKSDPYALVRLGTQTFCSRVIDEELN
1		1	PQWGETYEVMVHEVPGQEIEVEVFDKDPDKDDFLGRMKLDVGKV
1		1	LQASVLDDWFPLQGGQGQVHLRLEWLSLLSDAEKLEQVLQWNWG
			VSSRPDPPSAAILVVYLDRAQDLPMVTSELYPPQLKKGNKEPNP
			MVQLSIQDVTQESKAVYSTNCPVWEEAFRFFLQDPQSQELDVQV
1		}	
1		1	KDDSRALTLGALTLPLARLLTAPELILDQWFQLSSSGPNSRLYM
			KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR
			KLVMRILYLDSSEICFPTVPGCPGAWDVDSENPQRGSSVDAPPR PCHTTPDSQFGTBHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY
			PCHTTPDSQFGTBHVLRIHVLEAQDLIAKDRFLGGLVKGKSDPY

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
Ì	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
[amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
Í	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ļ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	pedacuce	Codon, /=possible nucleotide deletion,
		 	\=possible nucleotide insertion)
	j		ERLTPRPTAAELEEVLQVNSLIQTQKSAELAAALLSIYMERAED
			LPLRKGTKHLSPYATLTVGDSSHKTKTISQTSAPVWDESASFLI
ì			RKPHTESLELQVRGEGTGVLGSLSLPLSELLVADQLCLDRWFTL
1)	SSGQGQVLLRAQLGILVSQHSGVEAHSHSYSHSSSSLSEEPELS
1			GGPPHITSSAPEV\RQRLTHVDSPLEAPAGPLGQVKLTLWYYSE
1		ľ	ERKLVSIVHGCRSLRQNGRDPPDPYVSLLLLPDKNRGTKRRTSQ
}		1	KKRTLSPEFNERFEWELPLDEAQRRKLDVSVKSNSSFMSREREL
5428	3	1839	LGKVQLDLAETDLSQGVARWYDLMDNKDKGSS
	1	1639	SSRSERLSACAIAPPWLVSSRPARPAQLQRPGKMVEDGAEELED
Í			LVHFSVSELPSRGYGVMEEIRRQGKLCDVTLKIGDHKFSAHRIV
j		ĺ	LAASIPYPHAMFTNDMMECKQDEIVMQGMDPSALEALINFAYNG
		[NLAIDQQNVQSLLMGASFLQLQSIKDACCTFLRERLHPKNCLGV
			ROFAETMMCAVLYDAANSFIHQHFVEVSMSEEFLALPLEDVLEL
J			VSRDELNVKSEEQVFEAALAWVRYDREQRGTFL\RNLQSNIRLL
			FCRPQFLSDRVQQDDLVRCCHKCRDLVDEAKDYLLMPERRPHLP
1			AFRTRPRCCTSIAGLIYAVGGLNSAGDSLNVVEVFDPIANCWER
1			CRPMTTARSRVGVAVVNGLLYAIGGYDGQLRLSTVQAYNTETDT
İ			WTRVGSMNSKRSAMGTVVLDGQIYVCGGYDGNSSLSSVETYSPE
ĺ			TDKWTVVTSMSSNRSAA\GVTVFEGRIYVSGGHDGLQIFSSVEH
ļ		1	YNHHTATWHPAAGMLNKRCRHGAASLGSKMFVCGGYDGSGFLSI
			AEMYSSV\ADQWCLIVPM\HTRR\SRVSLGGPAVGRLYAVWGVT
			TGQSNL\SSVGDVLTPETDCWTFM\APMACHEGGVGVGCIPLLT
5429	828	202	RREDALSSEGCLWPSESTVSGNGIPEPQVYAPPRPTDRLAVPPF
1			AQRERFHRFQPTYPYLQHEIDLPPTISLSDGBEPPPYQGPCTLQ
1			LRDPEQQLELNRESVRAPPNRTIFDSDLMDSARLGGPCPPSSNS
1 !			GISATCYGSGGRMEGPPP\TYSEVIGHYPGSSFQHQQSSGPPSL
1)			LEGTRLHHTHIAPLESAAIWSKEKDKQKGHPL
5430	441	1507	QKRRKRRKKIMKTIQPKMHNSISWAIFTGLAALCLFQGVPVRS
1			GDATFPKAMDNVTVRQGESATLRCTIDNRVTRVAWLNRSTILYA
1 1	}		GNDKWCLDPRVVLLSNTQTQYSIEIQNVDVYDEGPYTCSVQTDN
	i		HPKTSRVHLIVQVSPKIVEISSDISINEGNNISLTCIATGRPEP
{			TVTWRHISPKAVGFVSEDBYLEIQGITREQSGDYECSASNDV\A
1 1	}	į	APV\VRRVKVTVNYPPYISEAKGTGVPVGQKGTLQCEASAVPSA
1	•		EFQWYKDDKRLI/EGKKGVKVENRPFLSKLIFFNVSEHDYGNYT
1 [CVASNKLGHTNASIMLFGPGAVSEVSNGTSRRAGCVWLLPLLVL
L !			HLLLKF
5431	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
[LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
			KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
	}		GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
ļ i		i	SDGEISICMEHMDGGSLDQVLKEAKRIPEEILGKVSIAVLRGLA
(ł	YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
		1	FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP
			DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
		l	AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
		j	DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
5432	2	1312	AAAAPGSRRRRPLPDRPHMAHGYEAPPPPAPRSPAWRARSKPV\
	1	ľ	LPGITINP\TIAEGPSP\TSEGASEANLVDLQKKLEELELDEQQ
}	1	·	KKRLEAFLTQKAKVGELKDDDFERISELGAGNGGVVTKVQHRPS
	ļ		GLIMARKLIHLEIKPAIRNQIIRELQVLHECNSPYIVGFYGAFY
[SDGEISICMEHMDGGSLDQVLKEAKRIPBEILGKVSIAVLRGLA
}	ł		YLREKHQIMHRDVKPSNILVNSRGEIKLCDFGVSGQLIDSMANS
	i i		FVGTRSYMAPERIOGETHY CHOCKET KLCDFGV SGQLIDSMANS
			FVGTRSYMAPERLQGTHYSVQSDIWSMGLSLVELAVGRYPIPPP DAKELEAIFGRPVVDGEEGEPHSISPRPRPPGRPVSGHGMDSRP
		1	AMAI FELLOVI INTERPRIT DEGLESS TO SPRENCE TO SERVICE TO
J		'	AMAIFELLDYIVNEPPPKLPNGVFTPDFQEFVNKCLIKNPAERA
5433	360	1885	DLKMLTNHTFIKRSEVEEVDFAGWLCKTLRLNQPGTPTRTAV
			SVQEDKVGFEDPLHLCSWRARACPCTWPHC/CTGLLECLGFAGV
i	t .	i ·	LFGWPSLVFVFKNEDYFKDLCGPDAGPIGNATGQADCKAQDERF
		I	SLIFTLGSFMNNFMTFPTGYIFDRFKTTVARLIAIFFYTTATLI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	
			P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			IAFTSAGSAVLLFLAMPMLTIGGILFLITNLQIGNLFGOHRSTI
1			ITLYNGAFDSSSAVFLIIKLLYEKGISLR/VLLHLHLCLQYLAC
1	İ		STHFPPDAPGAHPIPTAPQLQLWPVPWEWHHKGREG/QQLSMKT
	1		GSYSQRSSFQRRKRPQGQGRSRNSAPSGATL/CSRRFAWHLVWL
ł	Į.		SVIQLWHYLFIGTLNSLLTNMAGGDMARVSTYTNAFAFTQFGVL
1			CAPWNGLLMDRLKQKYQKEARKTGSSTLAVALCSTVPSLALTSL
			LCLGFALCASVPILPLQYLTFILQVISRSFLYGSNAAFLTLAFP
1			SEHFGKLFGLVMALSAVVSLLQFPIFTLIKGSLQNDPFYVNVMF
1	<u> </u>	_	MLAILLTFFHPFLVYRECRTWKESPSAIA
5434	66	652	RYAALIISLIQHKLLWRNQHCSRCVIMSPAQSAGLNWLF/GSGK
1			HGPFLGCSQYPACDYVRPLKSSADGHIVKVLEGQVCPACGANLV
1			LRQGRFGMFIGCINYPECEHTBLIDKPDETAITCPQCRTGHLVQ
1			RRSRYGKTFHSCDRYPECQFAINFKPIAGECPECHYPLLIEKKT
1	1	1	AQGVKHFCASKQCGKPVSAE
5435	4704	1597	PGDSSQRLAEMSNAKERKHAKKMRNQPTNVTLSSGFVADRGVKH
-:	1 ./53	1337	HSGGEKPFQAQKQEPHPGTSRQRQTRVNPHSLPDPEVNEOSSSK
		1	GMFRKKGGWKAGPEGTSOEIPKYITASTFAOARAAEISAMLKAV
ì			_ : : : : : : : : : : : : : : : : : : :
ł			TQKSSNSLVFQTLPRHMRRRAMSHNVKRLPRRLQEIAQKEAEKA
1			VHQKKEHSKNKCHKARRCHMNRTLEFNRRQKKNIWLETHIWHAK
1		İ	RFHMVKKWGYCLGERPTVKSHRACYRAMTNRCLLQDLSYYCCLE
J		}	LKGKEEEILKALSGMCNIDTGLTFAAVHCLSGKRQGSLVLYRVN
			KYPREMLGPVTFIWKSQRTPGDPSESRQLWIWLHPTLKQDILEE
ł			IKAACQCVEPIKSAVCIADPLPTPSQEKSQTELPDEKIGKKRKR
ļ			KDDGENAKPIKKIIGDGTRDPCLPYSWISPTTGIIISDLTMEMN
ļ			RFRLIGPLSHSILTEAIKAASVHTVGEDTEETPHRWWIETCKKP
j			DSVSLHCRQEAIFELLGGITSPAEIPAGTILGLTVGDPRINLPQ
i			KKSKALPNPEKCQDNEKVRQLLLEGVPVECTHSFIWNQDICKSV
ļ		ļ	TENKISDQDLNRMRSELLVPGSQLILGPHESKIPILLIQQPGKV
i			TGEDRLGWGSGWDVLLPKGWGMAFWIPFIYRGVRVGGLKESAVH
į	(SQYKRSPNVPGDFPDCPAGMLFAEEQAKNLLEKYKRRPPAKRPN
1	J	1	
1		1	YVKLGTLAPFCCPWEQLTQDWESRVQAYEEPSVASSPNGKESDL
i	ľ		RRSEVPCAPMPKKTHQPSDEVGTSIEHPREAEEVMDAGCQESAG
1			PERITDQEASENHVAATGSHLCVLRSRKLLKQLSAWCGPSSEDS
	1	j	RGGRRAPGRGQQGLTREACLSILGHFPRALVWVSLSLLSKGSPE
ļ)]	PHTMICVPAKEDFLQLHEDWHYCGPQESKHSDPFRSKILKQKEK
			KKREKRQKP\GRASSDGPAGEEPVAGQEALTLGLWSGPLPRVTL
1		1	HCSRTLLGFVTQGDFSMAVGCGEALGFVSLTGLLDMLSSQPAAQ
1		1	RGLVLLRPPASLQYRFARIAIEV
5436	1781	635	ASDSIPWSEARTTRKLAQRGCQWSLPERMPLVVFCGLPYSGKSR
Į	_	1	RAEELRVALAAEGRAVYVVDDAAVLGAEDPAVYGDSAREKALRG
			ALRASVERRLSRHDVVILDSLNYIKGFRYELY\CLARAARTPLC
1		1	LVYCVRPGGPIAGPQVAGANENPGRNVSVSWRPRAEEDGRAQAA
1			GSSVLRELHTADSVVNGSAQADVPKELEREESGAAESPALVTPD
1	['A
		1	SEKSAKHGSGAFYSPELLEALTLRFEAPDSRNRWDRPLFTLVGL
	1		EEPLPLAGIRSALFENRAPPPHQSTQSQPLASGSFLHQLDQVTS
	1	1	QVLAGLMEAQKSAVPGDLLTLPGTTEHLRFTRPLTMAELSRLRR
		ļ. <u>.</u>	QFISYTKMHPNNENLPQLANMFLQYLSQSLH
5437	739	1672	CQEAASEFGGPLHTPAMFLRRLGGWLPRPWGRRKPMRPDPPYPE
	1	1	PRRVDSSSENSGSDWDSAPETMEDVGHPKTKDSGALRVSRAASE
			PSKEEPQVEQLGSKRMDSLKWDQPISSTQESGRLEAGGASPKLR
1	1		WDHVDSGGTRRPGVSPEGGL\GVPGPGAPLEKPGRREKLLGWLR
	1		GEPGAPSRYLGGPEECLOISTNLTLHLLELLASALLALCSRPLR
[AALDTIGLRGPIGLWLHGLLSFLAALHGLHAVLSLLTAHPLHFA
1	1	Ĭ	
1			CLFGLLQALVLAVSLREPNGDEAATDWESEGLEREGEEQRGDPG
E (2 2	 	<u> </u>	KGL
5438	2443	1152	TKPRKRRHQPASQRQRPWSSDSTGDLLARGKGRKEENKGSDRVS
l	1	ĺ	LAPPSLRRPMMCQSEARQGPELRAAKWLHFPQLALRRRLGQLSC
ı	I	J	MSRPALKLRSWPLTVLYYLLPFGALRPLSRVGWRPVSRVALYKS
1	1		VPTRLLSRAWGRLNQVELPHWLRRPVYSLYIWTFGVNMKEAAVE
1			DLHHYRNLSEFFRRKLKPQARPVCGLHSVISPSDGRILNFGQVK
	1		NCEVEQVKGVTYSLESFLGPRMCTEDLPFPPAASCDSFKNQLVT
			

Deginning nucleotide location corresponding to first amino acid anino acid amino acid sequence sequenc	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
NO: nuclectide corresponding to first amino acid residue of saino acid residue of saino acid residue of saino acid sequence complete the complete sequence c	_	l .		
corresponding to first amino acid acid acid acid acid acid acid acid	1		l .	
to first maino acid residue of amino acid residue of amino acid sequence se	NO:	l .	1	
to first amino acid residue of amino acid anino acid anino acid anino acid sequence #TYPICOPIAN, Y=TYPICOINE, X=UNKNOWN, *=Stop Codon, /=possible nucleotide deletion, V=possible nucleotide insertion) #ENDELINGYHINGTHERPHYSICHSUMPHSFORMSTERIFFOSIASVNP GMARNIKELFCHINERVILTOMENGFFSLITAVGAT\MMGSIRIY EPROLUTINSPRINGKSYNDFSSVHTHNEGSDREVMALIGERIEJG FARSTVLIFFEARDONFOGLKTOOKIRFOSIAGASUMPHSFORMSTERIFFOSIAGASUMPHSFORM	l	location		
amino acid residue of anino acid sequence designed anino acid sequence codon, /=possible nucleotide deletion, /=possible nucle	1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
meind acid sequence anino acid sequence REGREINICHTYLATEOPHICHESTICHTYLATEOPHICHESTICHTYLATEOPHICHESTICHTYLATEOPHICHESTICHTYLATEOPHICHESTICHTYLATEOPHICHESTICHTYLATEOPHICHESTICHTYLATEOPHICHTYLATEOPHICHESTICHTYLATEOPHICHTYLATEOPHICHTYLATEOPHICHTYLATEOPHICHTYLATEOPHICHESTICHTYLATEOPHICHTYLATEOP		to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
meind acid sequence sequence sequence sequence sequence sequence #ESCRELIVICTIVIAGEOUNCHISTERTOWYSHERIPFOSLARSVNP COGO., /*possible nucleotide insertion) #ESCRELIVICTIVIAGEOUNCHISTERTOWYSHERIPFOSLARSVNP GMARWIRELFCHRERVULTODRKRIGFFSLITAVGAT, NAMSSIRIY EPROLUTINSPRHISKGSYNDFSSVITATURGEVRALIGELIC FRIEDRINGSPRINGSPRINGSPSVITATURGEVRALIGELIC FRIEDRINGSPRINGSPRINGSPSVITATURGEVRALIGELIC FRIEDRINGSPRINGSPRINGSPSVITATURGERALGSL ***INGSTITULIFERARDINFOLKTOOKIRFORALGSL ***INGSTITULIFERARDINFOLKTOOKIRFORALGSL ***INGSTITULIFERARDINFOLKTOOKIRFORALGSL ***INGSTITULIFERARDINFOLKTOOKIRFORALGSL ***SPRINGSPRI	Į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
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PERBLIKTINS PRISKSSYNDS FSTUTTIVREGUPHALISGEHLG/QS PRILGSTILL IERARDKIPHOLKITQKIRG KERAGISL 5440 693 253 EPIPVTPDHILVTHTHIV\QTFSPVNS\GQPPNYEMLKEEQEVA MLGAPINPAPPMSTVHIRSSTSVEDHVVMSLRYLIHINTICCUS FIAPATSVSKSBERMYGDTVTAGAATSTELHINIALILGIFMT ILLIIIPVLVVQAQR 1LLIIIPVLVVQAQR 5441 2 2054 CROGGNOFMYSPMKPELIKTQCSGFRMDPKICPADPAFFSFIN NSDLWVANIETGEERRLTFCHOGLSNVLDDPKSAGVATFV1QBE PROPTCYWWCCPTABMSGSEGKLKTILIVEDSEVEVIHVPSP ALBERKTDSVRYPRTGSKNPKIALKLAFFQTDSGGKIVSTOEKE LVQPPSSLFPKVEYIARAGWTRDSKYAMAMFLDRPQOWLQLVLL PPALFIPSTENERQ\RLASRAVPRNVQPVVVERVTNVNNVN DIFYPFOSEGBELGFLRAMECKTS-CHLIKVTAVLKSQSYDW SESPSSPGSGEGSCSITNAINVBETKLUYFQGTKOTFLEHHLVVS YRAAGSIVELLTTPGFSHSCSMSONFMPVSYSSVSTPCVHVY KLSGPDDDPILKQPRWBAGAMEAAKTHFHTSDVSLYSMYTYK HALQPGKKHPTULFVYGGPQVOLVNNSFKGIKVLRILVAGSYDW KLSGPDDDPILKQPRWBAGAMEAAKTHFHTSDVSLYSMYTYK HALQPGKKHPTULFVYGGPQVOLVNNSFKGIKVLRILVAGSYDW KLSGPDDDPILKQPRWBAGAMEAAKTHFHTSDVSLYSMYTYK HALQPGKKHPTULFVYGGPQVOLVNNSFKGIKVLRILLAGKY GFILDRNVHIFFHTNFLVSGLIRAGKPYQLQVALPVSPQTYPNRR HAIRCESGGRHYBEVTLLHFLQETL GFILDRNVHIFFHTNFLVSGLIRAGKPYQLQVALPVSPQTYPNRR HSIRCESGGHYBEVTLLHFLQETL GGCRSERKSPFMERAFRAKAPKGKGDAFKGAPKEAPPKEAPAE APKEAPPEDOSPTAEEPTSVFLKKPDSVSVETKKDAVVVAKVNK KSAAFTKKLDPATQVDRGNKIKLMUSISDPDLTLKNFRONGSIK HIGKVVLGDGGYVRLEVKAKDTCDSGGNTIDVBAPRODASGGSL ESFRKTISKKSKEDTAGRLDPSGLIKKREVDDDLG IPPBIWELLKGAKKSEYBKLAFQYGITDLRGMLKRLKKAKVEVK KSAAFTKKLDPATQVDRGNKIKLMUSISDPDLTLKNFRONGSIK KEPDAPTI KNFKKKHLELIKSTADADARVAVKDEKCFTTLEV KEPPVLIVTPLEDQOVFUGDRVEMAVEVSEGGAVTMKNEDVEL TREDSSKAFFENVEKKRITLISDSVDCBGRYYOTITNGQCC AELIVERKQLEVLQDIADLTVKASGQAVFKCEVSDEKVTGNYK NGVEVPSKRITISHNGFRHILIIBDVVDERTFERFRIE KRVDCSSFVIESAQREDEGRYTIKVTNPIGEDVASIFILQVVDVP DPPBARTISSGERMYBANTERFENVENTARIAGGSGGSSNAD/IV VVAGNKLALDV\SITCEABSPATVLLKOPUTTTEGRTPIE KRVDCSSFVIESAQREDEGRYTIKVTNPIGEDVASIFILQVVDVP DPPBARTISSGERWPANTERPSPATOLKGRILTKRVGENID LVVPSGCLESSERWPANTERPSPATOLKGARILFROYGNILAGRILFROYGVN IAGRSEPATLAQPVTTREIASPPRILGRIPTYRVENGAILFTGTTKK PPEYKRHDPRARKFITPLIDRIVVAKAGAPENTVYENKRHEGT TVSDLIVUNDEYTFROYTENIGGLISDS PGVSNTTARILLETGTTK PPEYKRHDPRARKFITPLIDRIVVAK]		1	
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RWMKLNFEVFTETTYESTKMIEGILYEMRVFAVNAIGVSQPSMN TKPFMPIAPTSEPLHLIVEDVTDTTTTLKWRPPNRIGAGGIDGY LVEYCLEGSEEWVPANTEPVERCGFTVKNLPTGARILFRVVGVN IAGRSEPATLAQPVTIRE I AEPPKIRLPRHLRQTYIRKVGEQLN LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVQAA RSDSGEYELSVQIENMKDTATIR IRVVEKAGPPINVMVKEVWGT NALVEWQAPKDDGNSE IMGYFVQKADKKTMEWFNVYERNRHTSC TVSDLIVGNEYYFRVYTENICGLSDSFGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV		1		
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LVEYCLEGSEEWVPANTEPVERCGFTVKNLPTGARILFRVVGVN IAGRSEPATLAQPVTIREIAEPPKIRLPRHLRQTYIRKVGEQLN LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAA RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV				- '
IAGRSEPATLAQPVTIREIAEPPKIRLPRHLRQTYIRKVGEQLN LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAA RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV	1]		
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RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV	1	1		
NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV		1		LVVPFQGKPRPQVVWTKGGAPLDTSRVHVRTSDFDTVFFVRQAA
NALVEWQAPKDDGNSEIMGYFVQKADKKTMEWFNVYERNRHTSC TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV				RSDSGEYELSVQIENMKDTATIRIRVVEKAGPPINVMVKEVWGT
TVSDLIVGNEYYFRVYTENICGLSDSPGVSKNTARILKTGITFK PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV	1	1	}	NALVEWQAPKDDGNSEIMGYFVOKADKKTMEWFNVYERNRHTSC
PPEYKEHDFRMAPKFLTPLIDRVVVAGYSAALNCAVRGHPKPKV VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV	ĺ	1		j
VWMKNKMEIREDPKFLITNYQGVLTLNIRRPSPFDAGTYTCRAV				
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	L			MEDGEVINECKDEAKANA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	
}	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
		N .	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
5443	66	1003	SRGQLDAGQSSEQHGGNRQPEQSRSRSSSSSSSPRRSRSAAEPA
ļ		1	MALSMPLNGLKEEDKEPLIELFVKAGSDGESIGNCPFSQRLFMI
			LWLKGVVFSVTTVDLKRKPADLQNLAPGTHPPFITFNSEVKTDV
Í	1		NKIEEFLBEVLCPPKYLKLSPKHPESNTAGMDIFAKFSAYIKNS
			RPEANEALERGLLKTLQKLDEYLNSPLPDEIDENSMEDIKFSTR
1			KFLDGNEMTLADCNLLPKLHIVKVVAKKYRNFDIPKEMTGIWRY
			LTNAYSRDEFTNTCPSDKEVEI\AYSDVAKRLHOVKSRLLKEVS
ļ			FMSSP
5444	2	344	SGPIGVTGAQMAKWLRDYLSFGGRRPPPQPPTPDYTESDILRAY
7333		""	RAQKNLDFEDPY*DSESRLEPDPAGPGDSKNPGDAKYGSPKHRL
1	1		
]	}		IKVEAADMARAKALLGGPGEELEADTEYLDPFDAQPHPAPPDDG
	1		YMEPYDAQWVMSELPGRGVQLYDTPYEEQDPETADGPPSGQKPR
1			QSRMPQEDERPADEYDQPWEWKKDHISRAFAVQFDSPEWERTPG
1		i	SAKELRRPPPRSPQPAERVDPALPLEKQPWFHGPLNRADAESLL
1			SLCKEGSYLVRLSETNPQDCSLSLRSSQGFLHLKFARTRENQVV
ľ			LGQHSGPFPSVPELVLHYSSRPLPVQGAEHLALLYPVVTQTP*Q
			*PDWGDRRPNGQVATGLPELWGAEAPSAAAHPGLHRERHPEGLP
J]		RAEKPGLRGPLLGLREPLGAGPRGPWGLQEPRRCQVWFSQAPAH
			QGGGCGYGQSQGPSGRPRGGAGSRH
5445	2364	486	ILSRGFLGSVEICIQLPLPASEPVLLLTWARRRWRETRSRREPT
ļ			TLRAQSVCPWWI*ETRMNRSIPVEVDESEPYPSQLLKPIPEYSP
			EBESEPPAPNIRNMAPNSLSAPTMLHNSSGDFSQAHSTLKLANH
1			QRPVSRQVTCLRTQVLEDSEDSFCRRHPGLGKAFPSGCSAVSEP
1			ASESVVGALPAEHQFSFMEKRNQWLVSQLSAASPDTGHDSDKSD
Į.			QSLPNASADSLGGSQEMVQRPQPHRNRAGLDLPTIDTGYDSQPQ
1	İ		DVLGIRQLERPLPLTSVCYPQDLPRPLRSREFPQFEPQRYPACA
			QMLPPNLSPHAPWNYHYHCPGSPDHQVPYGHDYPRAAYQQVIQP
1			ALPGQPLPGASVRGLHPVQKVILNYPSPWDQEERPAQRDCSFPG
1			LPRHQDQPHHQPPNRAGAPGESLECPAELRPQVPQPPSPAAVPR
			PPSNPPARGTLKTSNLPEELRKVFITYSMDTAMEVVKFVNFLLV
1			NGFQTAIDIFEDRIRGIDIIKWMERYLRDKTVMIIVAISPKYKQ
	ł	·	DVEGAESQLDEDEHGLHTKYIHRMMQIEFIKQGSMNFRFIPVLF
}	•	į	PNAKKEHVPTWLQNTHVYSWPKNKKNILLRLLREEEYVAPPRGP
			LPTLQVVPL
5446	972	161	SSWSWCTGRMRKTRLWGLLWMLFVSELRAATKLTEEKYELKEGQ
	1		TLDVKCDYTLEKFASSQKAWQIIRDGEMPKTLACTERPSKNSHP
1		1	VQVGRIILEDYHDHGLLRVRMVNLQVEDSGLYQCVIYQPPKEPH
		1	MLFDRIRLVVTKGFSGTPGSNENSTQNVYKIPPTTTKALCPLYT
		(TPRTVTQAPPKSTADVSTPDSEINLTNVTDIIRVPVFNIVILLA
			GGFLSKSLVFSVLPAVTLRSFVP*AHEPTRMSSDFQPHPSGSCA
1		1	KGGGRR
5447	207	617	MTARTLSLMASLVAYDDSDSEAETEHAGSFNATGQQKDTSGVAR
1		J	PPGQDFASGTLDVPKAGAQPTKHGSCEDPGGYRLPLAQLGRSDR
			GSCPSQRLQWPGKEPQVTFPIKEPSCSSLWTSHVPASHMPLAAA
l		l	RFKQVKLSRNFPKSSFHAQSESETVGKNGSSFQKKKCEDCVVPY
			TPRRLRQRQALSTETGKGKDVEPQGPPAGRAPAPLYVGPGVSEF
			IQPYLNSHYKETTVPRKVLFHLRGHRGPVNTIQWCPVLSKSHML
			LSTSMDKTFKVWNAVDSGHCLQTYSLHTEAVRAARWAPCGRRIL
1			1
		J	SGGFDFALHLTDLETGTQLFSGRSDFRITTLKFHPKDHNIFLCG
			GFSSEMKAWDIRTGKVMRSYKATIQQTLDILFLREGSEFLSSTD
	1		ASTRDSADRTIIAWDFRTSAKISNQIFHERFTCPSLALHPREPV
	1	J	FLAQTNGNYLALFSTVWPYRMSRRRRYEGHKVEGYSVGCECSPG
			GDLLVTGSADGRVLMYSFRTASRACTLQGHTQACVGTTYHPVLP
	1		SVLATCSWGGDMKIWH*AFHWLSLGEAIGDLAPARGYSGPGRSL
	<u> </u>		KSPSPSKSLLVLLCGRAMFQPATCPWQLPALSK
5448	194	1833	MASKVTDAIVWYQKKIGAYDQQIWEKSVEQREIKGLRNKPKKTA
1			HVKPDLIDVDLVRGSAFAKAKPESPWTSLTTKGIVRVVFFPFFF
			RWWLQVTSKVIFFWLLVLYLLQVAAIVLFCSTSSPHSIPLTEVI
			GPIWLMLLLGTVHCQIVSTRTPKPPLSTGGKRRKLRKAAHLEV
			HREGDGSSTTDNTQEGAVQNHGTSTSHSVGTVFRDLWHAAFFLS
1	1		GSKKAKNSIDKSTETDNGYVSLDGKKTVKSGEDGIQNHEPQCET
1	1	I	CONGRESO TELENGIASTERSKIAKSGERGIĞNUELÖCEL

beginning inclection corresponding corresponding corresponding corresponding corresponding corresponding corresponding to first amino acid amino acid amino acid amino acid amino acid sequence	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No: nucleotide location corresponding to first amino acid anino acid anino acid anino acid anino acid anino acid sequence corresponding to first anino acid anino acid anino acid sequence corresponding to first anino acid sequence corresponding to first anino acid sequence corresponding to first anino acid sequence corresponding to the correspo	1 -		1	Amitho acid segment containing signal peptide
cortesponding to first amino acid residue of amino acid amino acid sequence Proline, Q-Glutamine, R-Arginine, residue of amino acid amino acid sequence Proline, Q-Glutamine, R-Arginine, S-Serien, T-Threadney, X-Unknown, *-Stop Coden, '-possible nucleotide deletion, '-possible nucleotide deletion, '-possible nucleotide deletion, '-possible nucleotide insertion) IPPETEMENTALINESSENDERISESSESSESSESSESSESSESSESSESSESSESSESSES	1		1	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid amino acid amino acid amino acid amino acid sequence sequen	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
corresponding to first amino acid amino acid amino acid amino acid amino acid sequence sequen	j	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
to first amino acid residue of amino acid am	ļ.	corresponding	1	LaLeucine MaMethionine Nahanaragine
amino acid residue of amino acid sequence 8-Serine, T-Threonine, V-Valine, amino acid sequence 1RPETRAWITGTLENGFSUTGRITIONSEUS SERGER COCO. /=possible nuclectide deletion, V=possible nuclection, V=possible nuclectide deletion, V=possible nuclectide deletion, V=possible nuclectide deletion, V=possible nuclectide del	İ		j .	
residue of amino acid sequence (1		
amino acid sequence Codon, /=possible nucleotide deletion,	1		residue of	
### and acid sequence Codon, /*possible nucleotide deletion,]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence	1	amino acid	seguence	
IRPETAMYGILENGFSKDTGRT:THVSDEWSSEGGETGYSE. RRHVOPTSEGULARISHHYKHYKHYDDAPKSGTSSCSSCSSSS QDSESARPSSTEDVLMEDLHCASCUSSCTSSTDVENGCINFC VKERYADDPFROSKLUFMLSHSHEGLENSATVEGGENCKKADMS VLEISGMINMRYWSHIPGIGYGIFORAVSLILIGLTFYFFELSOA TUBEGLTARISASELIVALASSMEDILISHLISHIGGENCKKADMS VLEISGMINMRYWSHIPGIGYGIFORAVSLILIGLTFFYFELSOA SGTSCSSCSSSGSSGSSEARPSSTETEVLMEDLLICAGCHSSCT SETDVENNGINDCVKKEYRDDPFHOSILIPHLISSHEGLEXISAI VEKONDCKKADMSVLISGMINMRYWSHIPGIGYGIFORAVSLI LGUTPFVFRLSQATDLEQLTAKSASELYVLAFGSNEDVIVLSMV LISFYVVSLWIFFFLLCVARTYKYGVGIM SASKYTDAIVWYGKKIGAYDQGIMEKSVGORRIKGLRKFKKTA WKODLIOULUVGSAFAKAKPESPHISTLTKGIRVKYFYFPFFF RWHLQVTSKVIFFFLLUVLYLLQVAAIVLCCSTSSPHSIPLTEVI GPIWLMLLGTVHGOUTSTRYRFPLSTGGGRRKKARAHEV HREGOGSSTIDNTQGGAVQRHIGTSTSKVGTVTPOLMHAAFFLS GRKAANSIDKSTETDNTQGGAVQRHIGTSGGRRKKARAHEV HREGOGSSTIDNTQGGAVQRHIGTSGGRRKKARAHEV HREGOGSSTIDNTQGGAVQRHIGTSGGRRKKARAHEV HREGOGSSTIDNTQGGAVQRHIGTSGGRRKKARAHEV HREGOGSSTIDNTQGGAVQRHIGTSGGRRKKARAHEV HREGOGSSTIDNTQGGAVQRHIGTSGGRRKKARAHEV HREGOGSSTIDNTQGGAVQRHIGTSGGRRKKARAHEV KKEYTODFFKGHLUKSHHOLGKYRSGGGGTQHARAHEPQCET IRPETIANTGTLRNOPSKOTGRTITTVSDEWSSEGGFTGYSL GRKAANSIDKSTETDNTYSGAVGKTRSGGGRTGKRKARAHEV VKEYTODFFKGHLUKHASHHOLGKYRSGGGTGYGKKAAHEV VKEYTODFFKGHLUKHASHHOLGKYRSGGGTGYGKKAAHEV VKEYTODFFKGHLUKHASHHOLGKYRSGGGTGYGKCKAAMS VLEISGMINMRWISHTPGIGYTFGANVSLILLGLTPFYFRLOGA VKEYTODFFKGHLUKHASHHOLGKYRSGGTSAVGKAGMS VLEISGMINMRWISHTPGIGYTFGANVSLILLGLTPFYFRLOGA VKEYTODFFKGHLUKHASHHOLGKYLJAMIGTSTAVCKAAMS VLEISGMINMRWISHTPGIGYTFGANVSLILLGLTPFYFRLOGA SGTSCSSRGSSRGSSRGSSAPSSGFTGTVIMMGINFGCHSCT SETDVENHQINFCKKEYRDDFHGSHLWHKSHTPVRSLUM LIGHTPFYFRLSQATDLEQLTAMSASELYVIAFGSNEDVIVLSMI LIGHTPFYFRLSQATDLEQLTAMSASELYVIAFGSNEDVIVLSMI LIGHTPFYFRLSQATDLEQLTAMSASELYVIAFGSNEDVIVLSMI LIGHTPFYFRLSQATDLEQLTAMSASELYVIAFGSNEDVIVLSMI VLEGGGGRUKALGTURHTNAAAHTANGSLLBFLTDHTONGGGRELIFALITANG AGGRRGGATHATALGTARAHTANGSLLBFLTDHTONGGGRELIFALITANG AGGRRGGATHATALGTARAHTANGSLLBFLTDHTONGGGRELIFALITONG AGGRRGGATHATALGTARAHTANGSLLBFLTHDHTONGGGTHLB	1	1	1 204101100	
RRAYORTSBOYLARRIKSHHYKRHYPINDAPKSGTSCISSRCSSSRC ODSEARRESTEDVIKMELHIGHERISSTIVMEGNECKRAMS VLEISGHIMRRYWSHTPGIGVOTGFORWASILIGLIFTPYFISGA TÜLBGLTAHSASELYVIAPGSMEDVIVLSMYLISPYWKSLUWI FFELLCVARRIYKQVIM **TSBOYLARRISSHTYKGHYRIGHYRDAPK SGTSCSSRCSSSRGDSESARPSSTEDVLMEDLHCABCHSGCT SETDVENNIGINDEVKERVENDEPPHSELIPMLISSHPGLERISAT VWEGNOCKRAMSVLEISGMINNRYNSHTPGIGVOTGRANASLI LGIJTPYFWRISGANGKAFONDEVINSKYSTAPHOLHCABCHSGCT SETDVENNIGINDEVKERVENDEPPHSELVARPGINEDVIVLSMY LISPYWRSJWYIFFLLCVARRTYKQVGIM 194 1833 MASKYTDAITWYGKIGAYDQIMEKSVEQRETKGLERKEKKTA HVKPOLIDVULVGSASPAKAKPSBPMTSLTTKGIURWYPEPPFF RWHLOYTSKVIFFKLIGVYGATOMUTHSTENDEVTSTENDEN PLTEVT GPWIMLLIGTWIGOTUSTRTPKPPLSTGGRRRKLRKAAHLEV HREGOGSTITNTOGRAWONGHGTSTSKUGVTVENDHENDET GPWIMLLIGTWIGOTUSTRTPKPPLSTGGRRRKLRKAAHLEV HREGOGSTITNTOGRAWONGHGTSTSKUGVTVENDHENDET GRKAANSILNSTSTUNGVYSLOGKKTWASGEGOIGHNEOCET IRPETAMNYTGLLBANFENDORGTSTGSTSGTSGSSRGSSR ODESSAPBSBTEDVINBELLICHASCSGTSTTDTWENDINE GRKKAANSILNSTSTUNGVYSLOGKKTWASGEGOIGHNEOCET IRPETAMNYTGLISHPENDEVSTORGTHENDELICHACKSTSTSTOSKRGSSR ODESSAPBSBTEDVINBELLICHASCSGTSSTTDWINDINGTHEOCET IRPETAMNYTGLISHPENDERSTGTSTSCSGTSSTTDWINDINGTHEOCET REMUNDSTSBOYLARRIKSHHYKKHYPNBDAPKSGTSGTSGSSRGSSR ODESSAPBSBTEDVINBELLICHASCSGTSSTTDWINDINGTHEOCET IRPETAMNYTGLISHPENDELICHASCSGTSSTTDWINDINGTHEOCET REMUNDSTSBOYLARRIKSHHYKKHYPNBDAPKSGTSGTSGSRGSSR ODESSAPBSBTEDVINBELLICHASCSGTSTSTDWINDINGTHEOCET REMUNDSTSBOYLARRIKSHHYKKHYPNBDAPKSGTSGTSGSRGSSR ODESSAPBSBTEDVINBELLICHASCGTSTSTDWINDINGTHEOCET REMUNDSTSBOYLARRIKSHHYKKHYPNBDAPKSGTSGTSGSRGSSRGSTSGTSGTSGTSGTSGTSGTSGTSGTSGTSGTSGTSGTS		Bequence	<u> </u>	(=possible nucleotide insertion)
ODEBARRESTEDVIMEDLIHGABCUSSCTISTTVENKIGINPC VKKEYEDDPFROSILUPHIASHRIGHEKISATUVENKIKKAMS VLEISSMINNRWSHIPGIGYOI FORMASILULLITPYPELISGA TÜLEGÜLTAHSASELVIVIAPGSINEDVILSAMILIS EYVEVSLÜWI FPELLCVARETYKQVIIM-TSEGULENKISHHYKKHYPINDDAPK SGTSCSSSCSSSGSSESARPESTEDVIMEDLIHAGACUSSCT SETDVENHGINDCVKKEYEDDPHOSILUPHLISSHINGLEKISAT VREGNOCKKADMSVILSGAMINGVENKIPEIGYÖI FORMAVSLI LISPTVENLSGATDLEGÜTANSASELYVIAGSNEDVIVLSMW LISPTVENLSVANDLEGUTANSASELYVIAGSNEDVIVLSMW LISPTVENSLWII PFELLCVARETYKQVEN PERENTYTLYKKTA HVKPOLIDVLIVROSKATGAYDQQIWERVPEQNETKILRKPKKTA HVKPOLIDVLIVROSKATGAYDQQIWERVPEQNETKILRKPKKTA HVKPOLIDVLIVROSKAFAKAKPESPHTSITTKGIVVYFFFFFF GRILDVIRSVI FPKILULVILLQVAALTULCSTSS PSISTLITEV GPHIMILLIGITHVEQUIVASTATFFFFFISTGKRRKILRKAHLBEV HIRAGOSSTITONTOGAVQHATOTSSENGVIVELOHAAFFLS GSKKAKNSILIKSTETUNGVYSLOSKKTVESGEGG IQHIEDQGET IRREDIAMNOTILBANDSKUTORITIVSDEVSSEGGFTOYSL RRHVORTSBEVLRRKKSHIKKKHYPNEDAPKSGTSCSSRCSSSR QOSSSRAPBSETEDVIKBELLICARETSCSTSTITVURNIGINPC VKKEYRODPFRÖSHLEMLHSSRPGIRKISALTWEGNOCKKADMS VLBISGMINNRWNSHIPDIOTQTIFANSVLLILLIPPVYRLSQA TÜLEQUTAHSASELYVLAFGSSEDVIVLSMVILISPVVRSLUMI FPFLLCVARETYKQVISH-TSGAUKRKSHIKKKRSHIKKHYPNEDAPK SGTSCSSRCSSSRSSRSBSBARPSETEDVLIMBLILLCARCHSSCT SETDVENHQINDEVKKERPODPFROSHLEMLHSSRPGIRKISALTWEGNOCKKADMS VLBISGMINNRWNSHIPDIOTQTFRANSVLLILLIPPVYRLSQA TÜLEQUTAHSASELYVLAFGSSEDVIVLSMVILISPVVRSLUMI FPFLLCVARETYKQVISH-TSGAUKRKSHIKKHYPNEDAPK SGTSCSSRCSSRCSSRROBSSARPSETEDVLIMBLILLCARCHSSCT SETDVENHQINDEVKKERPODPFROSHLEMLHSSPPIDERDER SGTSCSSRCSSRCOBSSARPSETEDVLIMBLILLCARCHSSCT SETDVENHQINDEVKKERPODPFROSHLEMLHSSPPIDEVLIMBS FPFLYBLIVARGATARANSVLAGALERPLIKMSHINGHTENDAPK SGTSCSSRCSSRCOBSSRAPSTETEDVLIMBLILLCARCHSSCT SETDVENHQINGERCHEDUTAHSSELIPPTVINGHOORGHERINGT VKRSTRPIRGCHANTATION TORTON THE STANDARD THE STANDARD FPFLYRAGATARANSVLAGATERPHICHTSHANDARD FPFLYRAGATARANSVLAGATERPHICHTSHANDARD SGTSCSSRCOSSRCOBSRROPERTSTED TORTON THE STANDARD FPFLYRAGATARANSVLAGATERPTVATARGSRCHALL LITTPVARATAGATARANSVLAGATERPTVATARGSCHALL LITTPVARATAGATARANSVLAGATERPTVATARGATARANA AGCREEPEYEDAVARANSVLAGATARANSVLAGATARANSHILLDARA	1	1	1	IRPEETAWNTGTLRNGPSKDTQRTITNVSDEVSSEEGPETGYSL
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194 1833 MASKYTDAIVWYOKKIGAYDQOIMEKSVEGRETKGIENEPKETA. HYKPELIDUDLURGSARAKAPES MYSTKOIVENVEPPEPE RWMLQVTSKVIFPHLULYLLQVAAIVLFCSTSSPHSIPLTEVI GPIMMLLLGTVIKGTVSTRTPKPEPLSTGGRERKIRKAALEEV HREGOGSSTIDNTORGAVOUNIGTSTSHSVGTVFROLMHAAFILS GSKKAKNSIDKSTETDNOYVSLDGKKTVKSGEGG IONEPGCET IRPETTANTITLINDGSKOTORTITINNDESSSEGFETTYSI RRHVDRTSEGGLRINGTLINGGSKTOVSGEGGETTYSI RRHVDRTSEGGLRINGTLINGGSEGGETTYSI RRHVDRTSEGGLRINGTLINGGSEGGETTYSI RRHVDRTSEGGLRINGTLINGGSEGGETTYSI RRHVDRTSEGGLRINGTLINGGSEGGETTYSI RRHVDRTSEGGLRINGTLINGGSEGGETTYSI RRHVDRTSEGGLRINGTLINGGSTGSSSCSSSSS QDESSARPESSTEDVLWEIGHTYNESTDVENIGITING VKKEYRDDPFRQSHLDHLISHTGLEKISAIVWEGKTCKKADMS VLEISGMINMRVSHIP GIGVTFGNAVSLLIGITPFVFRLSQA TDLEQLTAHSASELYVIAFGSNEDVIVLWINTISFVVENSIVNI FFELLCVARRTYKQVGIM*TSEGVLRNKSHHYKKHYRENDAK SGTGSSKCSSSSKODESSARPESETTDVLWEDLLHCARCKSSCT SETDVENNGINPCVKKEYRDDPFHOSHLPWLHSHPEDEKISAI VWEGNDCKADMSVLEISGRIMMRVNSHI BCIGVGIFGNAVSLL LGITPFVFRLSQATDLEQLTHASASELYVIAFGSNEDVIVLSW TISFVUTNSQAATLSVORFLANASSAVEGBLEVFYGLFKGSNEDVIVLSW TISFVUTNSQAATLSVORFLANASSAVEGBLEVFYGLFVGGTGTLIGD YLKGTSRPLRGCLHAATLNGSLLARPLTPDVHEGCASEFSASDD VALGTSGFBLSAFDAWTODECTLEFTLTTOSROAPLAPQAGG RRGDFIYDDIFECHLRAVVERGGGVULHHNSVEVADGOPHEVSY HINAHALIS ISDOPYPTHSNGVLSVLEPBLIPGVPEPPGL PVERAFTGULHTS SUDOPYPTHSNGVLSVLEPBLIPGVPEPPGL PPFAMFTQLLTTSPLVVABGGTAMLEWRHVQPTLDLMEAELK SQVLFSVTRGAHYGELEDILIGADARKHYTLLDVVARRAFTHD GSBDTSDQLIVENSVTARVENSGLVSLEPBLIPFVLEPPFPGL PPFAMFTQLLTTSPLVVABGGTAMLEWRHVQPTLDLMEAELK SQVLFSVTRGAHYGELEDILIGAGARRHFTLLDVVARRAFTHD GSBDTSDQLIVENSVTARVENSGLSVLYNDGGRAGLIFFALLTRING AFGGREEBEVEDDAVOHHAPSTLARPSTARPLPPCVPPPGL PPFAMFTQLLTSPLVVASRGTAMLEWRHVQPTLDLMEAELK SQVLFSVTRGATVALLEFULFTANLLGEGGRAUPTLDFVURRAFFTH VSGLQASPPATLKVVATRAJQIHRSTGLRLAGGSAMPLIPAN LSVETNAYGGOVSVLFSTDPGHAYDTVINLALEEVQVGGBLISH SFPVTICRATUMLALEEPLITHOMTODETTIPQULTT VSGLQASPATLKVVATRAJQIHRSTGLRLAGGSAMPTYGA TARASEAVEDTFRFRVTAPFYFSPLYTFPHIGGGDDAVLTTV LLVVEGGSVSGHLAFFTYFFTHYAGGGRIL TDDVAFSDARRAFVLFHGABAGARI ILLOVSBOPDATLLEVOASSP YLEVANGSSLVVEGGGGTIDTAVLHLDTRIDIRSGGRALLE TODDLARRAFVLFHGAGAGGRI IOLOVSBOPDATLLEVOAS	1	1		
NVKDDLIDUDLYRGSAPAKARDES PWTSLTTKGIVRVVFFFFFF RWWLQVTSKVIFFWLLVLYLLQVAAIVLECSTSS PHSIPLTEVI GPIWLHLLGTVICQIVSTRTPKPPLSTGGRRKKLRKAAHLEV HREGDGSSTTDNTQEGAVQNNIGHTSTHSVGTVFFDLWHAAFFLS GSKKANNSIDKSTETDNGVSLDOKKTVKSGEGGIQNNEPQCET IRPETANNTGTLRNOPSKDTORT ITNVSDEVSEERGFTGVSL RRHVDRTSEGVLNRKSHLYKKYPPDEDAPKSGTSCSRCSSSR QDGSSAPBSSTEDULWBDLLHCABCHSSCTSRTDVENNIQINPC VKKEYRDDPFGSHLDWLHSLHCABCHSSCTSRTDVENNIQINPC VKKEYRDDPFGSHLDWLHSLHCABCHSSCTSRTDVENNIQINPC VKKEYRDDPFGSHLDWLHSLHGLEKISAIVWERGECKADMS VLEISGMIMNRVNSHIPGIGYQIFGNNAVLILGLTFFVFRLSQA TDLEQLTAHSASSLIVVIAFGSNEDVIVLSMVIISFVVRUSLIVNI FFFLLCVABRTYRQVGIM*TSEGVLNRKSHLYKKYPNEDDPR SGTSCSSRCSSSRQDSESARPESETDVLWBDLLHCABCHSSCT SETDVENNIQINPCVKEKEYRDDPFHQSHLPWLHSSHGLEKISAI VMEGNDCKKADMSVLRISGMIMNRVNSHIPGIGVQIPGNAVSLI LGITPFVERLQATDLEQLTAHSASELYVIAFGSNEDVIVLSMV 11SFVRNSLWHIFFFLLCVABRTYKQVGIM* SGTSCSRCSSRGSRESSFTDVLWBLLLLAGG GQGFASFFG*NHBEVTVAMALTDIDLQLGFSMSQFBALLLLAGG PADHLLLQLYGGGLLQATLYLQGEELRCTPAETLLSDBIPTTV LTVVEGNATLSVDGFIANSSAVEGAPLEVPYGLFVGGTGTLGLU YLGGTSFRLEGCLHAATLNGSLERLTPTGECABEFSASDD VALGFSGFHSLAAFPAMGTODESTLEFTLTTGSRQAPLAQGG RRGDFIYVDIFEGCHLAAVURKQGGTULLHNSVPYADGQPHEVSV HINARIELISVDQYPTHYSNRGVLSHEPROSLLIGGLDABASR HLQBHRLGLTPEATHASSLLCCMBDLSVNGGRRGLREALITHNNA AGCRLEEEEVEDDAYGHHAFSTLAFEANMELDPEPCVPEPGL PPVFANFTOLLTISPLVVABGGTANLEWRHQPTLDLWBAERJEH GSEDTSDQLVLEVSVTARVPMPSCLRGGGTYLLPIQVPRVMPUPP HIIFPRGSLMVILLHTQKPLGPEVFQAYDPDSACEGLTFOVLGT SGLEVERRDQFGFATTFSCRLEAGGSLYVYURCGGPAQLTTR VSDGLQASPPATLKVVAIRPAQIGHRSTGLEAGGSAMPLIPAN LSVETNANGQDVSVLFRTVTGALDGFGCLKGTYVLGGPAQDLTRR VSDGLQASPPATLKVVAIRPAQIGHRSTGURGGGGGLESGIS SPYTIGRATVMALLEFLEHITONTQCELTLGATLEATHAGANAPLIPPTOTAGGE SSGDAMMEWRGPYNALLGURGGTUNDALFFTIRFTGRAGGRRLL TTDDVARFDADGGRAVPLAGTTRIPTTYNALGERRLI SFPYTIGRATVMALLEGLEHITONTQCELTLGATLEAGGSAMPLTAN LSVETNANGGGRAVFLAGTURGGTYLDFTURGTERGGRRL TTDDVARFDADGGGATTDTAVHALDTGLEATLEATHAGA AFRAGERUS GARGAGGATDTATVHLDFTGLBARGRRLL TTDDVARFDADGGGATLGTGGGTTDTAVHALLGATLEATHAGARGRLL TDDVARFDAGGAGATAFAGGGATTDTAVHALDTRILDTRAGGRRLL TDDVARFDAGGGGTTDTAVHALDTRILDTRAGGRRLL TDDVARFDAGGAGATAFAGGALTAGGAD	F 440-			
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TQDKTTMVTSFTNEDLLRGRLVYQHDDSETTEDDIPFVATRQGE SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRLL TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYRF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYNT AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAABI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE	1]		
SSGDMAWEEVRGVFRVAIQPVNDHAPVQTISRIFHVARGGRRLL TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYRF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHVT AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE	l			
TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYRF TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP YLRVANGSSLVVPQGGGTIDTAVLHLIDTNLDIRSGDEVHYHVT AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE	1			
TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDTRSGDEVHYHVT AGPRWGQLVRAGQPATAFSQDLLDGAVLYSHNGSLSPEDTMAF SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE	I			
TQEDLRKRRVLFVHSGADRGWIQLQVSDGQHQATALLEVQASEP YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDTRSGDEVHYHVT AGPRWGQLVRAGQPATAFSQDLLDGAVLYSHNGSLSPEDTMAF SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAAEI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE	1	Į .		TTDDVAFSDADSGFADAQLVLTRKDLLFGSIVAVDEPTRPIYRF
YLRVANGSSLVVPQGGQGTIDTAVLHLDTNLDIRSGDEVHYHVT AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAABI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE	1	1		
AGPRWGQLVRAGQPATAFSQQDLLDGAVLYSHNGSLSPEDTMAF SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAABI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE	l			
SVEAGPVHTDATLQVTIALEGPLAPLKLVRHKKIYVFQGEAABI RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE	ì			
RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE	1			
LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE	1	[
LDPVQSFSQEAVDTGRVLYLHSRPEAWSDAFSLDVASGLGAPLE	1			RRDQLEAAQEAVPPADIVFSVKSPPSAGYLVMVSRGALADEPPS
	I			
O THE SERVICE OF THE	ł			
	L	L	L	O TO TO THE PROPERTY OF THE PR

CEO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì		to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding		
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LLGLSLQVLEPPQHGPLQKEDGPQARTLSAFSWRMVBEQLIRYV
	1		HDGSETLTDSFVLMANASEMDRQSHPVAFTVTVLPVNDQPPILT
			TNTGLOMWEGATAPIPAEALRSTDGDSGSEDLVYTIEOPSNGRV
1			VLRGAPGTEVRSFTQAQLDGGLVLFSHRGTLDGGFPFRLSDGEH
			TSPGHFFRVTAQKQVLLSLKGSQTLTVCPGSVQPLSSQTLRASS
			SAGTDPQLLLYRVVRGPQLGRLFHAQQDSTGEALVNFTQAEVYA
			GNILYEHEMPPEPFWEAHDTLELQLSSPPARDVAATLAVAVSFE
			1
	1		AACPQRPSHLWKNKGLWVPEGQRARITVAALDASNLLASVPSPQ
			RSEHDVLFQVTQFPSRGQLLVSEEPLHAGQPHFLQSQLAAGQLV
'			YAHGGGGTQQDGFHFRAHLQGPAGASVAGPQTSEAFAITVRDVN
	1		ERPPQPQASVPLRLTRGSRAPISRAQLSVVDPDSAPGEIEYEVQ
·		1	RAPHNGFLSLVGGGLGPVTRFTQADVDSGRLAFVANGSSVAGIF
			QLSMSDGASPPLPMSLAVDILPSAIEVQLRAPLEVPQALGRSSL
		1	SQQQLRVVSDREEPEAAYRLIQGPQYGHLLVGGRPTSAFSQFQI
			DQGEVVFAFTNFSSSHDHFRVLALARGVNASAVVNVTVRALLHV
	i	}	WAGGPWPQGATLRLDPTVLDAGELANRTGSVPRFRLLEGPRHGR
			VVRVPRARTEPGGSQLVEQFTQQDLEDGRLGLEVGRPEGRAPGP
		ĺ	AGDSLTLELWAQGVPPAVASLDFATEPYNAARPYSVALLSVPEA
		ļ	ARTEAGKPESSTPTGEPGPMASSPEPAVAKGGFLSFLEANMFSV
			IIPMCLVLLLLALILPLLFYLRKRNKTGKHDVQVLTAKPRNGLA
	}	ļ	GDTETFRKVEPGQAIPLTAVPGQGPPPGGQPDPELLQFCRTPNP
	1		ALKNGOYWV
5451	1	2274	RDSSEOGRTGDTLGRPSACMDALKPPCLWRNHERGKKDRDSCGR
2427	, •	22/4	KNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFNFLFSPLP
			1
		ĺ	TPALICILTFGAAIFLWLITRPQPVLPLLDLNNQSVGIEGGARK
1]		GVSQKNNDLTSCCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQ
			PYRWLSYKQVSDRAEYLGSCLLHKGYKSSPDQFVGIFAQNRPEW
			IISELACYTYSMVAVPLYDTLGPEAIVHIVNKADIAMVICDTPQ
			KALVLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSL
ł			YDAENLGKEHFRKPVPPSPEDLSVICFTSGTTGDPKGAMITHON
			IVSNAAAFLKCVEHAYEPTPDDVAISYLPLAHMFERIVQAVVYS
		}	CGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNE
)			AKTPLKKFLLKLAVSSKFKELQKGIIRHDSFWDKLIFAKIQDSL
ļ			GGRVRVIVTGAAPMSTSVMTFFRAAMGCQVYEAYGQTECTGGCT
ł		1	FTLPGDWTSGHVGVPLACNYVKLEDVADMNYFTVNNEGEVCIKG
ļ		j	TNVFKGYLKDPEKTQEALDSDGWLHTGDIGRWLPNGTLKIIDRK
İ	1		KNIFKLAQGEYIAPEKIENIYNRSQPVLQIFVHGESLRSSLVGV
		1	VVPDTDVLPSFAAKLGVKGSFEELCONQVVREAILEDLQKIGKE
1		1	SGLKTFEQVKAIFLHPEPFSIENGLLTPTLKAKRGELSKYFRTQ
1		l	IDSLYEHIQD
5452	1833	1138	SRVPSLCLSLSLSLSPSREPVAGAPGCGTAGPPAMATLWGGLLR
, ,,,,	1333	1 2230	LGSLLSLSCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENSG
1		1	HIYNKNISQKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSS
			1
1		1	VTIKVTIIIYLSILGLLLLYMVYLTLVEPILKRRLFGHAQLIQS
		J	DDDIGDHQPFANAHDVLARSRSRANVLNKVEYAQQRWKLQVQEQ
	<u> </u>	<u> </u>	RKSVFDRHVVLS
5453	111	1520	PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAV
		1	AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
1		1	PQEERSQQQDDIBELETKAVGMSNDGRFLKFDIEIGRGSFKTVY
			KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI
1		1	VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
}			RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
1			LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
1			LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII
)	EGCIRONKDERYSIKDLLNHAFFQEETGVRVELABEDDGEKIAI
			KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG
1		1	i e
L	4	<u> </u>	
5454	111	1520	
			AGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAKE
			PQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTVY
1	1	I	KGLDTETTVEVAWCELQDRKLTKSERQRFKEEAEMLKGLQHPNI
5454	111	1520	YVCEGDHKTMAKAIKDRVSLIKRKREQRQL* PSIPAAVPQSAPPEPHREETVTATATSQVAQQPPAAAAPGEQAAGPAPSTVPSSTSKDRPVSQPSLVGSKEEPPPARSGSGGGSAAPQEERSQQQDDIEELETKAVGMSNDGRFLKFDIEIGRGSFKTV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
1 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\≈possible nucleotide insertion)
			VRFYDSWESTVKGKKCIVLVTELMTSGTLKTYLKRFKVMKIKVL
1 (RSWCRQILKGLQFLHTRTPPIIHRDLKCDNIFITGPTGSVKIGD
1			LGLATLKRASFAKSVIGTPEFMAPEMYEEKYDESVDVYAFGMCM
1 [ļ	LEMATSEYPYSECQNAAQIYRRVTSGVKPASFDKVAIPEVKEII
1 1		ļ	EGCIRQNKDERYSIKDLLNHAFFQEETGVRVELAEEDDGEKIAI
1			KLWLRIEDIKKLKGKYKDNEAIEFSFDLERNVPEDVAQEMVESG
			YVCEGDHKTMAKAIKDRVSLIKRKREQRQL*
5455	1359	377	LTMVSPATRKSLPKVKAMDFITSTAILPLLFGCLGVFGLFRLLQ
1			WVRGKAYLRNAVVVITGATSGLGKECAKVFYAAGAKLVLCGRNG
]]		,	GALEELIRELTASHATKVQTHKPYLVTFDLTDSGAIVAAAAEIL
			QCFGYVDILVNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALT
1			KALLPSMIKRRQGHIVAISSIQGKMSIPFRSAYAASKHATQAFF
1			DCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTT
1			TAQGRSPVEVAQDVLAAVGKKKKDVILADLLPSLAVYLRTLAPG
1		<u> </u>	LFFSLMASRARKERKSKNS
5456	2	2332	CGAGLVAAGAVLVLYPASRAGERTRVPGSPAPSSLPLHSPGACG
		}	TEVDMDPQRSPLLEVKGNIELKRPLIKAPSQLPLSGSRLKRRPD
		!	QMEDGLEPEKKRTRGLGATTKITTSHPRVPSLTTVPQTQGQTTA
1		1	QKVSKKTGPRCSTAIATGLKNQKPVPAVPVQKSGTSGVPPMAGG
\' \			KKPSKRPAWDLKGQLCDLNAELKRCRERTQTLDQENQQLQDQLR
[1	DAQQQVKALGTERTTLEGHLAKVQAQAEQGQQELKNLRACVLEL
} })	EERLSTQEGLVQELQKKQVELQEERRGLMSQLEEKERRLQTSEA
		1	ALSSSQAEVASLRQETVAQAALLTEREERLHGLEMERRRLHNQL
} }		1	QELKGNIRVFCRVRPVLPGEPTPPPGLLLFPSGPGGPSDPPTRL
1			SLSRSDERRGTLSGAPAPPTRHDFSFDRVFPPGSGQDEVFEEIA
i i			MLVQSALDGYPVCIFAYGQTGSGKTFTMEGGPGGDPQLEGLIPR
1 1			ALRHLFSVAQELSGQGWTYSFVASYVEIYNETVRDLLATGTRKG QGGECEIRRAGPGSEELTVTNARYVPVSCEKEVDALLHLARONR
			AVARTAQNERSSRSHSVFQLQISGEHSSRGLQCGAPLSLVDLAG
1 1			SERLDPGLALGPGERERLRETQAINSSLSTLGLVIMALSNKESH
1			VPYRNSKLTYLLQNSLGGSAKMLMFVNISPLEENVSESLNSLRF
1 1			ASKVEPSVLFGTAQSNRKWKTDPDLCVCVCVCVCVCVCVCVCVP
} }			MSMYRVRGGRVAGGCFIGWRAPCPRAIK
5457	2	1540	DDFVERRRWTRTTCLVRSPPHVPVCGHACSWNGGSLDPLKGTPA
3.3.	_	1	LLRSAERLMRKVKKLRLDKENTGSWRSFSLNSEGAERMATTGTP
			TADRGDAAATDDPAARFQVQKHSWDGLRSIIHGSRKYSGLIVNK
1 1			APHDFOFVOKTDESGPHSHRLYYLGMPYGSRENSLLYSEIPKKV
		1	RKEALLLLSWKQMLDHFQATPHHGVYSREEELLRERKRLGVFGI
			TSYDFHSESGLFLFQASNSLFHCRDGGKNGFMVSPGPGCVSPMK
1 1	l	1	PLEIKTQCSGPRMDPKICPADPAFFSFINNSDLWVANIETGEER
1		1	RLTFCHQGLSNVLDDPKSAGVATFVIQEEFDRFTGYWWCPTASW
1		ľ	EGSEGLKTLRILYEEVDESEVEVIHVPSPALEERKTDSYRYPRT
1		1	GSKNPKIALKLAEFQTDSQGKIVSTQEKELVQPFSSLFPKVEYI
[ARAGWTRDGKYAWAMFLDRPQQWLQLVLLPPALFIPSTENEEQA
		}	ASLCQSCPQECPAVCGVRGGHQRLDQCS
5458	6642	4022	FVPGLREPQWEPAQPSATMSAPSEEEEYARLVMEAQPEWLRAEV
		1	KRLSHELAETTREKIQAAEYGLAVLEEKHQLKLQFEELEVDYEA
			IRSEMEQLKEAFGQAHTNHKKVAADGESREESLIQESASKEQYY
			VRKVLELQTELKQLRNVLTNTQSENERLASVAQBLKEINQNVEI
		1	QRGRLRDDIKEYKFREARLLQDYSELEEENISLQKQVSVLRQNQ
		1	VEFEGLKHEIKRLEEETEYLNSQLEDAIRLKEISERQLEEALET
			1
			LKTEREQKNSLRKELSHYMSINDSFYTSHLHVSLDGLKFSDDAA
			EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS
			EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG
			EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG
			EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ
			EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS
			EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML
			EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALIRILQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKEKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML DYYREGQGGAGRTSPGGRTSPEARGRRSPILLPKGLLAPEAGRA
			EPNNDAEALVNGFEHGGLAKLPLDNKTSTPKKEGLAPPSPSLVS DLLSELNISEIQKLKQQLMQMEREKAGLLATLQDTQKQLEHTRG SLSEQQEKVTRLTENLSALRRLQASKERQTALDNEKDRDSHEDG DYYEVDINGPEILACKYHVAVAEAGELREQLKALRSTHEAREAQ HAEEKGRYEAEGQALTEKVSLLEKASRQDRELLARLEKELKKVS DVAGETQGSLSVAQDELVTFSEELANLYHHVCMCNNETPNRVML

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	•	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
l .	beginning	1	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ĺ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	1	l .	
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			REQITTLRTVLKANKQTAEVALANLKSKYENEKAMVTETMMKLR
	1	İ	NELKALKEDAATFSSLRAMFATRCDEYITQLDEMQRQLAAAEDE
1			KKTLNSLLRMAIQQKLALTQRLELLELDHEQTRRGRAKAAPKTK
İ			PATPSVSHTCACASDRAEGTGLANQVFCSEKHSIYCD
		1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	
5459	316	1262	RGGHRLSGMASNFNDIVKQGYVRIRSRRLGIYQRCWLVFKKASS
1		1	KGPKRLEKFSDERAAYFRCYHKVTELNNVKNVARLPKSTKKHAI
		1	GIYFNDDTSKTFACESDLEADEWCKVLQMECVGTRINDISLGEP
	i	i	DLLATGVEREQSERFNVYLMPSPNLGCYMGECALQITYEYICLW
l			DVQNPRVKLISWPLSALRRYGRDTTWFTFEAGRMCETGEGLFIF
1		(QTRDGEAIYQKVHSAALAIAEQHERLLQSVKNSMLQMKMSERAA
			=
ì		1	SLSTMVPLPRSAYWQHITRQHSTGQLYRLQDVSSPLKLHRTETF
l		<u> </u>	PAYRSEH
5460	45	2097	RPGCRAGELSTGSRARERVRNRVSAPCGQDSRRCDPEVLRGRSP
		1	GLGLAEMPSCGACTCGAAAVRLITSSLASAQRGISGGRIHMSVL
ł	1	1	GRLGTFETQILQRAPLRSFTETPAYFASKDGISKDGSGDGNKKS
1		1	ASEGSSKKSGSGNSGKGGNQLRCPKCGDLCTHVETFVSSTRFVK
ļ	1	1	-
		1	CEKCHHFFVVLSEADSKKSIIKEPESAAEAVKLAFQQKPPPPPK
}		ł	KIYNYLDKYVVGQSFAKKVLSVAVYNHYKRIYNNIPANLRQQAE
1		Į.	VEKQTSLTPRELEIRRREDEYRFTKLLQIAGISPHGNALGASMQ
ļ	1.	1	QQVNQQIPQEKRGGEVLDSSHDDIKLEKSNILLLGPTGSGKTLL
		1	AQTLAKCLDVPFAICDCTTLTQAGYVGEDIESVIAKLLQDANYN
ļ	}	1	VEKAQQGIVFLDEVDKIGSVPGIHQLRDVGGEGVQQGLLKLLEG
Ì			TIVNVPEKNSRKLRGETVQVDTTNILFVASGAFNGLDRIISRRK
}		}	
		\	NEKYLGFGTPSNLGKGRRAAAAADLANRSGESNTHQDIEEKDRL
}		}	LRHVEARDLIEFGMIPEFVGRLPVVVPLHSLDEKTLVQILTEPR
			NAVIPQYQALFSMDKCELNVTEDALKAIARLALERKTGARGLRS
Ì		•	IMEKLLLEPMFEVPNSDIVCVEVDKEVVEGKKEPGYIRAPTKES
1		1	SEEEYDSGVEEEGWPRQADAANS
5461	1481	160	INPPPPPKSPCGRARKWRRRRRPGAPEAAVMELPSGPGPERLFD
3401	1401	100	
		1	SHRLPGDCFLLLVLLLYAPVGFCLLVLRLFLGIHVFLVSCALPD
		ì	SVLRRFVVRTMCAVLGLVARQEDSGLRDHSVRVLISNHVTPFDH
ł			NIVNLLTTCSTPLLNSPPSFVCWSRGFMEMNGRGELVESLKRFC
1		1	ASTRLPPTPLLLFPEEEATNGREGLLRFSSWPFSIQDVVQPLTL
			QVQRPLVSVTVSDASWVSELLWSLFVPFTVYQVRWLRPVHRQLG
		[EANEEFALRVOOLVAKELGOTGTRLTPADKABHMKRORHPRLRP
	}		OSAQSSFPPSPGPSPDVQLATLAQRVKEVLPHVPLGVIQRDLAK
ſ			TGCVDLTITNLLEGAVAFMPEDITKGTQSLPTASASKFPSSGPV
1			
L	<u> </u>	<u> </u>	TPQPTALTFAKSSWARQESLQERKQALYEYARRRFTERRAQEAD
5462	663	3353	KIKERQMSANNSPPSAQKSVLPTAIPAVLPAASPCSSPKTGLSA
		1	RLSNGSFSAPSLTNSRGSVHTVSFLLQIGLTRESVTIEAQELSL
1		J	SAVKDLVCSIVYQKFPECGFFGMYDKILLFRHDMNSENILQLIT
1			SADEIHEGDLVEVVLSALATVEDFQIRPHTLYVHSYKAPTFCDY
}	1	į.	CGEMLWGLVRQGLKCEGCGLNYHKRCAFKIPNNCSGVRKRRLSN
[VSLPGPGLSVPRPLQPEYVALPSEESHVHQEPSKRIPSWSGRPI
i			·-
1			WMEKMVMCRVKVPHTFAVHSYTRPTICQYCKRLLKGLFRQGMQC
			KDCKFNCHKRCASKVPRDCLGEVTFNGEPSSLGTDTDIPMDIDN
1	1	1	NDINSDSSRGLDDTEEPSPPEDKMFFLDPSDLDVERDEEAVKTI
1			SPSTSNNIPLMRVVQSIKHTKRKSSTMVKEGWMVHYTSRDNLRK
1			RHYWRLDSKCLTLFONESGSKYYKEIPLSEILRISSPRDFTNIS
1			QGSNPHCFEIITDTMVYFVGENNGDSSHNPVLAATGVGLDVAQS
1		İ	WEKAIRQALMPVTPQASVCTSPGQGKDHKDLSTSISVSNCQIQE
1			
1	1	1	NVDISTVYQIFADEVLGSGQFGIVYGGKHRKTGRDVAIKVIDKM
			RFPTKQESQLRNEVAILQNLHHPGIVNLECMFETPERVFVVMEK
1			LHGDMLEMILSSEKSRLPERITKFMVTQILVALRNLHFKNIVHC
1	1		DLKPENVLLASAEPFPOVKLCDFGFARIIGEKSFRRSVVGTPAY
1	1		LAPEVLRSKGYNRSLDMWSVGVIIYVSLSGTFPFNEDEDINDQI
1	}		
1	1		QNAAFMYPPNPWREISGEAIDLINNLLQVKMRKRYSVDKSLSHP
1	ļ		WLQDYQTWLDLREFETRIGERYITHESDDARWEIHAYTHNLVYP
i	-		KHFIMAPNPDDMEEDP
5463	237	1012	LLSVTMTTSRCSHLPEVLPDCTSSAAPVVKTVEDCGSLVNGQPQ
1	1	1	YVMQVSAKDGQLLSTVVRTLATQSPFNDRPMCRICHEGSSQEDL
1			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	1	l .	S=Serine, T=Threonine, V=Valine,
}	amino acid	residue of	1
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
Ĺ	sequence		\=possible nucleotide insertion)
			LSPCECTGTLGTIHRSCLEHWLSSSNTSYCELCHFRFAVERKPR
1			PLVEWLRNPGPQHEKRTLFGDMVCFLFITPLATISGWLCLRGAV
			DHLHFSSRLEAVGLIALTVALFTIYLFWTLVSFRYHCRLYNBWR
1			RTNQRVILLIPKSVNVPSNQPSLLGLHSVKRNSKETVV
5464	195	677	SPSMNPRKKVDLKLIIVGAIGVGKTSLLHQYVHKTFYEEYQTTL
			GASILSKIIILGDTTLKLQIWDTGGQERVRSMVSTFYKGSDGCI
ì			LAFDVTDLESFEALDIWRGDVLAKIVPMEQSYPMVLLGNKIDLA
1	}]	DRKYQSILENHLTESIKLSPDQSRSRCC
EASE	5278	3348	KGDPREFIRVHREALECDYVSAHLHEWIDLIFGYKQQGPAAVEA
5465	54/0	3340	VNVFHHLFYEGQVDIYNINDPLKETATIGFINNFGQIPKQLFKK
			PHPPKRVRSRLNGDNAGISVLPGSTSDKIFFHHLDNLRPSLTPV
1		İ	KELKEPVGQIVCTDKGILAVEQNKVLIPPTWNKTFAWGYADLSC
1			RLGTYESDKAMTVYECLSEWGQILCAICPNPKLVITGGTSTVVC
			VWEMGTSKEKAKTVTLKQALLGHTDTVTCATASLAYHIIVSGSR
1	}		DRTCIIWDLNKLSFLTQLRGHRAPVSALCINELTGDIVSCAGTY
1			IHVWSINGNPIVSVNTFTGRSQQIICCCMSEMNEWDTQNVIVTG
			HSDGVVRFWRMEFLQVPETPAPEPAEVLEMQEDCPEAQIGQEAQ
	ļ		DEDSSDSEADEQSISQDPKDTPSQPSSTSHRPRAASCRATAAWC
1		·	TDSGSDDSRRWSDQLSLDEKDGFIFVNYSEGQTRAHLQGPLSHP
1		ľ	HPNPIEVRNYSRLKPGYRWERQLVFRSKLTMHTAFDRKDNAHPA
	}		EVTALGISKDHSRILVGDSRGRVFSWSVSDQPGRSAADHWVKDE
			GGDSCSGCSVRFSLTERRHHCRNCGQLFCQKCSRFQSEIKRLKI
1	1		SSPVRVCQNCYYNLQHERGSEDGPRNC
5466	3	992	HACAHASAHASGRLVRWWRKRRSVMGIOTSPVLLASLGVGLVTL
1 2 2 3 3		1	LGLAVGSYLVRRSRRPQVTLLDPNEKYLLRLLDKTTVSHNTKRP
			RPALPTAHHTLGLPVGKHIYLSTRIDGSLVIRPYTPVTSDEDQG
1	}	j	YVDLVIKVYLKGVHPKFPEGGKMSQYLDSLKVGDVVEFRGPSGL
			LTYTGKGHFNIQPNKKSPPEPRVAKKLGMIAGGTGITPMLQLIR
1	1		AILKVPEDPTQCFLLFANQTEKDIILREDLEELQARYPNRFKLW
			FTLDHPPKDWAYSKGFVTADMIREHLPAPGDDVLVLLCGPPPMV
	ľ	\	
L		<u> </u>	QLACHPNLDKLGYSQKMRFTY
5467	2103	4	GEALRVGTRGCRRDLPDPQARIFIQKKDLEEDESVTAAHLKSRG
	1		RSPRKIDQFCNSSNMVHGSVTFRDVAIDFSQEEWECLQPDQRTL
			YRDVMLENYSHLISLAGSSISKPDVITLLEQEKEPWMVVRKETS
			RRYPDLELKYGPEKVSPENDTSEVNLPKQVIKQISTTLGIEAFY
1			FRNDSEYRQFEGLQGYQEGNINQKMISYEKLPTHTPHASLICNT
	1	1	HKPYECKECGKYFSCGSNLIQHQSIHTGEKPYKCKECGKAFQLH
1			IQLTRHQKFHTGEKTFECKECGKAFNLPTQLNRHKNIHTVKKLF
1			ECKECGKSFNRSSNLTQHQSIHAGVKPYQCKECGKAFNRGSNLI
	1		QHQKIHSNEKPFVCKECGMAFRYHYQLIEHCQIHTGEKPFECKE
	1		CGKAFTLLTKLVRHQKIHTGEKPFECRECGKAFSLLNQLNRHKN
	1		IHTGEKPFECKECGKSFNRSSNLVQHQSIHAGIKPYECKECGKG
		1	FNRGAHLIQHQKIHSNEKPFVCRECEMAFRYHCQLIEHSRIHTG
			DKPFECQDCGKAFNRGSSLVQHQSIHTGEKPYECKECGKAFRLY
1		1	LOLSOHOKTHTGEKPFECKECGKFFRRGSNLNOHRSIHTGKKPF
		į.	ECKECGKAFRLHMHLIRHQKLHTGEKPFECKECGKAFRLHMQLI
		1	RHOKLHTGEKPFECKECGKVFSLPTOLNRHKNIHTGEKAS
5468	225	2976	SFLTDLFOSLAOLENLCKQLYETTDTTTRLQAEKALVEFTNSPD
3400	245	29/0	CLSKCQLLLERGSSSYSQLLAATCLTKLVSRTNNPLPLEQRIDI
		1	RNYVINYLATRYKLATFVTQALIQLYARITKLGWFDCQKDDYVF
	1		
j		Į.	RNAITDVTRFLQDSVEYCIIGVTILSQLTNEINQVSATAFLIEA
		1	DTTHPLTKHRKIASSFRDSSLFDIFTLSCNLLKQASGKNLNLND
1		ì	ESQHGLLMQLLKLTHNCLNFDFIGTSTDESSDDLCTVQIPTSWR
1			SAFLDSSTLQLSTIGRCEYEKTCALLVQLFDQSAQSYQELLQSA
1	1		SASPMDIAVQEGRLTWLVYIIGAVIGGRVSFASTDEQDAMDGEL
1			VCRVLQLMNLTDSRLAQAGNEKLELAMLSFFEQFRKIYIGDQVQ
			KSSKLYRRLSEVLGLNDETMVLSVFIGKIITNLKYWGRCEPITS
1			KTLQLLNDLSIGYSSVRKLVKLSAVQFMLNNHTSEHFSFLGINN
1			QSNLTDMRCRTTFYTALGRLLMVDLGEDEDQYEQFMLPLTAAFE
1		1	AVAOMFSTNSFNBOEAKRTLVGLVRDLRGIAFAFNAKTSFMMLF
1			EWIYPSYMPILORAIELWYHDPACTTPVLKLMAELVHNRSQRLQ
L	<u>. 1</u>	1,	1

	Table 12 To State 1	5	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
140:		1	
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	
1			P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	1 "	1	
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	}	\=possible nucleotide insertion)
			
l .			FDVSSPNGILLFRETSKMITMYGNRILTLGEVPKDQVYALKLKG
1			ISICFSMLKAALSGSYVNFGVFRLYGDDALDNALQTFIKLLLSI
ł		{	PHSDLLDYPKLSQSYYSLLEVLTQDHMNFIASLEPHVIMYILSS
i		ì	
ľ	1	i	ISEGLTALDTMVCTGCCSCLDHIVTYLFKQLSRSTKKRTTPLNQ
	1		ESDRFLHIMQQHPEMIQQMLSTVLNIIIFEDCRNQWSMSRPLLG
ŀ	1	ì	LILLNEKYFSDLRNSIVNSQPPEKQQAMHLCFENLMEGIERNLL
· ·		ŀ	
1			TKNRDRFTQNLSAFRREVNDSMKNSTYGVNSNDMMS
5469	134	2653	DOEFETSLVPWHLPMGWLCSGLLFPVSCLVLLOVASSGNMKVLO
		1	
			EPTCVSDYMSISTCEWKMNGPTNCSTELRLLYQLVFLLSEAHTC
1			VPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPS
1	}	!	EHVKPRAPGNLTVHTNVSDTLLLTWSNPYPPDNYLYNHLTYAVN
1	1		
1		i	IWSENDPADFRIYNVTYLEPSLRIAASTLKSGISYRARVRAWAQ
Ī	1	ĺ	CYNTTWSEWSPSTKWHNSYREPFEQHLLLGVSVSCIVILAVCLL
1		1	_
[1	1	CYVSITKIKKEWWDQIPNPARSRLVAIIIQDAQGSQWEKRSRGQ
J	1	1	EPAKCPHWKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFQGSGK
1	1		SAWCPVEISKTVLWPESISVVRCVELFEAPVECEEEEEVEEEKG
	1	1	
1			SFCASPESSRDDFQEGREGIVARLTESLFLDLLGEENGGFCQQD
ł			MGESCLLPPSGSTSAHMPWDEFPSAGPKEAPPWGKEOPLHLEPS
1			PPASPTQSPDNLTCTETPLVIAGNPAYRSFSNSLSQSPCPRELG
]		1	
i		ł	PDPLLARHLEEVEPEMPCVPQLSEPTTVPQPEPETWEQ1LRRNV
J	Į	1	LQHGAAAAPVSAPTSGYQEFVHAVEQGGTQASAVVGLGPPGEAG
	l		YKAFSSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDPA
1		1	
1	1	ŧ	PVPVPLFTFGLDREPPRSPQSSHLPSSSPEHLGLEPGEKVEDMP
1	Į.	1	KPPLPQEQATDPLVDSLGSGIVYSALTCHLCGHLKQCHGQEDGG
			QTPVMASPCCGCCCGDRASPPTTPLRAPDPSPGGVPLEASLCPA
1	į	{	
		ŀ	SLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKIVNFVSVGPTYM
ľ	i	1	RVS
1			
E470	1 - 1	7410	
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF
5470	17	1418	
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF
5470		1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNMPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF
5470	17	1418	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT
			TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNIHDIIFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFMTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE
5470	1868	658	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV
			TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNIHDIIFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE
			TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFMTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR
			TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAATAAAAAAGVEMAAAAAQGGGGEPRRTEGV GPGVPGEVEMVKGQFFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR
			TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFFKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAATAAAAAAGVEMAAAAAQGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHGTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR
			TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAATAAAAAAGVEMAAAAAQGGGGEPRRTEGV GPGVPGEVEMVKGQFFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR
			TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIFILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD
			TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWIPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENB RSSAPPGPQRAAAATAAAAAAQGGGGEPRRTEGV GPGVPGEVEMVKQQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS
			TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIFILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD
			TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKQPPDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL
			TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPPDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBRAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP
			TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPDRAAAATAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ
			TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVVLTASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPPDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBRAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP
		658	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAATAAAAAAGVEMAAAAAQGGGGEPRRTEGV GGGVPGEVEMVKGQPFDVGPRYTCLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIPPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP
5471	1868		TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFFKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAATAAAAAAQVEMAAAAAQGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIMSVGCILAEMLS NRPIPPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR
5471	1868	658	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWPHA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAATAAAAAAGVGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHOTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTPHR
5471	1868	658	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFFKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAATAAAAAAQVEMAAAAAQGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIMSVGCILAEMLS NRPIPPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR
5471	1868	658	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKQQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLERAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA
5471	1868	658	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPORAAAATAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPPDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBRAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEA
5471	1868	658	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKQQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLERAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA
5471	1868	658	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPONPGYLGPAPEEA IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA
5471	1868	658 753	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPRSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNFGYLGPAPEEA IATQILACRGFSGHNLEYLRVRDVMQLCGPQAQDEHLAAIVDA VGTMLPCFCPTEQALALV
5471	1868	658	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTDLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRFWQGDTFHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNFGYLGPAPEEA IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA VGTMLPCFCPTEQALALV
5471	1868	658 753	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPRSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTPHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNFGYLGPAPEEA IATQILACRGFSGHNLEYLRVRDVMQLCGPQAQDEHLAAIVDA VGTMLPCFCPTEQALALV
5471	1868	658 753	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFFKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPPDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHGTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWTRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIPPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRFWQGDTFHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEA IATQILACRGFSGHNLEYLLVRDVMQLCGPQAQDEHLAAIVDA VGTMLPCFCPTEQALALV FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPQEEG KEMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLEELEKQMTS
5471	1868	658 753	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAAQGVEMAAAAAQGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIMSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEA IATQILACRGFSGHNLEYLLVRVDVMOLCGPQAQDEHLAAIVDA VGTMLPCFCPTEQALAV FMNVKLLIQDLEDIEQVPVMDAQYKIITKTAHLITKESPQEEG KEMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLEELEKQMTS FYDSLGKINEIITVLEREAQSSALFKQKHQELLACQENCKKTLT
5471	1868	658 753	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFFKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAATAAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPPDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHGTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWTRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIPPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRFWQGDTFHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEA IATQILACRGFSGHNLEYLLVRDVMQLCGPQAQDEHLAAIVDA VGTMLPCFCPTEQALALV FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPQEEG KEMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLEELEKQMTS
5471	1868	658 753	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPORAAAATAAAAAGVEMAAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPPDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALMIFGYGSLVWRPDFAYSDSRVGFVRGYSRRFWQGDTFHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEA IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA VGTMLPCFCPTEQALALV FMNVKLLIQDLEDIEGVPVMDAQYKIITKTAHLITKESPQEEG KEMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLBELEKQMTS FYDSLGKINEIITVLEREAQSSALPKQKHQELLACQENCKKTLIT LIEKGSQSVQKFVTLSNVLKHPDQTRLQRQIADIHVAFQSMVKK
5471	1868	658 753	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAGVEMAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRFFWQGDTFHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEEA IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA VGTMLPCFCPTEQALALV FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPQEEG KEMFATMSKLKEQLTKVKECYSPLLYESQULIPLEELEKQMTS FYDSLGKINEIITVLEREAQSSALPKQKHQELLACQENCKKTLT LIEKGSQSVQKFVTLSNVLKHFPQTTLQRQIADIHVAFQSNVKK TGDWKKHVETNSRLMKKFEESRAELEKVLRIAQEGLBEKGDPEE
5471	1868	658 753	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAAGVEMAAAAAQGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPRSDSKALDLLDRMITFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNFGYLGPAPEEA IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA VGTMLPCFCPTEQALALV FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPQEEG KEMFATMSKLKEQLTKVKECYSPLLYESQQLLIPLEELEKCMTS FYDSLGKINEIITVLEREAQSSALFKQKHQELLACQENCKKTLT LIEKGSQSVQKFVTLSNVLKHFDQTRLQRQIADIHVAFQSMVKK TGDMKKHVETNSRLMKKFEESRAELEKVLRIAQEGLBEKGDPEE LLRRHTEFFSQLDQRVLNAFLKACDELTDILPEQQQGLQGAVR
5471	1868	658 753	TACRIRTSLNRGIAAVKEDAVEMLASYGLAYSLMKFFTGPMSDF KNVGLVFVNSKRDRTKAVLCMVVAGAIAAVFHTLIAYSDLGYYI INKLHHVDESVGSKTRRAFLYLAAFPFMDAMAWTHAGILLKHKY SFLVGCASISDVIAQVVFVAILLHSHLECREPLLIPILSLYMGA LVRCTTLCLGYYKNIHDIIPDRSGPELGGDATIRKMLSFWWPLA LILATQRISRPIVNLFVSRDLGGSSAATEAVAILTATYPVGHMP YGWLTEIRAVYPAFDKNNPSNKLVSTSNTVTAAHIKKFTFVCMA LSLTLCFVMFWTPNVSEKILIDIIGVDFAFAELCVVPLRIFSFF PVPVTVRAHLTGWLMTLKKTFVLAPSSVLRIIVVLIASLVVLPYL GVHGATLGVGSLLAGFVGESTMDAIAACYVYRKQKKKMENESAT EGEDSAMTDMPPTEEVTDIVEMREENE RSSAPPGPQRAAAATAAAAAGVEMAAAAQGGGGGEPRRTEGV GPGVPGEVEMVKGQPFDVGPRYTQLQYIGEGAYGMVSSAYDHVR KTRVAIKKISPFEHQTYCQRTLREIQILLRFRHENVIGIRDILR ASTLBAMRDVYIVQDLMETDLYKLLKSQQLSNDHICYFLYQILR GLKYIHSANVLHRDLKPSNLLINTTCDLKICDFGLARIADPEHD HTGFLTEYVATRWYRAPEIMLNSKGYTKSIDIWSVGCILAEMLS NRPIFPGKHYLDQLNHILGILGSPSQEDLNCIINMKARNYLQSL PSKTKVAWAKLFPKSDSKALDLLDRMLTFNPNKRITVEEALAHP YLEQYYDPTDEPVAEEPFTFAMELDDLPKERLKELIFQETARFQ PGVLEAP LYVMARYLSDEEVAVSIDRLCKANGRSPSIPFGTVRIPGRARVR DPQALWIFGYGSLVWRPDFAYSDSRVGFVRGYSRFFWQGDTFHR GSDKMPGRVVTLLEDHEGCTWGVAYQVQGEQVSKALKYLNVREA VLGGYDTKEVTFYPQDAPDQPLKALAYVATPQNPGYLGPAPEEEA IATQILACRGFSGHNLEYLLRVRDVMQLCGPQAQDEHLAAIVDA VGTMLPCFCPTEQALALV FMNVKLLIQDLEDIEQRVPVMDAQYKIITKTAHLITKESPQEEG KEMFATMSKLKEQLTKVKECYSPLLYESQULIPLEELEKQMTS FYDSLGKINEIITVLEREAQSSALPKQKHQELLACQENCKKTLT LIEKGSQSVQKFVTLSNVLKHFPQTTLQRQIADIHVAFQSNVKK TGDWKKHVETNSRLMKKFEESRAELEKVLRIAQEGLBEKGDPEE

Predicted beginning nucleotide location nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence Predicted end residue of amino acid residue of amino acid sequence Predicted end residue of amino acid sequence Predicted end residue of amino acid sequence Predicted end residue of amino acid sequence Predicted end residue of amino acid residue of end residue of amino acid residue of amino acid residue of end residue of end residue of end residue of end residue of end res	PV PFS PFS PFS PFS PFS PFS PFS PFS PFS PFS
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location corresponding to first amino acid residue of amino acid residue of amino acid sequence N=Peroline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, R=Arginine, P=Proline, Q=Glutamine, R=Arginine, R=	PV RFS RRG LLS DTE DRG VVR AEN LDK
L=Leucine, M=Methionine, N=Asparagine, p=Proline, Q=Glutamine, R=Arginine, amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, amino acid sequence M=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, amino acid sequence M=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, amino acid sequence M=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, amino acid sequence M=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, v=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, v=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, v=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, v=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, V=Valine, v=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, v=Sterine, V=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, v=Sterine, V=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, v=Sterine, T=Threonine, v=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, v=Sterine, V=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, v=Sterine, T=Threonine, v=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, T=Threonine, v=Tryptophan, Y=Tyrosine, X=Unknown, *=Sterine, V=Sterine, V=Sterine, V=Sterine, V=Sterine, V=Sterine, V=Sterine, V=Sterine, V=Sterine, V=Sterine, V=Sterine, V=Sterine, V=	IPV RFS RG LS OTE ORG IVR AEN IDK
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to first amino acid residue of amino acid residue of amino acid sequence W=Tryptophan, Y=Tyrosine, X=Unknown, *=Sto Codon, /=possible nucleotide deletion, =possible nucleotide insertion) KMMPQEGSEKITKEHRVFFSDKGPHHLCEKRLQLIEELCVK RDPVRDTPGTCHVTLKELRAAIDSTYRKIMEDPDKWKDYTS EFSSWISTNETQLKGIKGEAIDTANHGEVKRAVEEIRNGVT ETLSWLKSRLKVLTEVSSENEAQKQGDELAKLSSSFKALVT EVEKMLSNFGDCVQYKEIVKNSLEELISGSKEVQEQABKILI NLFEAQQLLLHHQQKTKRISAKKRDVQQIAQAQQEGGLP HEELRKLESTLDCLERSRERQERRIQVTLRKWBRFETNKET YLFQTGSSHERFLSFSSLESLSSELEQTKEFSKRTESIAVQ, LVXEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEEEYV S S S474 2 780 TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQ, LVXEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEEEYV S CECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAW LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGR LQQAYGYGFYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLY PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF S475 2 506 ARGHLESISLTCQTTPPPSSPCLLHSPETFIHTMPPNLTGY VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTV STFRNYTVQFDVGVEFFEBLIRSVDGRKCQTIVTWEEEHLVC GEVPNRGWRHWLEGEMLYJELTARDAVCEQVFRVR S5476 192 1457 SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLS PSTRASEVLCSTNVSHYBELQVEIGRGFDNLTSVHLARHTFT VTIKITNLENCNDERLKALQKAVILSHFFRHPNITTYWTVF	IPV RFS RG LS OTE ORG IVR AEN IDK
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KLMPQEGSEKIIKEHRVFFSDKGPHHLCEKRLQLIEELCVKI RDPVRDTPGTCHVTLKELRAAIDSTYRRIMEDPDKWKDYTSI EFSSWISTNETQLKGIKGEAIDTANHGEVKRAVEEIRNGVTI ETLSWLKSRLKVLTEVSSENEAQKQGDELAKLSSSFKALVTI EVEKMLSNFGDCVQYKEIVRNSLEELISGSKEVQEGABKILI NLFEAQQLLLHHQQKTKRISAKKRDVQQQIAQAQQGEGGLPI HBELRKLESTLDGLERSRERQERRIQVTLRKWERFETNKET YLFQTGSSHERFLSFSSLESLSELEQTKEFSKRTESIAVQ. LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEEEYV S SA74 2 780 TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQ LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEEEYV S LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINI QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAW LQDSTNTAYVGSAVMTDETSVVSSPPPTTAYAAPAPEVGR LQQAYGYGFYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLY PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTV STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVC GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVR 5476 192 1457 SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLS PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPT VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF	RFS CRG LLS OTE ORG VVR LEN LDK STI
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EFSSWISTNETQLKGIKGEAIDTANHGEVKRAVEEIRNGVT ETLSWLKSRLKVLTEVSSENEAQKQGDELAKLSSSFKALVTI EVERMLSNFGDCVQYKEIVRNSLEELISGSKEVQEQABKILI NLFEAQQLLLHHQQKTKRISAKKRDVQQQIAQAQQGEGGLPI HBELRKLESTLDGLERSRERQERRIQVTLRKWERFETNKET YLFQTGSSHERFLSFSSLESLSSELEQTKEFSKRTESIAVQ. LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEEEYV S 5474 2 780 TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQ LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINI. QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAW LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGR LQQAYGYGYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLY PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF 5475 2 506 ARGWLESLSTCQTTPPPSSPCLLHSPETFIHTMPPNLTGY VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTV STFRNTTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVC GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVR 5476 192 1457 SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLS PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPT VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF	CRG LLS OTE ORG VVR LEN LDK STI
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EVEKMLSNFGDCVQYKEIVKNSLEELISGSKEVQEQABKILD NLFEAQQLLLHHQQKTKRISAKKRDVQQQIAQAQQGEGGLPI HBELRKLESTLDGLERSRERQERRIQVTLRKWERFETNKET YLFQTGSSHERFLSFSSLESLSSELEQTKEFSKRTESIAVQ. LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEBEYV S 5474 2 780 TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQ. LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINI: QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAW LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGR LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLY PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF ARGWESLSLTCQTTPPPSSPCLLHSPETFIHTMPPNLTGY VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTV STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVC GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVR 5476 192 1457 SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLS PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPT VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF	OTE ORG IVR AEN IDK STI
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HBELRKLESTLDGLERSRERQERRIQVTLRKWERFETNKET YLFQTGSSHERFLSFSSLESLSSELEQTKEFSKRTESIAVQ. LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEBEYV S 5474 2 780 TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQ. LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINI. QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAW. LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGR. LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLY. PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF. PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF. VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTV. STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVC. GEVPNRGWRHWLEGEMLYLELTARDAVCEQUFRKVR. SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLS. PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPT. VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF	VR EN IDK STI
YLFQTGSSHERFLSFSSLESLSSELEQTKEFSKRTESIAVQ. LVKEASEIPLGPQNKQLLQQQAKSIKEQVKKLEDTLEBEYV S 5474 2 780 TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQ. LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINI: QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAW LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGR LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLY PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF 5475 2 506 ARGWLESLSITCQTTPPPSSPCLLHSPETFIHTMPPNLTGY VSQKNMEDYLQALNISLAVRXIALLLKPDKEIEHQGNHMTV STFRNYTVOFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVC GEVPNRGWRHWLGEMLYLELTARDAVCEQVPRKVR 5476 192 1457 SDSMSLLDCFCTSRTQVESLRPEKGSETSIHQYLVDEPTLS PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPT VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF	ETI ETI ETI
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S 5474 2 780 TPDVRQLQASRRGIAVASWCSPRWFAGEEMAFVKSGWLLRQ LKRMKKNWFDLMSDGHLIYYDDQTRQNIEDKVHMPMDCINI QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAW LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPDEVGR LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLY PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF 5475 2 506 ARGWLESLSTCQTTPPPSSPCLLHSPETFIHTMPPNLTGY VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTV STFRNYTVOFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVC GEVPNRGWRHWLGEMLYLELTARDAVCEQVFRKVR 5476 192 1457 SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLS PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPT VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF	TI TG
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LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINI QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAW LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGR LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLY PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF 3475 2 506 ARGWESISLTCQTTPPPSSPCLLHSPETFIHTMPPNLTGY VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTV STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVC GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVR 5476 192 1457 SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLS PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPT VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF	2TG
LKRWKKNWFDLWSDGHLIYYDDQTRQNIEDKVHMPMDCINI QECRDTQPPDGKSKDCMLQIVCRDGKTISLCAESTDDCLAW LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGR LQQAYGYGPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLY PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF 3475 2 506 ARGWLESLSLTCQTTPPPSSPCLLHSPETFIHTMPPNLTGY VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTV STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVC GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVR 5476 192 1457 SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLS PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPT VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF	TG Tra
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LQDSRTNTAYVGSAVMTDETSVVSSPPPYTAYAAPAPEVGR LQQAYGYPYGGAYPPGTQVVYAANGQAYAVPYQYPYAGLY PANQVIIRERYRDNDSDLALGMLAGAATGMALGSLFWVF \$475 2 506 ARGWLESISITCOTTPPPSSPCLLHSPETFIHTMPPNLTGY VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTV STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVC GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVR 5476 192 1457 SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLS PSTRASEVLCSTNV9HYELQVEIGRGFDNLTSVHLARHTPT VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF	
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5475 2 506 ARGWLESLSTTQTTPPPSSPCLLHSPETFIHTMPPNLTGY VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTV STFRNTTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVC GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRVR 5476 192 1457 SDEMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLS PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPT VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF	-22
VSQKNMEDYLQALNISLAVRKIALLLKPDKEIEHQGNHMTV STFRNYTVQFDVGVEFEEDLRSVDGRKCQTIVTWEEEHLVC GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRVR 5476 192 1457 SDSMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLS PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPT VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF	
VSQKNMEDYLQALNISLÄVRKIALLLKPDKEIEHQGNHMTV STFRNYTVOFDVGVEFEEDLKSVDGRKCQTIVTWEEEHLVC GEVPNRGWRHWLEGEMLYLELTARDAVCEQVFRKVR 5476 192 1457 SDEMSLLDCFCTSRTQVESLRPEKQSETSIHQYLVDEPTLS PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPT VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF	
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PSTRASEVLCSTNVSHYELQVEIGRGFDNLTSVHLARHTPT VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF	10D
VTIKITNLENCNEERLKALQKAVILSHF FRHPNITTYWTVF	
VTIKITNLENCNEERLKALQKAVILSHFFRHPNITTYWTVF SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNILFGAVR	
SWLWVISPFMAYGSASQLLRTYFPEGMSETLIRNILFGAVR	rvg
	SLN
YLHONGCIHRSIKASHILISGDGLVTLSGLSHLHSLVKHGQ	
AVYDFPQFSTSVQPWLSPELLRQDLHGYNVKSDIYSVGITA	CEL
ASGQVPFQDMHRTQMLLQKLKGPPYSPLDISIFPQSESRMK	vico.
SGVDSGIGESVLVSSGTHTVNSDRLHTPSSKTFSPAFFSLV	5TC
LQQDPEKRPSASSLLSHVFFKQMKEESQDSILSLLPPAYNK	PSI
SLPPVLPWTEPECDFPDEKDSYWEF	
THE PARTY OF THE P	SRI
5477 3 1044 RGNSRLRYSHEDELQLPRDFELFETGRQLLDEVEVALEPAG VOEKVFKGLDLLEKAAEMLSQLDLFSRNEDLEEIASTDLKY	
PAFQGALTMKQVNPSKRLDHLQRAREHFINYLTQCHCYHVA	ere
LPKTMNNSAENHTANSSMAYPSLVAMASQRQAKIQRYKQKK	ELE
HRLSAMKSAVESGQADDERVREYYLLHLQRWIDISLEEIES	IDQ
EIKILRERDSSREASTSNSSRQERPPVKPFILTRNMAQAKV	
GYPSLPTMTVSDWYEQHRKYGALPDQGIAKAAPBEFRKAAQ	
EQEEKEEEDDEQTLHRAREWDDWKDTHPRGYGNRQNMG	
THE STATE OF THE S	n izm
5478 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASL	DVI.
VKVWATHRQKFLFSLSQHINNVRCAKFSPDGRLIVSASDDK	T.A.K
LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTV	KVW
DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKI	PDF
MEGRLLYTLHGHQGPATTVAFSRTGEYFASGGSDBQVMVWK	SNF
DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKI	KOC
3 1	
LENQQLIMQRATP	
5479 2 835 KTVRIWVPNVKGESTVFRAHTATVRSVHFCSDGQSFVTASL	
VKVWATHRQKFLFSLSQHINWVRCAKFSPDGRLIVSASDDK	
LWDKSSRECVHSYCEHGGFVTYVDFHPSGTCIAAAGMDNTV	
DVRTHRLLQHYQLHSAAVNGLSFHPSGNYLITASSDSTLKI	LDL
MEGRILYTLHGHQGPATTVAFSRTGEYFASGGSDEQVMVWW	SNF
MEGRELYTENGHQGPAIIVAPSRIGEIFASGGDEQVWVW	200
DIGDHGEVTKVPRPPATLASSMGNLTVSILEQRLTLEEDKL	V QC
LENQQLIMQRATP	
5480 444 1952 LSLTSRMEEAELVKGRLQAITDKRKIQEEISQKRLKIEEDK	LKH
OHLKKKALREKWLLDGISSGKEQEEMKKQNQQDQHQIQVLE	
LRLEKEIQDLEKAELQISTKERAILKKLKSIERTTEDIIRS	
EREERAEESIEDIYANIPDLPKSYIPSRLRKEINEEKEDDE	
KALYAMEIKVEKDLKTGESTVLSSIPLPSDDFKGTGIKVYI	1 X 2(1)
KSVYAVSSNHSAAYNGTDGLAPVEVEELLRQASERNSKSPI	
EPVYANPPYRPTTPORETVTPGPNFQERIKIKTNGLGIGVN	EYH
HNMGNGLSEERGNNFNHISPIPPVPHPRSVIQQAEEKLHTE	EYH
Indigrade productive and the state of the st	EYH ESI

SEQ	Predicted	Predicted end	Danton notes
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	1 2	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide		Glutamic Acid, F=Phenylalanine, G=Glycine,
ľ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
J	sequence] -	\=possible nucleotide insertion)
 	 	 	LMTPWEESNVMQDKDAPSPKPRLSPRETIFGKSEHQNSSPTCQE
1	1	1	
			DEEDVRYNIVHSLPPDINDTEPVTMIFMGYQQAEDSEEDKKFLT
i	ŀ	ł	GYDGIIHAELVVIDDEEEEDEGEAEKPSYHPIAPHSQVYQPAKP
			TPLPRKRSEASPHEKHKS
5481	3	1422	NSPGSVCLCQCVCPSLLHCLPPLLLLLLLLLLLHESPQPPALRV
]	<u>l</u>	J	VATSSDRNFMNKHQKPVLTGQRFKTRKRDEKEKFEPTVFRDTLV
	li di di di di di di di di di di di di di]	QGLNEAGDDLEAVAKFLDSTGSRLDYRRYADTLFDILVAGSMLA
1	l	1	PGGTRIDDGDKTKMTNHCVFSANEDHETIRNYAQVFNKLIRRYK
		ł	YLEKAFEDEMKKLLLFLKAFSETEQTKLAMLSGILLGNGTLPAT
t		ľ	ILTSLFTDSLVKEGIAASFAVKLFKAWMAEKDANSVTSSLRKAN
ĺ		ļ	
1		[LDKRLLELFPVNRQSVDHFAKYFTDAGLKELSDFLRVQQSLGTR
	1	j	KELQKELQERLSQECPIKEVVLYVKEEMKRNDLPETAVIGLLWT
1			CIMNAVEWNKKEELVAEQALKHLKQYAPLLAVFSSQGQSELILL
1	1	1	QKVQEYCYDNIHFMKAFQKIVVLFYKADVLSEEAILKWYKEAHV
	<u></u>	L	AKGKSVFLDQMKKFVEWLQNABEESESEGEEN
5482	1492	528	THVVMTGMCYAPHQVLSYINGVTTSKPGVSLVYSMPSRNLSLRL
1	1		EGLQEKDSGPYSCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPS
1	1		CRLQGVPHVGANVTLSCQSPRSKPAVQYQWDRQLPSFQTFFAPA
1	1	ļ	LDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTAQCNVTLEVSTGP
	i		GAAVVAGAVVGTLVGLGLLAGLVLLYHRRGKALEEPANDIKEDA
1	ļ		IAPRTLPWPKSSDTISKNGTLSSVTSARALRPPHGPPRPGALTP
			TPSLSSQALPSPRLPTTDGAHPQPISPIPGGVSSSGLSRMGAVP
5483			VMVPAQSQAGSLV
5483	1	788	FFFFKGCRAGRGNESDYRKLEEMHQRFLVSERSKDDLQLRLTRA
}	1	•	ENRIKQLETDSSEEISRYQEMIQKLQNVLESERENCGLVSEQRL
			KLQQENKQLRKETESLRKIALEAQKKAKVKISTMEHEFSIKERG
ſ	[FEVOLREMEDSNRNSIVELRHLLATQQKAANRWKEETKKLTESA
1]		EIRINNLKSELSRQKLHTQELLSQLEMANEKVAENEKLILEHOE
			KANRLQRRLSQAEERAASASQQLSVITVQRRKAASLMNLENI
5484	3	1997	IMADMEDLFGSDADSEAERKDSDSGSDSDSDQENAASGSNASGS
Ĭ			ESDQDERGDSGQPSNKELFGDDSEDEGASHHSGSDNHSERSDNR
[1		SEASERSDHEDNDPSDVDQHSGSEAPNDDEDEGHRSDGGSHHSE
}]		AEGSEKAHSDDEKWGREDKSDQSDDEKIQNSDDEERAQGSDEDK
ļ			
ł			LQNSDDDEKMQNTDDEERPQLSDDERQQLSEEEKANSDDERPVA
1			SDNDDEKQNSDDEEQPQLSDEEKMQNSDDERPQASDEEHRHSDD
ſ	(EEEQDHKSESARGSDSEDEVLRMKRKNAIASDSEADSDTEVPKD
1]		NSGTMDLFGGADDISSGSDGEDKPPTPGQPVDENGLPQDQQEEE
1 -			PIPETRIEVEIPKVNTDLGNDLYFVKLPNFLSVEPRPFDPQYYE
	}		DEFEDEEMLDEEGRTRLKLKVENTIRWRIRRDEEGNEIKESNAR
	, ,		IVKWSDGSMSLHLGNEVFDVYKAPLQGDHNHLFIRQGTGLQGQA
1	1		VFKTKLTFRPHSTDSATHRKMTLSLADRCSKTQKIRILPMAGRD
			PECQRTEMIKKEEERLRASIRRESQQRRMREKQHQRGLSASYLE
	į i		PDRYDEEEEGEESISLAAIKNRYKGGIREERARIYSSDSDEGSE
1	1		EDKAQRLLKAKKLTSDEVRPNLFNSRGLSCTQEPTALNEELTDQ
			AGTN
5485	161	1074	
-100	101	70/4	KRKILSSMMDSEAHEKRPPILTSSKQDISPHITNVGEMKHYLCG
1	[CCAAFNNVAITFPIQKVLFRQQLYGIKTRDAILQLRRDGFRNLY
]		RGILPPLMQKTTTLALMPGLYEDLSCLLHKHVSAPEFATSGVAA
			VLAGTTEAIFTPLERVQTLLQDHKHHDKFTNTYQAFKALKCHGI
		ļ	GEYYRGLVPILFRNGLSNVLFFGLRGPIKEHLPTATTHSAHLVN
			DFICGGLLGAMLGFLFFPINVVKTRIQSQIGGEFQSFPKVFQKI
L		İ	WLERDRKLINLPRGAHLNYHRSLISWGIINATYEFLLKVI
5486	1404	142	IPGSTISWSPAAARGLSVCRCCRLHPASAMDLFGDLPEPERSPR
	1		PAAGKEAQKGPLLFDDLPPASSTDSGSGGPLLFDDLPPASSGDS
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		.	GSLATSISQMVKTEGKGAKRKTSEEEKNGSEELVEKKVCKASSV
		ļ	IFGLKGYVAERKGEREEMQDAHVILNDITEECRPPSSLITRVSY
			FAVFDGHGGIRASKFAAQNLHQNLIRKFPKGDVISVEKTVKRCL
1			LDTFKHTDEEFLKQASSQKPAWKDGSTATCVLAVDNILYIANLG
			DSRAILCRYNEESQKHAALSLSKEHNPTQYEERMRIQKAGGNVR
[L		DGRVLGVLEVSRSIGDGQYKRCGVTSVPDIRRCQLTPNDRFILL

SEO	I Decade at a second	Predicted end	
ID	Predicted beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, R=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ĭ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence		\=possible nucleotide insertion)
			ACDGLFKVFTPEEAVNFILSCLEDEKIOTREGKSAADARYEAAC
Î			NRLANKAVQRGSADNVTVMVVRIGH
5487	535	182	AVSLEQIRGLQTPAPVPLPLQPCPSNCDMERVTLALLLLAGLTA
	1		LEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGK
1	i	Į.	CKCKSSQKQHSPVPEKAIPLITPGSATTC
5488	1072	259	AMAASGEPQRQWQEEVAAVVVVGSCMTDLVSLTSRLPKTGETIH
3400	1072	239	
1	1	l .	GHKFFIGFGGKGANQCVQAARLGAMTSMVCKVGKDSFGNDYIEN
			LKQNDISTEFTYQTKDAATGTASIIVNNEGQNIIVIVAGANLLL
į.	1		NTEDLRAAANVISRAKVMVCQLEITPATSLEALTMARRSGVKTL
İ	Ì		FNPAPAIADLDPQFYTLSDVFCCNESEAEILTGLTVGSAADAGE
İ			AALVLLKRGCQVVIITLGAEGCVVLSQTEPEPKHIPTEKVKAVD
ł		}	TTVSFKI
5489	81	893	GKGPVAAFIDQSNIFLTDPKIFLGOWREEPKMPLLLLGETEPLK
1			LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
1	1		LFPTVEMVIKVFVATSSGSIAIRKKOOEVVGFLEANKIDFKELD
1			IAGDEDNRRWMRENVPGEKKPONGIPLPPOIFNEEQYCGDFDSF
(1		FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG
1			NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEGEEP
	ļ		GEDEDS
5490	81		
3490	81	893	GKGPVAAFIDQSNIFLTDPKIFLGQWREEPKMPLLLLGRTEPLK
			LERDCRSPVEPWAAASPDLALACLCHCQDLSSGAFPNRGVLGGV
l .			LFPTVEMVIKVFVATSSGSIAIRKKQQEVVGFLEANKIDFKELD
	E .		IAGDEDNRRWMRENVPGEKKPQNGIPLPPQIFNEEQYCGDFDSF
i	1		FSAKEENIIYSFLGLAPPPDSKGSEKAEEGGETEAQKEGSEDVG
			NLPEAQEKNEEEGETATEETEEIAMEGAEGEAEEEEETAEGEEP
			GEDEDS
5491	204	1194	GSAPRLSLGPTGAQARDPDWWARPPSRPYTQSKEDRPDTEGRSE
		,	QGDMASSFLPAGAITGDSGGELSSGDDSGEVEFPHSPEIEETSC
			LAELFEKAAAHLQGLIQVASREQLLYLYARYKQVKVGNCNTPKP
1	j		SFFDFEGKQKWEAWKALGDSSPSQAMQEYIAVVKKLDPGWNPQI
1	1	1	PEKKGKEANTGFGGPVISSLYHEETIREEDKNIFDYCRENNIDH
l			ITKAIKSKNVDVNVKDEEGRALLHWACDRGHKELVTVLLOHRAD
			1 -
1	1		INCQDNEGQTALHYASACEFLDIVELLLQSGADPTLRDQDGCLP
			EEVTGCKTVSLVLQRHTTGKA
5492	3	1896	ASKNPLSAVCTTGIMSSLAVRDPAMDRSLRSVFVGNIPYEATEE
(1	1	QLKDIFSEVGSVVSFRLVYDRETGKPKGYGFCEYQDQETALSAM
1	1		RNLNGREFSGRALRVDNAASEKNKEELKSLGPAAPIIDSPYGDP
1			IDPEDAPESITRAVASLPPEQMFELMKQMKLCVQNSHQEARNML
1	1		LQNPQLAYALLQAQVVMRIMDPEIALKILHRKIHVTPLIPGKSQ
1			SVSVSGPGPGPGPGLCPGPNVLLNQQNPPAPQPQHLARRPVKDI
			PPLMQTPIQGGIPAPGPIPAAVPGAGPGSLTPGGAMQPQLGMPG
1	l		VGPVPLERGQVQMSDPRAPIPRGPVTPGGLPPRGLLGDAPNDPR
1	1		GGTLLSVTGEVEPRGYLGPPHQGPPMHHASGHDTRGPSSHEMRG
1	1		GPLGDPRLLIGEPRGPMIDQRGLPMDGRGGRDSRAMETRAMETE
)			VLETRVMERRGMETCAMETRGMEARGMDARGLEMRGPVPSSRGP
1	1		MTGGIQGPGPINIGAGGPPQGPRQVPGISGVGNPGAGMOGTGIO
1	1		GTGMQGAGIQGGGMQGAGIQGVSIQGGGIQGGGIQGASKQGGSQ
			PSSFSPGQSQVTPQDQEKAALIMQVLQLTADQIAMLPPEQRQSI
}	1		LILKEQIQKSTGAS
5402	+	1076	
5493	1	1876	RAPMMTKAVPEEPRKPGRLTQALNSPLTWEHVWICVPGGTPDCL
1	1		TDTFRVKRPHLRRSASNGHVPGTPVYREKEDMYDEIIELKKSLH
			VQKSDVDLMRTKLRRLEEENSRKDRQIEQLLDPSRGTDFVRTLA
	1		EKRPDASWVINGLKQRILKLEQQCKEKDGTISKLQTDMKTTNLE
}	1		EMRIAMETYYEEVHRLQTLLASSETTGKKPLGEKKTGAKRQKKM
			GSALLSLSRSVQELTEENQSLKEDLDRVLSTSPTISKTQGYVEW
1	1		SKPRLLRRIVELEKKLSVMESSKSHAAEPVRSHPPACLASSSAL
}	}		HRQPRGDRNKDHERLRGAVRDLKEERTALQEQLLQRDLEVKQLL
			QAKADLEKELECAREGEEERREREEVLREEIQTLTSKLQELQEM
1	1		KKEEKEDCPEVPHKAQELPAPTPSSRHCEQDWPPDSSBEGLPRP
L	J		RSPCSDGRRDAAARVLQAQWKVYKHKKKKAVLDEAAVVLQAAFR

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	Grucamic Acid, Fernenylatanine, GeGlycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
ł	amino acid	1	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
(amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	ľ	1	GHLTRTKLLASKAHGSEPPSVPGLPDQSSPVPRVPSPIAQATGS
j	ļ		PVQEEAIVIIQSALRAHLARARHSATGKRTTTAASTRRRSASAT
			HGDASSPPFLAALPDPSPSGPQAVAPLPGDDVNSDDSDDIVIAP
L	<u></u>	<u> </u>	SLPTKNFPV
5494	71	536	RSKAKIGTPTREVPSTDMKVRRESSSSLTHRPAPSPATPRLLGT
Į	İ	}	RRVLLGVSEGTGCADAMELVLVFLCSLLAPMVLASAAEKEKEMD
Ĭ	1	ĺ	PFHYDYQTLRIGGLVFAVVLFSVGILLILSRRCKCSFNQKPRAP
1	,		GDEEAQVENLITANATEPOKAEN
5495	273	2168	DSLLLIQVDTMPFTLHLRSRLPSAIRSLILQKKPNIRNTSSMAG
1			ELRPASLVVLPRSLAPAFERFCQVNTGPLPLLGQSEPEKWMLPP
			QGAISETRMGHPQFWKYEFGACTGSLASLEQYSEQLKDMVAFFL
			GCSFSLEEALEKAGLPRRDPAGHSQAGAYKTTVPCVTHAGFCCP
1			I/V/TMPPI PKDVI PGI //PAGGG GGPOGODININGPPRI A TITOT
1			LVVTMRPIPKDKLEGLVRACCSLGGEQGQPVHMGDPELLGIKEL
1			SKPAYGDAMVCPPGEVPVFWPSPLTSLGAVSSCETPLAFASIPG
ì	ł		CTVMTDLKDAKAPPGCLTPERIPEVHHISQDPLHYSIASVSASQ
			KIRELESMIGIDPGNRGIGHLLCKDELLKASLSLSHARSVLITT
İ	ľ		GPPTHFNHEPPEETDGPPGAVALVAFLQALEKEVAIIVDQRAWN
ì	[LHQKIVEDAVEQGVLKTQIPILTYQGGSVEAAQAFLCKNGDPQT
	1		PRFDHLVAIERAGRAADGNYYNARKMNIKHLVDPIDDLFLAAKK
	1		IPGISSTGVGDGGNELGMGKVKEAVRRHIRHGDVIACDVEADFA
j]		VIAGVSNWGGYALACALYILYSCAVHSQYLRKAVGPSRAPGDQA
			WTQALPSVIKEEKMLGILVQHKVRSGVSGIVGMEVDGLPFHNTH
5496			AEMIQKLVDVTTAQV
3496	3	2408	QDTKMHEIYKGNITPQLNKNTLKTSAATDVWAVYFSQFWIDYEG
			MKSGKGRPISFVDSFPLSIWICQPTRYAESQKEPQTCNQVSLNT
1			SQSESSDLAGRLKRKKLLKEYYSTESEPLTNGGQKPSSSDTFFR
1			FSPSSSEADIHLLVHVHKHVSMQINHYQYLLLLFLHESLILLSE
1			NLRKDVEAVTGSPASQTSICIGILLRSAELALLLHPVDOANTLK
ł			SPVSESVSPVVPDYLPTENGDFLSSKRKQISRDINRIRSVTVNH
1			MSDNRSMSVDLSHIPLKDPLLFKSASDTNLQKGISFMDYLSDKH
	(LGKISEDESSGLVYKSGSGEIGSETSDKKDSFYTDSSSVLNYRE
1			DSNILSFDSDGNQNILSSTLTSKGNETIESIFKAEDLLPEAASL
			SENLDISKEETPPVRTLKSQSSLSGKPKERCPPNLAPLCVSYKN
			MKRSSSQMSLDTISLDSMILEEQLLESDGSDSHMFLEKGNKKNS
			TTNYRGTAESVNAGANLQNYGETSPDAISTNSEGAQENHDDLMS
			VVVFKITGVNGEIDIRGEDTEICLQVNQVTPDQLGNISLRHYLC
(NRPVGSDQKAVIHSKSSPEISLRFESGPGAVIHSLLAEKNGFLQ
		j	CHIKNFSTEFLTSSLMNIQHFLEDETVATVMPMKIQVSNTKINL
			KDDSPRSSTVSLEPAPVTVHIDHLVVERSDDGSFHIRDSHMLNT
		l	GNDLKENVKSDSVLLTSGKYDLKKQRSVTQATQTSPGVPWPSQS
] !]		ANFPEFSFDFTREQLMEENESLKQELAKAKMALAEAHLEKDALL
			HHIKKMTVE
5497	1821	3308	SISKLLKRRSNIDAYLLSNSCAFFAPRLFSLASQIIREQQSPNV
1			CFIYKYSGFPSLECQCHFVSPHSSCYINFFSFPPPFFVCFQLSN
		j	GFSHYSLSSESHVGPTGAGLFPHCLPASRLLPRVTSVHLPDYAH
[YYTIGPGMFPSSQIPSWKDWAKPGPYDQPLVNTLQRRKEKREPD
Į į		}	PNGGGPTTASGPPAAAEEAQRPRSMTVSAATRPGEEMEACEELA
1			LALSRGLQLDTQRSSRDSLQCSSGYSTQTTTPCCSEDTIPSQVS
į i			DYDYFSVSGDQEADQQEFDKSSTIPRNSDISQSYRRMFQAKRPA
, ,		j	STAGLPTTLGPAMVTPGVATIRRTPSTKPSVRRGTIGAGPIPIK
1 1			TOVI DIRECTIVE DE DE DE DE DE DE DE DE DE DE DE DE DE
		1	TPVI PVKTPTVPDLPGVLPAPPDGPEERGEHSPESPSVGEGPQG
j l	}		VTSMPSSMWSGQASVNPPLPGPKPSIPEEHRQAIPESEAEDQER
]	ĺ	ſ	EPPSATVSPGQIPESDPADLSPRDTPQGEDMLNAIRRGVKLKKT
5498	2434	1465	TTNDRSAPRFS
3436	2434	1492	ILTHQEIFTGEKPCECGKASIQMSHLSQQKIYSGENPFACKVCG
			KVFSHKSNLTEHEHFHTREKPFECNECGKAFSQKQYVIKHQNTH
1	}	į.	TGEKLFECNECGKSFSQKENLLTHQKIHTGEKPFECKDCGKAFI
			QKSNLIRHQRTHTGEKPFVCKECGKTFSGKSNLTEHEKIHIGEK
	1	1	PFKCSECGTAFGQKKYLIKHQNIHTGEKPYECNECGKAFSORTS
, ,	J	ļ	LIVHVRIHSGDKPYECNVCGKAFSQSSSLTVHVRSHTGEKPYGC
Ll			NECGKAFSQFSTLALHLRIHTGKKPYQCSECGKAFSQKSHHIRH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
]	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Ì	amino acid	residue of	
1			S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	<u> </u>	\=possible nucleotide insertion)
	<u> </u>	<u> </u>	QKIHTH
5499	324	926	GFGQIGRGHKITTYPFSPRKSGRKGMAQSQGWVKRYIKAFCKGF
	i	}	FVAVPVAVTFLDRVACVARVEGASMQPSLNPGGSQSSDVVLLNH
ł			WKVRNFEVHRGDIVSLVSPKNPEQKIIKRVIALEGDIVRTIGHK
1	1	<u> </u>	NRYVKVPRGHIWVEGDHHGHSFDSNSFGPVSLGLLHAHATHILW
1			PPERWQKLESVLPPERLPVQREEE
5500	1978	1286	KPDWRLQNLPPRLYLWRSSRFGFGHLKKRLOMDFKIEHTWDGFP
3300	}]	VKHEPVFIRLNPGDRGVMMDISAPFFRDPPAPLGEPGKPFNELW
1			DYEVVEAFFLNDITEQYLEVELCPHGQHLVLLLSGRRNVWKQEL
	}		1
	1		PLSFRVSRGETKWEGKAYLPWSYPPPNVTKFNSFAIHGSKDKRS
			YEALYPVPQHELQQGQKPDFHCLEYFKSFNFNTLLGEEWKQPES
	<u> </u>		DLMTIEKCDI
5501	2927	2226	CRPPVSARVAPGHQGAVGGSGRRPARVEVVDAAARPSSRPFSLP
		ł	AAIMLALISRLLDWFRSLFWKEEMELTLVGLQYSGKTTFVNVIA
		[SGQFSEDMIPTVGFNMRKVTKGNVTIKIWDIGGQPRFRSMWERY
1		1	CRGVNAIVYMIDAADREKIEASRNELHNLLDKPQLQGIPVLVLG
			NKRDLPNALDEKQLIEKMNLSAIQDREICCYSISCKEKDNIDIT
		1	LQWLIQHSKSRRS
5502	3	824	NSAFPVWVPERTALLTCPLGAAPGSSREAPGIAGPPNSTAMSKL
			GKFFKGGGSSKSRAAPSPQEALVRLRETEEMLGKKQEYLENRIQ
i		ľ	REIALAKKHGTONKRAALQALKRKKRFEKOLTOIDGTLSTIEFO
1		}	REALENSHINTEVLRNMGFAAKAMKSVHENMDLNKIDDLMOEIT
1		Ì	EQQDIAQEISEAFSQRVGFGDDFDEDELMAELEELEQEELNKKM
1		l .	TNIRLPNVPSSSLPAQPNRKPGMSSTARRSRAASSQRAEEEDDD
]	IKQLAAWAT
	 		1 <u></u>
5503	216	654	KGVRRRGRVRSDSEDSHLGYFKMSFLLPKLTSKKEVDQAIKSTA
			EKVLVLRFGRDEDPVCLQLDDILSKTSSDLSKMAAIYLVDVDQT
1		1	AVYTQYFDISYIPSTVFFFNGQHMKVDYGGEDPALRSIKAVRRT
			SPAGTLGEKPVNS
5504	58	3563	QLSFSFQAPVTFDDITVYLLQEEWVLLSQQQKELCGSNKLVAPL
}		1	GPTVANPELFRKFGRGPEPWLGSVQGQRSLLEHHPGKKQMGYMG
			EMEVQGPTRESGQSLPPQKKAYLSHLSTGSGHIEGDWAGRNRKL
1		1	LKPRSIQKSWFVQFPWLIMNEEQTALFCSACREYPSIRDKRSRL
1			IEGYTGPFKVETLKYHAKSKAHMFCVNALAARDPIWAARFRSIR
			DPPGDVLASPEPLFTADCPIFYPPGPLGGFDSMAELLPSSRAEL
1	ļ	ļ	EDPGGDGAIPAMYLDCISDLRQKEITDGIHSSSDINILYNDAVE
			SCIQDPSAEGLSEEVPVVFEELPVVFEDVAVYFTREEWGMLDKR
1			QKELYRDVMRMNYELLASLGPAAAKPDLISKLERRAAPWIKDPN
			GPKWGKGRPPGNKKMVAVREADTQASAADSALLPGSPVEARASC
i			CSSSICEEGDGPRRIKRTYRPRSIQRSWFGQFPWLVIDPKETKL
		1	FCSACIERPNLHDKSSRLVRGYTGPFKVETLKYHEVSKAHRLCV
		1	NTVEIKEDTPHTALVPEISSDLMANMEHFFNAAYSIAYHSRPLN
		1	DFEKILQLLQSTGTVILGKYRNRTACTQFIKYISETLKREILED
		1	VRNSPCVSVLLDSSTDASEQACVGIYIRYFKQMEVKESYITLAP
1]	1	LYSETADGYFETIVSALDELDIPFRKPGWVVGLGTDGSAMLSCR
			GGLVEKFQEVIPQLLPVHCVAHRLHLAVVDACGSIDLVKKCDRH
		ľ	IRTVFKFYQSSNKRLNELQEGAAPLEQEIIRLKDLNAVRWVASR
			RRTLHALLVSWPALARHLQRVAEAGGQIGHRAKGMLKLMRGFHF
	ļ		VKFCHFLLDFLSIYRPLSEVCQKEIVLITEVNATLGRAYVALES
1			LRHQAGPKEEEFNASFKDGRLHGICLDKLEVAEQRFQADRERTV
1.			LTGIEYLQQRFDADRPPQLKNMEVFDTMAWPSGIELASFGNDDI
1			LNLARYFECSLPTGYSEEALLBEWLGLKTIAQHLPFSMLCKNAL
1		}	AQHCRFPLLSKLMAVVVCVPISTSCCERGFKAMNRIRTDERTKL
			SNEVLNMLMMTAVNGVAVTEYDPQPAIQHWYLTSSGRRFSHVYT
		1	CAQVPARSPASARLRKEEMGALYVEEPRTQKPPILPSREAAEVL
		1	KDCIMEPPERLLYPHTSQEAPGMS
5505	3312	1219	NCSPRSLSAAKMSNRNNNKLPSNLPQLQNLIKRDPPAYIEEFLQ
2203	1 3312	1219	QYNHYKSNVEIFKLQPNKPSKELAELVMPMAQISHCYPEYLSNF
		1	
		1	PQEVKDLLSCNHTVLDPDLRMTFCKALILLRNKNLINPSSLLEL
L		<u> </u>	FFELFRCHDKLLRKTLYTHIVTDIKNINAKHKNNKVNVVLQNFM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
)	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į.	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
(residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
		Bequeince	\=possible nucleotide insertion)
L	sequence	Ļ <u> </u>	•
	i .	1	YTMLRDSNATAAKMSLDVMIELYRRNIWNDAKTVNVITTACFSK
			VTKILVAALTFFLGKDEDEKQDSDSESEDDGPTARDLLVQYATG
1	l .	i	KKSSKNKKKLEKAMKVLKKHRKKKKPEVFNFSAIHLIHDPQDFA
1	!		EKLLKQLECCKERFEVKMMLMNLISRLVGIHELFLFNFYPFLQR
			FLQPHQREVTKILLFAAQASHHLVPPEIIQSLLMTVANNFVTDK
ļ			NSGEVMTVGINAIKEITARCPLAMTEELLQDLAQYKTHKDKNVM
1			MSARTLIHLFRTLNPQMLQKKFRGKPTEASIEARVQEYGELDAK
			DYIPGAEVLEVEKERNAENDEDGWESTSLSEBEDADGEWIDVOH
1	1	1	SSDEEQQEISKKLNSMPMEERKAKAAAISTSRVLTQEDFQKIRM
ĺ	1		_ ==
ì		1	AQMRKELDAAPGKSQKRKYIEIDSDEEPRGELLSLRDIERLHKK
1			PKSDKETRLATAMAGKTDRKEFVRKKTKTNPFSSSTNKEKKKQK
1 .	.[NFMMMRYSQNVRSKNKRSFREKQLALRDALLKKKKRMK
5506	1	1531	FRGDLCGQRGGSAPGEGGSSAWPAPAHPLPEREREALCPGRS
1			CSGGGGEETPGTTPVWSPLEGGGDEELRPNPYVRFPYRWWAVVV
ŀ		1	LAAFPSLGAGGETPEAPPESWTQLWFFRPVVNAAGYASFMVPGY
1			LLVQYFRRKNYLETGRGLCFPLVKACVFGNEPKASDEVPLAPRT
1		1	EAAETTPMWQALKLLFCATGLQVSYLTWGVLQERVMTRSYGATA
Ì]	1	TSPGERFTDSQFLVLMNRVLALIVAGLSCVLCKQPRHGAPMYRY
i		1	SFASLSNVLSSWCOYEALKFVSFPTQVLAKASKVIPVMLMGKLV
İ	}	1	SRRSYEHWEYLTATLISIGVSMFLLSSGPEPRSSPATTLSGLIL
		1	
1	}	i	LAGYIAFDSFTSNWQDALFAYKMSSVQMMFGVNFFSCLFTVGSL
	1	1	LEQGALLEGTRFMGRHSEFAAHALLLSICSACGQLFIFYTIGQF
	-	[GAAVFTIIMTLRQAFAILLSCLLYGHTVTVVGGLGVAVVFAALL
1	1		LRVYARGRLKQRGKKAVPVESPVQKV
5507	3704	1271	PRGTRRCRPAGRASRRARRRPPCPGPAAPGSLEIGGFGTAAGKK
i	.	1	VAVADVQFGPMRFHQDQLQVLLVFTKEDNQCNGFCRACEKAGFK
		ì	CTVTKEAQAVLACFLDKHHDIIIIDHRNPRQLDAEALCRSIRSS
ŀ	ì	1	KLSENTVIVGVVRRVDREELSVMPFISAGFTRRYVENPNIMACY
1		j	NELLQLEFGEVRSQLKLRACNSVFTALENSEDAIEITSEDRFIQ
1		ļ	YANPAFETTMGYQSGELIGKELGEVPINEKKADLLDTINSCIRI
1	1		GKEWQGIYYAKKKNGDNIQQNVKIIPVIGQGGKIRHYVSIIRVC
			NGNNKAEKISECVOSDTHTDNOTGKHKDRRKGSLDVKAVASRAT
}	}	1	EVSSORRHSSMARIHSMTIEAPITKVINIINAAQESSPMPVTEA
	İ		· · · · · · · · · · · · · · · · · · ·
1			LDRVLEILRTTELYSPOFGAKDDDPHANDLVGGLMSDGLRRLSG
1			NEYVLSTKNTQMVSSNIITPISLDDVPPRIARAMENEEYWDFDI
1			FELEAATHNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIE
1		1	ANYHSSNPYHNSTHSADVLHATAYFLSKERIKETLDPIDEVAAL
1			IAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHHAALAF
			QLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVN
			KFVNSINKPLATLEENGETDKNQEVINTMLRTPENRTLIKRMLI
į			KCADVSNPCRPLQYCIEWAARISEEYFSQTDEEKQQGLPVVMPV
1			FDRNTCSIPKSQISFIDYFITDMFDAWDAFVDLPDLMQHLDNNF
.1			KYWKGLDEMKLRNLRPPPE
5508	1151	691	LSSVFSRRSASMFAVGCSMGPFLHYWYLSLDRLFPASGLRGFPN
2208	1121	031	VLKKVLVDQLVASPLLGVWYFLGLGCLEGQTVGESCQELREKFW
1	1		1
			EFYKADWCVWPAAQFVNFLFVPPQFRVTYINGLTLGWDTYLSYL
	<u> </u>		KYRSPVPLTPPGCVALDTRAD
5509	1238	619	RKSRGCQNALSASGPAAAAAAIMVRKLKFHEQKLLKQVDFLNWE
1			VTDHNLHELRVLRRYRLQRREDYTRYNQLSRAVRELARRLRDLP
Į	1		ERDQFRVRASAALLDKLYALGLVPTRGSLELCDFVTASSFCRRR
1		1	LPTVLLKLRMAQHLQAAVAFVEQGHVRVGPDVVTDPAFLVTRSM
1	1		EDFVTWVDSSKIKRHVLEYNEERDDFDLEA
5510	96	1195	PAGAHLSSGSSEPLVEPGRGRVGARVKGERGLQASGSAPGRSKM
1 3323		1	AEGEROPPPDSSREAPPATONFIIPKKEIHTVPDMGKWKRSQAY
1			ADYIGFILTLNEGVKGKKLTFEYRVSEAIEKLVALLNTLDRWID
	1		i e
1	1	I	ETPPVDQPSRFGNKAYRTWYAKLDERAENLVATVVPTHLAAAVP
			EVAVYLKESVGNSTRIDYGTGHEAAFAAFLCCLCKIGVLRVDDQ
1			IAIVFKVFNRYLEVMRKLQKTYRMEPAGSQGVWGLDDFQFLPFI
	1		WGSSQLIDHPYLEPRHFVDEKAVNENHKDYMFLECILFITEMKT
l			GPFAEHSNQLWNISAVPSWSKVNQGLIRMYKAECLEKFPVIQHF
j	}	1	KFGSLLPIHPVTSG
		_ 1	

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	35455	\=possible nucleotide insertion)
5511	276	1980	KLSRVLNLPPENLITSISAVPISQKEEVADFQLSVDSLLEKDND
		1	HSRPDIQVQAKRLAEKLRCDTVVSEISTGQRTVNFKINRELLTK
1			TVLQQVIEDGSKYGLKSELFSGLPQKKIVVEFSSPNVAKKPHVG
1		ĺ	HLRSTIIGNFIANLKEALGHQVIRINYLGDWGMQFGLLGTGFQL
1			FGYEEKLQSNPLQHLFEVYVQVNKEAADDKSVAKAAQEFFQRLE
1			LGDVQALSLWQKFRDLSIEEYIRVYKRLGVYFDEYSGESFYREK
1			SQEVLKLLESKGLLLKTIKGTAVVDLSGNGDPSSICTVMRSDGT
		·	SLYATRDLAAAIDRMDKYNFDTMIYVTDKGQKKHFQQVFQMLKI
1			MGYDWAERCQHVPFGVVQGMKTRRGDVTFLEDVLNEIQLRMLQN
1			MASIKTTKELKNPQETAERVGLAALIIQDFKGLLLSDYKFSWDR
ĺ			VFQSRGDTGVFLQYTHARLHSLEETFGCGYLNDFNTACLQEPQS
			VSILQHLLRFDEVLYKSSQDFQPRHIVSYLLTLSHLAAVAHKTL
	<u></u>		QIKDSPPEVAGARLHLFKAVRSVLANGMKLLGITPVCRM
5512	120	1015	DPSLLLTITVTGVTVLVLVLKSMNSRRREPITLQDPEAKYPLPL
			IEKEKISHNTRRFRFGLPSPDHVLGLPVGNYVQLLAKIDNELVV
ì	İ		RAYTPVSSDDDRGFVDLIIKIYFKNVHPQYPEGGKMTQYLENMK
1			IGETIFFRGPRGRLFYHGPGNLGIRPDQTSEPKKTLADHLGMIA
			GGTGITPMLQLIRHITKDPSDRTRMSLIFANQTEEDILVRKELE
1			EIARTHPDQFDLWYTLDRPPIGWKYSSGFVTADMIKEHLPPPAK
	<u></u>		STLILVCGPPPLIQTAAHPNLEKLGYTQDMIFTY
5513	2	837	ARWRLPSDSPRIPPAGAETPGRGSCRNYLPSSSPPPPEPSSFPS
			PPTSRGGPGSRDTMSDSEEESQDRQLKIVVLGDGASGKTSLTTC
			FAQETFGKQYKQTIGLDFFLRRITLPGNLNVTLQIWDIGGQTIG
}			GKMLDKYIYGAQGVLLVYDITNYQSFENLEDWYTVVKKVSEESE
1	ļ		TQPLVALVGNKIDLEHMRTIKPEKHLRFCQENGFSSHFVSAKTG
ĺ	1		DSVFLCFQKVAAEILGIKLNKAEIEQSQRVVKADIVNYNQEPMS
5514	1295		RTVNPPRSSMCAVQ
2214	1295	449	VNRPSWIMGNFRGHALPGTFFFIIGLWWCTKSILKYICKKQKRT
}	}		CYLGSKTLFYRLEILBGITIVGMALTGMAGEQFIPGGPHLMLYD
	}		YKQGHWNQLLGWHHFTMYFFFGLLGVADILCFTISSLPVSLTKL
ł	ľ		MLSNALFVEAFIFYNHTHGREMLDIFVHQLLVLVVFLTGLVAFL
İ			EFLVRNNVLLELLRSSLILLQGSWFFQIGFVLYPPSGGPAWDLM
	'	'	DHENILFLTICFCWHYAVTIVIVGMNYAFITWLVKSRLKRLCSS EVGLLKNAEREOESEEBM
5515	1572	260	FVRLVGRGDCDPLLSVCLTTMPLYEGLGSGGEKTAVVIDLGEAF
]	200	TKCGFAGETGPRCIIPSVIKRAGMPKPVRVVQYNINTEELYSYL
			KEFIHILYFRHLLVNPRDRRVVIIESVLCPSHFRETLTRVLFKY
	j		FEVPSVLLAPSHLMALLTLGINSAMVLDCGYRESLVLPIYEGIP
	ļ		VLNCWGALPLGGKALHKBLETQLLEQCTVDTSVAKEQSLPSVMG
	1		SVPEGVLEDIKARTCFVSDLKRGLKIQAAKFNIDGNNERPSPPP
			NVDYPLDGEKILHILGSIRDSVVEILFEQDNEEQSVATLILDSL
			IQCPIDTRKQLAENLVVIGGTSMLPGFLHRLLAEIRYLVEKPKY
]		KKALGTKTFRIHTPPAKANCVAWLGGAIFGALQDILGSRSVSKE
	<u>L</u>		YYNQTGRIPDWCSLNNPPLEMMFDVGKTQPPLMKRAFSTEK
5516	3	735	NSREPPQAGPGPSPRKSPTASSFLFPWRPLASSFWMGAQGAQES
	}		IKAMWRVPGTTRRPVTGESPGMHRPEAMLLLLTLALLGGPTWAG
1			KMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSVQVKLGDSW
			DVKLGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMYTSKDR
			YFYFGKLDGQISSAYPSQEGQVLVGIYGQYQLLGIKSIGFEWNY
			PLEEPTTEPPVNLTYSANSPVGR
5517	246	499	SEIYVAMRTDSSKMTDVESGVANFASSARAGRRNALPDIQSSAA
F6-5			TDGTSDLPLKLEALSVKEDAKEKDEKTTQDQLEKPQNEEK
5518	3	1375	DAWADAWVRAWDLNMDFPCLWLGLLLPLVAALDFNYHRQEGMEA
] [FLKTVAQNYSSVTHLHSIGKSVKGRNLWVLVVGRFPKEHRIGIP
1			EFKYVANMHGDETVGRELLLHLIDYLVTSDGKDPEITNLINSTR
			IHIMPSMNPDGFEAVKKPDCYYSIGRENYNQYDLNRNFPDAFEY
1			NNVSRQPETVAVMKWLKTETFVLSANLHGGALVASYPFDNGVQA
			TGALYSRSLTPDDDVFQYLAHTYASRNPNMKKGDECKNKMNFPN
ĺ		1	GVTNGYSWYPLQGGMQDYNYIWAQCFEITLELSCCKYPREEKLP
L	L		SFWNNNKASLIEYIKQVHLGVKGQVFDQNGNPLPNVIVEVQDRK

SEQ Predicted Predicted end Amino acid segment	
ID beginning nucleotide (A=Alanine, C=Cyste	containing signal peptide
NO: nucleotide location Glutamic Acid, F=Ph	eine, D=Aspartic Acid, E= henylalanine, G=Glycine,
location corresponding H=Histidine, I=Isol	
	onine, N=Asparagine,
to first amino acid P=Proline, Q=Glutam	
amino acid residue of S=Serine, T=Threoni	ine, V=Valine,
	rosine, X=Unknown, *=Stop
1 1 - T	nucleotide deletion,
sequence \=possible nucleoti	
1 I	PGSYIINVTVPGHDPHITKVIIPEKS
1 1 -	DSIPVSNPSCPMIPLYRNLPDHSAAT
KPSLFLFLVSLLHIFFK	
	TEAKGPTMGKESGWDSGRAAVAAVVG
	SVGIAASSIAAKMMSTAAIANGGGVA
	ISKVIGGFAGTALGAWLGSPPSS
3 I	LAMTKTSTCIYHFLVLSWYTFLNYYI
1 1	NKYMTLLNLLLQTIFYGVTCLDDVLK
RTKGGKDIKFLTAFRDLLE	FTTLAFPVSTFVFLAFWILFLYNRDL
IYPKVLDTVIPVWLNHAMH	HTF1FP1TLAEVVLRPHSYPSKKTGL
TLLAAASIAYISRILWLYF	FETGTWVYPVFAKLSLLGLAAFFSLS
YVFIASIYLLGEKLNHWKW	WSVQILQRWRLESVGICFQWPDWKS
PAKHQLVKNIR	
	NPKAEEDRPLEDVPQEAEGNPQPSEE
	QGFKEDTPVRHLDPEEMIRGVDELER
LREEIRRVRNKFVMMHWKQ	
	SLIWKVDFPYQDKLVGYITNYSRRF
	CLVEDPAGCVWGVAYRLPVGKEEEVK
1 1	(PKDPTTKPFSVLLYIGTCDNPDYLG
PAPLEDIAEQIFNAAGPSG	RNTEYLFELANSIRNLVPEEADEHL
FALEKLVKERLEGKQNLNC	
	PVFDDKEDVNFDHFQILRAIGKGSFG
KVCIVQKRDTEKMYAMKYM	MKQQCIERDEVRNVFRELEILQEIE
HVFLVNLWYSFQDEEDMFM	MVVDLLLGGDLRYHLQQNVQFSEDTV
	IHRDVKPDNILLDERGHAHLTDFNI
	MAPEIFHSFVNGGTGYSFEVDWWSV
	SNAVESLVQLFSTVSVQYVPTWSKEM
	QDVQAAPALAGVLWDHLSEKRVEPG
1 1	IILESRPLHKKKKRLAKNKSRDNSRD
	FVIFNREKLKRSQDLPREPLPAPES
RDAAEPVEDEAERSALPMO	
	GGCFPSPTMELRCGGLLFSSRFDSG
, ,	GGASALTSGIASSPDYEFNVWTRPD
i I I	GGMPGKLIKINIMNMNKQSKLYSQG
	RPTFEMTETQFVLSFVHRFVEGRGA
1 1 1	NQLDQRFPENHPTHSSPLDTIYYHR
; ; ;	CHGLREDREPRLEQLFPDTSTPRPF
	PSSFVFNGFLDFILRPDDPRAQTLR
	HYRTDSRGVNLNRQYLKPDAVLHPA
	QSSSEHQPSSCLPPDAPVSDLEKAN
	WKQTEPAEQKLNSVWIMPQQSAGLE
, , ,	LHGHASKRGCFMYGNSFSDESTQVE
	CNFSEKNMYARDRRDGQSKEGSGRV
	TGRSVNSIPAACHDNGRASPPPPPA
	AALDMAECNPWPRIVLSEHSSLTNL
1	VGVNKKRGLRTPPKSHNGLPVSCSE
	SSQQNSPQMKNSPSFPFHGSRPAGL
	GKPVWEPLQHVFGCLGHCWGK
	QTQLVINKLPEKVAKHVTLVRESGS
	VASGQEKHLLFEVQPGSDSSAFWKV
1 1	RIMNLYQFIQLYKDITSQAAGVLAQ
	SLWMGRVKQLTDEERCCICMDGRAD
, ,	RHRNCPICRLQMTGANESWVVSDAP
TEDDMANYILMMADEAGQP	
	PRGLEVIMLRVAWRTLSLIRTRAVI
1 1 -	WGLQPRSLLLQAARGYVVRKPAQSR
[LDDDPPPSTLLKDYONVPG	IEKVDDVVKRLLSLEMANKKEMLKI
1 1	
KQEQFMKKIVANPEDTRSL	EARIIALSVKIRSYEEHLEKHRKDK
KQEQFMKKIVANPEDTRSL AHKRYLLMSIDQRKKMLKNI	EARIIALSVKIRSYEBHLEKHRKDK LRNTNYDVFEKICWGLGIEYTFPPL FQETQKLKKRRRALKAAAAAQKQAK

SEO	Predicted	Predicted end	Amino agid aggment cont
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
j	corresponding	corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	i	L=Leucine, M=Methionine, N=Asparagine,
ì	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	residue of		S=Serine, T=Threonine, V=Valine,
1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
——	sequence		\=possible nucleotide insertion)
			RRNPDSPAKAIPKTLKDSQ
5527	3225	565	LLRKYLLHQNPLLLRHQPNRTCISFSATMKLKDTKSRPKQSSCG
ļ			KFQTKGIKVVGKWKEVKIDPNMFADGQMDDLVCFEELTDYQLVS
ł			PAKNPSSLFSKEAPKRKAQAVSEEEEEEEGKSSSPKKKIKLKKS
ĺ			KNVATEGTSTQKEFEVKDPELRAQGDDMVCDDPEAGEMTSENLV
1	į.		QTAPKKKKNKGKKGLEPSQSTAAKVPKKAKTWIPEVHDQKADVS
1			AWKDLFVPRPVLRALSFLGFSAPTPIQALTLAPAIRDKLDILGA
(i	J	AETGSGKTLAFAIPMIHAVLQWQKRNAAPPPSNTEAPPGETRTE
1			AGAETRSPGKAEAESDALPDDTVIESEALPSDIAAEARAKTGGT
			VSDQALLFGDDDAGEGPSSLIREKPVPKQNENEEENLDKEQTGN
			LKQELDDKSATCKAYPKRPLLGLVLTPTRELAVQVKQHIDAVAR
l	1		FTGIKTAILVGGMSTQKQQRMLNRRPEIVVATPGRLWELIKEKH
1			YHLRNLRQLRCLVVDEADRMVEKGHFAELSQLLEMLNDSQYNPK
1	[ROTLVFSATLTLVHQAPARILHKKHTKKMDKTAKLDLLMQKIGM
1			RGKPKVIDLTRNEATVETLTETKIHCETDEKDFYLYYFLMOYPG
1			RSLVFANSISCIKRLSGLLKVLDIMPLTLHACMHQKQRLRNLEO
1			FARLEDCVLLATDVAARGLDIPKVQHVIHYQVPRTSEIYVHRSG
ı			RTARATNEGLSLMLIGPEDVINFKKIYKTLKKDEDIPLFPVOTK
1			YMDVVKERIRLARQIEKSEYRNFQACLHNSWIEQAAAALEIELE
			EDMYKGGKADQQEERRRQKQMKVLKKELRHLLSQPLFTESOKTK
ł			YPTQSGKPPLLVSAPSKSESALSCLSKQKKKKTKKPKEPQPEQP
			QPSTSAN
5528	3	895	GPFLSACRMWGACKVKVHDSLATISITLRRYLRLGATMAKSKFE
i .			YVRDFEADDTCLAHCWVVVRLDGRNFHRFAEKHNFAKPNDSRAL
			QLMTKCAQTVMEELEDIVIAYGQSDEYSFVFKRKTNWFKRRASK
j			FMTHVASQFASSYVFYWRDYFEDQPLLYPPGFDGRVVVYPSNQT
		•	LKDYLSWRQADCHINNLYNTVFWALIQQSGLTPVQAQGRLQGTL
)			AADKNEILFSEFNINYNNEPPMYRKGTVLIWQKVDEVMTKEIKL
			PTEMEGKKMAVTRTRTKPCKPSHLPRAPCLRWL
5529	48	640	TFRLVSAHLKTRKLINPEAAERRWRDWDSRQGWLSVKMQRVSGL
1			LSWTLSRVLWLSGLSEPGAARQPRIMEEKALEVYDLIRTIRDPE
]			KPNTLEELEVVSESCVEVQEINEEEYLVIIRFTPTVPHCSLATL
ł			IGLCLRVKLQRCLPFKHKLEIYISEGTHSTEEDINKQINDKERV
			AAAMENPNLREIVEQCVLEPD
5530	4541	2606	AQIVHAISYCHKLHVGHRDLKPENVVFFEKQGLVKLTDFGFSNK
			FQPGKKLTTSCGSLAYSAPEILLGDEYDAPAVDIWSLGVILFML
1 1			VCGQPPFQEANDSETLTMIMDCKYTVPSHVSKECKDLITRMLQR
			DPKRRASLEEIENHPWLQGVDPSPATKYNIPLVSYKNLSEEEHN
			SIIQRMVLGDIADRDAIVEALETNRYNHITATYFLLAERILREK
1 1			QEKEIQTRSASPSNIKAQFRQSWPTKIDVPQDLEDDLTATPLSH
,			ATVPQSPARAADSVLNGHRSKGLCDSAKKDDLPELAGPALSTVP
			PASLKPTASGRKCLFRVEEDEEEDEEDKKPMSLSTQVVLRRKPS
			VTNRLTSRKSAPVLNQIFEEGESDDEFDMDENLPPKLSRLKMNI
]]	j		ASPGTVHKRYHRRKSQGRGSSCSSSETSDDDSESRRRLDKDSGF
			TYSWHRRDSSEGPPGSEGDGGGQSKPSNASGGVDKASPSENNAG
[]		ļ	GGSPSSGSGGNPTNTSGTTRRCAGPSNSMQLASRSAGELVESLK
	ļ	}	LMSLCLGSQLHGSTKYIIDPQNGLSFSSVKVQEKSTWKMCISST
1	ļ		GNAGQVPAVGGIKFFSDHMADTTTELERIKSKNLKNNVLQLPLC
Ll			EKTISVNIQRNPKEGLLCASSPASCCHVI
5531	24	515	GSQPRAPRPRDSMERPEPELIRQSWRAVSRSPLEHGTVLFARLF
	1		ALEPDLLPLFQYNCRQFSSPEDCLSSPEFLDHIRKVMLVIDAAV
	1		TNVEDLSSLEEYLASLGRKHRAVGVKLSSFSTVGESLLYMLEKC
			LGPAFTPATRAAWSQLYGAVVQAMSRGWDGE
5532	3395	1402	SDWMVVGKRKMIIEDETEFCGEELLHSVLQCKSVFDVLDGEEMR
	i		RARTRANPYEMIRGVFFLNRAAMKMANMDFVFDRMFTNPRDSYG
	1	ļ	KPLVKDREAELLYFADVCAGPGGFSEYVLWRKKWHAKGFGMTLK
		ľ	GPNDFKLEDFYSASSELFEPYYGEGGIDGDGDITRPENISAFRN
	1	ľ	FVLDNTDRKGVHFLMADGGFSVEGQENLQEILSKQLLLCOFLMA
	1	ł	LSIVRTGGHFICKTFDLFTPFSVGLVYLLYCCFRRVCLFKPITS
			RPANSERYVVCKGLKVGIDDVRDYLFAVNIKLNQLRNTDSDVNL

	15	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	1 -	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	amino acid		
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	(\=possible nucleotide insertion)
		 	VVPLEVIKGDHEFTDYMIRSNESHCSLQIKALAKIHAFVQDTTL
	1	1	SEPROAEIRKECLRLWGIPDOARVAPSSSDPKSKFFELIOGTEI
			DIFSYKPTLLTSKTLEKIRPVFDYRCMVSGSEQKFLIGLGKSQI
			YTWDGRQSDRWIKLDLKTELPRDTLLSVEIVHELKGEGKAQRKI
			SAIHILDVLVLNGTDVREQHFNQRIQLAEKFVKAVSKPSRPDMN
		l	PIRVKEVYRLEEMEKIFVRLEMKIIKGSSGTPKLSYTGRDDRHF
	ĺ		VPMGLYIVRTVNEPWTMGFSKSFKKKFFYNKKTKDSTFDLPADS
		1	1
			IAPFHICYYGRLFWEWGDGIRVHDSQKPQDQDKLSKEDVLSFIQ
		İ	MHRA
5533	94	789	MKERRAPQPVVARCKLVLVGDVQCGKTAMLQVLAKDCYPETYVP
2233	''		TVFENYTACLETEEORVELSLWDTSGSPYYDNVRPLCYSDSDAV
			LLCFDISRPETVDSALKKWRTEILDYCPSTRVLLIGCKTDLRTD
			LSTLMELSHQKQAPISYEQGCAIAKQLGPEIYLEGSAFTSEKSI
		Į.	HSIFRTASMLCLNKPSPLPQKSPVRSLSKRLLHLPSRSELISPT
			FKKEKAKXCSIM
5534	3 -	605	LVRGRARAANPGRVGAMDGLRQRVEHFLEQRNLVTEVLGALEAK
JJJ4		1	TGVEKRYLAAGAVTLLSLYLLFGYGASLLCNLIGFVYPAYASIK
		ļ	AIESPSKDDDTVWLTYWVVYALFGLAEFFSDLLLSWFPFYYVGK
		1	
	1	1	CAFLLFCMAPRPWNGALMLYQRVVRPLFLRHHGAVDRIMNDLSG
	1	1	RALDAAAGITRNVKPSQTPQPKDK
5535	1029	332	KSFMDSEARLCSLVELSDTQDBTQKSDSENEDLKIDCLQESQEL
3333	1 2023		NLOKLKNSERILTEAKOKMRELTVNIKMKEDLIKELIKTGNDAK
	}	1	
	1	1	SVSKQYTLKVTKLEHDABQAKVELTETQKQLQELENKDLSDVAM
	}	1	KVKLQKEFRKKVDAAKLRVQVLQKKQQDSKKLASLSIQNEKRAN
		1	ELEQSVDHMKYQKIQLQRKLQEENEKRKQLDAVIKRDQQKIKVI
1		1	LSYIPAKYNMKC
5536	942	282	AAATAASLSPRGCRLRTPSSDVSPSRAPPPSAAPLPTGRAQMSP
2236	342	1	SGRLCLLTIVGLILPTRGQTLKDTTSSSSADATIMDIQVPTRAP
		1	·-
	1	}	DAVYTELQPTSPTPTWPADETPQPQTQTQQLEGTDGPLVTDPET
}	1		HKSTKAAHPTDDTTTLSERPSPSTDVQTDPQTLKPSGFHEDDPF
l		1	FYDEHTLRKRGLLVAAVLFITGIIILTSGKCRQLSRLCRNHCR
5537	3	2391	RARVSSPOLRVFRSGRPRRLRVLRINRTSVALRLAGTGRFVAKT
, ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,		1	PGHPGSWEMGLLTFRDVAVEFSLEEWEHLEPAQKNLYQDVMLEN
ì		1	YRNLVSLGLVVSKPDLITFLEQRKEPWNVKSEBTVAIQPDVFSH
1			
l			YNKDLLTEHCTEASFQKVISRRHGSCDLENLHLRKRWKREECEG
		1	HNGCYDEKTFKYDQFDESSVESLFHQQILSSCAKSYNFDQYRKV
1	1		FTHSSLLNQQEEIDIWGKHHIYDKTSVLFRQVSTLNSYRNVFIG
1			EKNYHCHNSEKTLNQSSSPKNHQENYFLEKQYKCKEFEEVFLQS
I			MHGOEKQEQSYKCNKCVEVCTQSLKHIQHQTIHIRENSYSYNKY
1			
1			DKDLSQSSNLRKQIIHNEEKPYKCEKCGDSLNHSLHLTQHQIIP
1			TEEKPYKWKECGKVFNLNCSLYLTKQQQIDTGENLYKCKACSKS
1			FTRSSNLIVHQRIHTGEKPYKCKECGKAFRCSSYLTKHKRIHTG
1			EKPYKCKECGKAFNRSSCLTQHQTTHTGEKLYKCKVCSKSYARS
	,		SNLIMHORVHTGEKPYKCKECGKVFSRSSCLTQHRKIHTGENLY
			KCKVCAKPFTCFSNLIVHERIHTGEKPYKCKECGKAFPYSSHLI
1		1	RHHRIHTGEKPYKCKACSKSFSDSSGLTVHRRTHTGEKPYTCKE
			CGKAFSYSSDVIQHRRIHTGQRPYKCEECGKAFNYRSYLTTHQR
	1		SHTGERPYKCEECGKAFNSRSYLTTHRRRHTGERPYKCDECGKA
1			FSYRSYLTTHRRSHSGERPYKCEECGKAFNSRSYLIAHQRSHTR
ł	ĺ		
L			EKL
5538	926	161	HSMMMKIPWGSIPVLMLLLLLGLIDISQAQLSCTGPPAIPGIPG
1			IPGTPGPDGQPGTPGIKGEKGLPGLAGDHGEFGEKGDPGIPGNP
1	1		GKVGPKGPMGPKGGPGAPGAPGPKGESGDYKATQKIAFSATRTI
ì			NVPLRRDQTIRFDHVITNMNNNYEPRSGKFTCKVPGLYYFTYHA
1	ł .		
1	1		SSRGNLCVNLMRGRERAQKVVTFCDYAYNTFQVTTGGMVLKLEQ
1		1	GENVFLQATDKNSLLGMEGANSIFSGFLLFPDMEA
5539	38	1258	HRGPSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPG
3333	1	1	IVDGPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREK
	l .	1	DEIYGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCS
	i	1	
l _		.1	SDSFNEDIAAFAKQVRSERPLFSSNPELDNLVIQAIQVLRFHLL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	Talencine, Machine, Kabysine,
1	to first	1	L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			ELEKVHDLCDNFCHRYITCLKGKMPIDLVIBDRDGGCREDFEDY
}			PASCPSLPDQNNMWIRDHEDSGSVHLGTPGPSSGGLASQSGDNS
		}	SDQGDGLDTSVASPSSGGEDEDLDQERRRNKKRGIFPKVATNIM
			RAWLFQHLSHPYPSEEQKKQLAQDTGLTILQVNNWFINARRRIV
1	1		QPMIDQSNRTGQGAAFSPEGQPIGGYTETQPHVAVRPPGSVGMS
			LNLEGEWHYL
5540	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
]	1 1110	PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
1			CDANI ACEDEMINALIDEDVODUDEDDO DI DEGLE CONTRE
			GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKRKKDEI
ł	}	ľ	YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
			FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
1	1	<i>[</i>	KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
			SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
			EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
1	}		LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
		L	QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5541	148	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
	Ì		PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
	1		GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
•	1		YGHPLPPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
L	ļ		FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
Ī			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
ļ			SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
ĺ	1		EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
1			LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
-		•	QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5542	148	1440	
3242	140	1440	PPLGAGAGVHARSPHPARRLPLTTAGVGGRAPDLLPTPWRQHRG
}	ļ	•	PSGAAAPGCALPRGQALEGPRSCRRPQPMARRYDELPHYPGIVD
[GPAALASFPETVPAVPGPYGPHRPPQPLPPGLDSDGLKREKDEI
1	l		YGHPLFPLLALVFEKCELATCSPRDGAGAGLGTPPGGDVCSSDS
			FNEDNTAFAKQVRSERPLFSSNPELDNLMIQAIQVLRFHLLELE
Į.			KGKMPIDLVIEDRDGGCREDFEDYPASCPSLPDQNNIWIRDHED
			SGSVHLGTPGPSSGGLASQSGDNSSDQGVGLDTSVASPSSGGED
1			EDLDQEPRRNKKRGIFPKVATNIMRAWLFQHLSHPYPSEEQKKQ
Į			LAQDTGLTILQVNNWFINARRRIVQPMIDQSNRTGQGAAFSPEG
L	<u> </u>	L	QPIGGYTETEPHVAFRAPASVGDEFGTRKEEWHYL
5543	2405	665	RWVREQPWPLRTSEAVKTPALRPFPGPRGVSPFPKPDWGKSPAP
1			KRPFSDSGAFWSPERRPGVLEAPRRRPVPASFRAVPPKPTRVHG
			SSASRDRVLARTMIVADSECRABLKDYLRFAPGGVGDSGPGEEQ
1		1	RESRARRGPRGPSAFIPVEEVLREGAESLEQHLGLEALMSSGRV
			DNLAVVMGLHPDYFTSFWRLHYLLLHTDGPLASSWRHYIAIMAA
1			ARHOCSYLVGSHMAEFLOTGGDPEWLLGLHRAPEKLRKLSETNK
!			LLAHRPWLITKEHIQALLKTGEHTWSLAELIQALVLLTHCHSLS
			SFVFGCGILPEGDADGSPAPQAPTPPSEQSSPPSRDPLNNSGGF
1			ESARDVEALMERMQQLQESLLRDEGTSQEEMESRFELEKSESLL
1			
]		VTPSADILEPSPHPDMLCFVEDPTFGYEDFTRGAQAPPTFRAQ
1			DYTWEDHGYSLIQRLYPEGGQLLDEKFQAAYSLTYNTIAMHSGV
			DTSVLRRAIWNYIHCVFGIRYDDYDYGEVNQLLERNLKVYIKTV
1			ACYPEKTTRRMYNLFWRHFRHSEKVHVNLLLLEARMQAALLYAL
5544	1000		RAITRYMT
2544	1895	514	LGGLLGRQRLLLRMGAGRLGAPMERHGRASATSVSSAGEQAAGD
			PEGRRQEPLRRRASSASVPAVGASAEGTRRDRLGSYSGPTSVSR
		ļ	QRVESLRKKRPLFPWFGLDIGGTLVKLVYFEPKDITAEEBEEEV
		ļ	ESLKSIRKYLTSNVAYGSTGIRDVHLELKDLTLCGRKGNLHFIR
		[FPTHDMPAFIQMGRDKNFSSLHTVFCATGGGAYKFEQDFLTIGD
}]	}	LQLCKLDELDCLIKGILYIDSVGFNGRSQCYYFENPADSEKCQK
		Ì	LPFDLKNPYPLLLVNIGSGVSILAVYSKDNYKRVTGTSLGGGTF
			FGLCCLLTGCTTFEEALEMASRGDSTKVDKLVRDIYGGDYERFG
	[LPGWAVASSFGNMMSKEKREAVSKEDLARATLITITNNIGSIAR
]	ļ	MCALNENINQVVFVGNFLRINTIAMRLLAYALDYWSKGQLKALF
(SEHEGYFGAVGALLELLKIP
	·		

SBQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	9	j .	H-Histidine, I-Isoleucine, K-Lysine,
	location	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ.	sequence	1	\=possible nucleotide insertion)
5545	802	131	GAMWSAGRGGAAWPVLLGLLLALLVPGGGAAKTGAELVTCGSVL
3313	1		KLLNTHHRVRLHSHDIKYGSGSGQQSVTGVEASDDANSYWRIRG
1	ł		GSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFPSPLSNNQEV
			SAFGEDGEGDDLDLWTVRCSGQHWEREAAVRFQHVGTSVFLSVT
}	1		
Į.		Į.	GEQYGSPIRGQHEVHGMPSANTHNTWKAMEGIFIKPSVEPSAGH
l	1	l	DEL
5546	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
Į.	Į	ł	RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
	ļ	ļ	LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
1	ł	Ì	SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
			NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
1	1	ł	KLLQEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
	}		AVAGRGNMRAQQSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
{		Į.	FVSKTEEELOAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
1		1	
	1	1	RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
ļ			EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
	1	L	CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRPGKRVA
5547	1592	146	FVPRGGHSSMGQSGRSRHQKRARAQAQLRNLEAYAANPHSFVFT
1	1	1	RGCTGRNIRQLSLDVRRVMEPLTASRLQVRKKNSLKDCVAVAGP
1			LGVTHFLILSKTETNVYFKLMRLPGGPTLTFQVKKYSLVRDVVS
{	1		SLRRHRMHEQQFAHPPLLVLNSFGPHGMHVKLMATMFQNLFPSI
			NVHKVNLNTIKRCLLIDYNPDSQELDFRHYSIKVVPVGASRGMK
1	1	1	KLLOEKFPNMSRLQDISELLATGAGLSESEAEPDGDHNITELPQ
Į.			AVAGRGNMRAQOSAVRLTEIGPRMTLQLIKVQEGVGEGKVMFHS
1	((FVSKTEEELQAILEAKEKKLRLKAQRQAQQAQNVQRKQEQREAH
}			_
ì			RKKSLEGMKKARVGGSDEEASGIPSRTASLELGEDDDEQEDDDI
i			EYFCQAVGEAPSEDLFPEAKQKRLAKSPGRKRKRWEMDRGRGRL
I		İ	CDQKFPKTKDKSQGAQARRGPRGASRDGGRGRGRGRPGKRVA
5548	1	2153	DOTGPPETIAFTFPRSTMEPLCPLLLVGFSLPLARALRGNETTA
1	ĺ		DSNETTTTSGPPDPGASQPLLAWLLLPLLLLLLLLLLAAYFFRF
	·	1	RKQRKAVVSTSDKKMPNGILEEQEQQRVMLLSRSPSGPKKYFPI
	1	1	PVEHLEEEIRIRSADDCKQFREEFNSLPSGHIQGTFELANKEEN
1	j		REKNRYPNILPNDHSRVILSQLDGIPCSDYINASYIDGYKEKNK
	1	1	FIAAOGPKOETVNDFWRMVWEQKSATIVMLTNLKERKEEKCHQY
	i		WPDQGCWTYGNIRVCVEDCVVLVDYTIRKFCIQPQLPDGCKAPR
	i	i	LVSOLHFTSWPDFGVPFTPIGMLKFLKKVKTLNPVHAGPIVVHC
ļ	ļ	}	SAGVGRTGTFIVIDAMMAMMHAEQKVDVFEFVSRIRNQRPQMVQ
]	TDMQYTFIYQALLEYYLYGDTELDVSSLEKHLQTMHGTTTHFDK
	1		IGLEEEFRKLTNVRIMKENMRTGNLPANMKKARVIQIIPYDFNR
1	ļ		VILSMKRGQEYTDYINASFIDGYRQKDYFIATQGPLAHTVEDFW
		1	RMIWEWKSHTIVMLTEVQEREQDKCYQYWPTEGSVTHGEITIEI
Ĭ	}	1	KNDTLSEAISIRDFLVTLNQPQARQEEQVRVVRQFHFHGWPEIG
1			IPAEGKGMIDLIAAVQKQQQQTGNHPITVHCSAGAGRTGTFIAL
1			SNILERVKAEGLLDVFQAVKSLRLQRPHMVQTLEQYEFCYKVVQ
	\		DFIDIFSDYANFK
5549	915	256	FEATGGKRLAFKMAGTARHDREMAIQAKKKLTTATDPIERLRLQ
1 3343	313	1	CLARGSAGIKGLGRVFRIMDDDNNRTLDFKEFMKGLNDYAVVME
	1	1	KEEVEELFORFDKDGNGTIDFNEFLLTLRPPMSRARKEVIMQAF
		1	RKLDKTGDGVITIEDLREVYNAKHHPKYQNGEWSEEQVFRKFLD
	1	1	
			NFDSPYDKDGLVTPEEFMNYYAGVSASIDTDVYFIIMMRTAWKL
5550	2364	1210	RKRKVFLKMRRLNRKKTLSLVKELDAFPKVPESYVETSASGGTV
			SLIAFTTMALLTIMEFSVYQDTWMKYEYEVDKDFSSKLRINIDI
			TVAMKCQYVGADVLDLAETMVASADGLVYEPTVFDLSPQQKEWQ
			RMLQLIQSRLQEEHSLQDVIFKSAFKSTSTALPPREDDSSQSPN
		}	ACRIHGHLYVNKVAGNFHITVGKAIPHPRGHAHLAALVNHESYN
		1	FSHRIDHLSFGELVPAIINPLDGTEKIAIDHNQMFQYFITVVPT
		1	KLHTYKISADTHQFSVTERERIINHAAGSHGVSGIFMKYDLSSL
		Į.	
		1	MVTVTEEHMPFWQFFVRLCGIVGGIFSTTGMLHGIGKFIVEIIC
	}	1	
			CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH
5551	211	1700	CRFRLGSYKPVNSVPFEDGHTDNHLPLLENNTH MORDHTMDYKESCPSVSIPSSDEHREKKKFFTVYKVLVSVGRSE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
{	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
 	sequence	 	\=possible nucleotide insertion)
]	WFVFRRYAEFDKLYNTLKKQFPAMALKIPAKRIFGDNFDPDFIK QRRAGLNEFIQNLVRYPELYNHPDVRAFLQMDSPKHQSDPSEDE
1	1	1	DERSSQKLHSTSQNINLGPSGNPHAKPTDFDFLKVIGKGSFGKV
			LLAKRKLDGKFYAVKVLQKKIVLNRKEQKHIMAERNVLLKNVKH
	Ĭ	ļ	PFLVGLHYSFQTTEKLYFVLDFVNGGELFFHLQRERSFPEHRAR
}	}	ļ	FYAAEIASALGYLHSIKIVYRDLKPENILLDSVGHVVLTDFGLC
	-		KEGIAISDTTTTFCGTPEYLAPEVIRKQPYDNTVDWWCLGAVLY
	}		EMLYGLPPFYCRDVAEMYDNILHKPLSLRPGVSLTAWSILEELL
			EKDRQNRLGAKEDFLEIQNHPFFESLSWADLVQKKIPPPFNPNV
i			AGPDDIRNFDTAFTEETVPYSVCVSSDYSIVNASVLEADDAFVG
5552	2748	930	FSYAPPSEDLFL
	2/30	930	LGPAAGAAMGKKHKKKHKAEWRSSYEDYADKPLEKPLKLVLKVGG SEVTELSGSGHDSSYYDDRSDHERERHKEKKKKKKKKSEKEKHL
,	1		DDEERRKRKEEKKRKREREHCDTEGEADDFDPGKKVEVEPPPDR
			PVRACRTQPAENESTPIQQLLEHFLRQLQRKDPHGFFAFPVTDA
ļ	ļ		IAPGYSMIIKHPMDFGTMKDKIVANEYKSVTEFKADFKLMCDNA
			MTYNRPDTVYYKLAKKILHAGFKMMSKQAALLGNEDTAVEEPVP
			EVVPVQVETAKKSKKPSREVISCMFEPEGNACSLTDSTAEEHVL
			ALVEHAADEARDRINRFLPGGKMGYLKRNGDGSLLYSVVNTAEP
			DADEEETHPVDLSSLSSKLLPGFTTLGFKDERRNKVTFLSSATT
			ALSMQNNSVFGDLKSDEMELLYSAYGDETGVQCALSLQEFVKDA
			GSYSKKVVDDLLDQITGGDHSRTLFQLKQRRNVPMKPPDEAKVG DTLGDSSSSVLEFMSMKSYPDVSVDISMLSSLGKVKKELDPDDS
			HLNLDETTKLLQDLHEAQAERGGSRPSSNLSSLSNASERDQHHL
		f	GSPSRLSVGEQPDVTHDPYEFLQSPEPAASAKT
5553	74	1095	LGREAVYLVSRMDGPVAEHAKQEPFHVVTPLLESWALSQVAGMP
			VFLKCENVQPSGSFKIRGIGHFCQEMAKKGCRHLVCSSGGNAGI
			AAAYAARKLGIPATIVLPESTSLQVVQRLQGEGAEVQLTGKVWD
			EANLRAQELAKRDGWENVPPFDHPLIWKGHASLVQELKAVLRTP
1			PGALVLAVGGGGLLAGVVAGLLEVGWQHVPIIAMETHGAHCFNA
			AITAGKLVTLPDITSVAKSLGAKTVAARALECMQVCKIHSEVVE DTEAVSAVQQLLDDERMLVEPACGAALAAIYSGLLRRLQAEGCL
			PPSLTSVVVIVCGGNNINSRELQALKTHLGOV
5554	166	2318	CSGRTGGRGSLRPAENVCLTCKLSGAETRGLLCPALRTWIMKVL
			GRSFFWVLFPVLPWAVQAVEHEEVAQRVIKLHRGRGVAAMQSRQ
			WVRDSCRKLSGLLRQKNAVLNKLKTAIGAVEKDVGLSDEEKLFO
ļ	i		VHTFEIFQKELNESENSVFQAVYGLQRALQGDYKDVVNMKESSR
	ļ	•	QRLEALREAAIKEETEYMELLAABKHQVEALKNMQHQNQSLSML
			DEILEDVRKAADRLEEBIEEHAFDDNKSVKGVNFEAVLRVEEEE
	i		ANSKQNITKREVEDDLGLSMLIDSQNNQYILTKPRDSTIPRADH HFIKDIVTIGMLSLPCGWLCTAIGLPTMFGYIICGVLLGPSGLN
]	ļ		SIKSIVQVETLGEFGVFFTLFLVGLEFSPEKLRKVWKISLQGPC
			YMTLLMIAFGLLWGHLLRIKPTQSVFISTCLSLSSTPLVSRFLM
	ļ		GSARGDKEGDIDYSTVLLGMLVTQDVQLGLFMAVMPTLIQAGAS
	į		ASSSIVVEVLRILVLIGQILFSLAAVFLLCLVIKKYLIGPYYRK
			LHMESKGNKEILILGISAFIFLMLTVTELLDVSMELGCFLAGAL
			VSSQGPVVTEEIATSIEPIRDFLAIVFFASIGLHVFPTFVAYEL
			TVLVFLTLSVVVMKFLLAALVLSLILPRSSQYIKWIVSAGLAQV
ŀ			SEFSFVLGSRARRAGVISREVYLLILSVTTLSLLLAPVLWRAAI
5555	212	1425	TRCVPRPERRSSL
		1473	LSLRTRETPAPPRCEAASQGRVGWRADAAAEEAVRSVWNRTRDR GTMAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRSASIKDIK
	-		KAYRKLALQLHPDRNPDDPQAQEKFQDLGAAYEVLSDSEKRKQY
		[DTYGEEGLKDGHQSSHGDIFSHFFGDFGFMFGGTPRQQDRNIPR
- 1		į	GSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQE
}		Ì	MRTTQLGPGRFQMTQEVGCDECPNVKLVNEERTLEVEIEPGVRD
ļ		ļ	GMEYPFIGEGEPHVDGEPGDLRFRIKVVKHPIFERRGDDLYTNV
Ì	1	ĺ	TISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGL
	. 1		PNFDNNNIKGSLIITFDVDFPKEQLTEEAREGIKQLLKQGŞVQK
5556	5835		VYNGLQGY
	3033	3346	RTRGMSKNCVPMEFEEYLLRMFQGTFYLLQKITKDNNAHTVKSR

070	Thursday - bard	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
[amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł	sequence		\=possible nucleotide insertion)
}	Sequence		LEELDESYIEKFTDFLRLFVSVHLRRIESYSQFPVVEFLTLLFK
			YTFHOPTHEGYFSCLDIWTLFLDYLTSKIKSRLGDKEAVLNRYE
{	}	ł	DALVLLLTEVLNRIOFRYNOAOLEELDDETLDDDQQTEWQRYLR
		ĺ	QSLEVVAKVMELLPTHAFSTLFPVLQDNLEVYLGLQQFIVTSGS
)		1	GHRLNITAENDCRRLHCSLRDLSSLLQAVGRLAEYFIGDVFAAR
ļ		İ	FNDALTVVERLVKVTLYGSQIKLYNIETAVPSVLKPDLIDVHAQ
ľ	Ì		SLAALQAYSHWLAQYCSEVHRQNTQQFVTLISTTMDAITPLIST
ļ		}	KVQDKLLLSACHLLVSLATTVRPVFLISIPAVQKVFNRITDASA
			LRLVDKAQVLVCRALSNILLLPWPNLPENEQQWPVRSINHASLI
}	1	ł	SALSRDYRNLKPSAVAPORKMPLDDTKLIIHQTLSVLEDIVENI
}			SGESTKSRQICYQSLQESVQVSLALFPAFIHQSDVTDEMLSFFL
1	1	1	TLFRGLRVQMGVPFTEQIIQTFLNMFTREQLAESILHEGSTGCR
1		1	VVEKFLKILQVVVQEPGQVFKPFLPSIIALCMEQVYPIIAERPS
1			PDVKAELFELLFRTLHHNWRYFFKSTVLASVQRGIAEEQMENEP
		1	
	1		QFSAIMQAFGQSFLQPDIHLFKQNLFYLETLNTKQKLYHKKIFR
1			TAMLFQFVNVLLQVLVHKSHDLLQEEIGIAIYNMASVDFDGFFA
1		į	AFLPEFLTSCDGVDANQKSVLGRNFKMDRVRRERGRAKRRAEWA
	L	<u> </u>	RKPGTCAARRGHIEASGRGLCPPCSLAAAHEMPADLVL
5557	1712	491	VILGAGLRDKDMWIPVVGLPRRLRLSALAGAGRFCILGSEAATR
ļ		1	KHLPARNHCGLSDSSPQLWPEPDFRNPPRKASKASLDFKRYVTD
1	1		RRLAETLAQIYLGKPSRPPHLLLECNPGPGILTQALLEAGAKVV
Į.	1	1	ALESDKTFIPHLESLGKNLDGKLRVIHCDFFKLDPRSGGVIKPP
ì	ļ]	AMSSRGLFKNLGIEAVPWTADIPLKVVGMFPSRGEKRALWKLAY
I			DLYSCTSIYKFGRIEVNMFIGEKEFQKLMADPGNPDLYHVLSVI
}	1		WQLACEIKVLHMEPWSSFDIYTRKGPLENPKRRELLDQLQQKLY
			LIQMIPRONLFTKNLTPMNYNIFFHLLKHCFGRRSATVIDHLRS
i			LTPLDARDILMQIGKQEDEKVVNMHPQDFKTLFETIERSKDCAY
1)	1	KWLYDETLEDR
			RAGCTHPOVPADLGAPAEPRRPOKTCVCLLQPQPGGQRGPTTMI
5558	1509	96	
l .	1	j	TGVFSMRLWTPVGVLTSLAYCLHQRRVALAELQEADGQCPVDRS
ļ			LLKLKMVQVVFRHGARSPLKPLPLEEQVEWNPQLLEVPPQTQFD
1	}		YTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQLTKVGMQQMFA
	ì		LGERLRKNYVEDIPFLSPTFNPQEVFIRSTNIFRNLESTRCLLA
f			GLFQCQKEGPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTA
1	}	1	SLQPGISEDLKKVKDRMGIDSSDKVDFFILLDNVAAEQAHNLPS
l l	,		CPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFLHILES
1			NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPP
1	1		FAVDLTMELYQHLESKEWFVQLYYHGKEQVPRGCPDGLCPLDMF
			LNAMSVYTLSPEKYHALCSQTQVMEVGNEE
5559	150	1983	PLAATAHFAKMSRVAKYRROVSEDPDIDSLLETLSPEEMEELEK
1 2333	1 230		ELDVVDPDGSVPVGLRQRNQTEKQSTGVYNREAMLNFCEKETKK
			LMOREMSMDESKOVETKTDAKNGEERGRDASKKALGPRRDSDLG
1			KEPKRGGLKKSFSRDRDEAGGKSGEKPKEEKIIRGIDKGRVRAA
1			
			VDKKEAGKDGRGEERAVATKKEERKKGSDRNTGLSRDKDKKREE
}	1		MKEVAKKEDDEKVKGERRNTDTRKEGEKMKRAGGNTDMKKEDEK
			VKRGTGNTDTKKDDEKVKKNEPLHEKEAKDDSKTKTPEKQTPSG
1	1		PTKPSEGPAKVEEEAAPSIFDEPLERVKNNDPEMTEVNVNNSDC
J			ITNEILVRFTEALEFNTVVKLFALANTRADDHVAFAIAIMLKAN
ì			KTITSLNLDSNHITGKGILAIFRALLQNNTLTELRFHNQRHICG
1			GKTEMEIAKLLKENTTLLKLGYHFELAGPRMTVTNLLSRNMDKQ
1			RQKRLQEQRQAQEAKGEKKDLLEVPKAGAVAKGSPKPSPQPSPK
		1	PSPKNSPKKGGAPAAPPPPPPPPLAPPLIMENLKNSLSPATQRKM
1		İ	GDKVLPAQEKNSRDQLLAAIRSSNLKQLKKVEVPKLLQ
5560	 9	921	SSVVEFSALSVSMACLSPSQLQKFQQDGFLVLEGFLSAEECVAM
3360	,	724	QQRIGEIVAEMDVPLHCRTEFSTQEEEQLRAQGSTDYFLSSGDK
1			
			IRFFFEKGVFDEKGNFLVPPEKSINKIGHALHAHDPVFKSITHS
	-		FKVQTLARSLGLQMPVVVQSMYIFKQPHFGGEVSPHQDASFLYT
			EPLGRVLGVWIAVEDATLENGCLWFIPGSHTSGVSRRMVRAPVG
		(SAPGTSFLGSEPARDNSLFVPTPVQRGALVLIHGEVVHKSKQNL
			SDRSRQAYTPHLMEASGTTWSPENWLQPTAELPFPQLYT
5561	2175	1775	CYFIFQFFSSPYPGLHPHQTPAPLPNPGLYPPPVSMSPGQPPPQ
		 	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
10.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ		amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	to first		
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j.	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			QLLAPTYFSAPGVMNFGNPSYPYAPGALPPPPPPHLYPNTQAPS
Į	1		QVYGGVTYYNPAQQQVQPKPSPPRRTPQPVTIKPPPPEVVSRGS
			S
5562	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
	1		LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
1	}		LASFLDFITYSYMIDNVILLITGTLHQRSIAELVPKCHPLGSFE
1	1		QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
1	1		IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
1	ļ		
(Į		INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA
1			DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNQFHF
			GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5563	342	1385	SSGKNDMAAAGAAGLVRGLKAGVLSQADYLNLVQCETLEDLKLH
1		Ī	LQSTDYGNFLANEASPLTVSVIDDRLKEKMVVEFRHMRNHAYEP
1	1	Į.	LASFLDFITYSYMIDNVILLITGTLHQRSIABLVPKCHPLGSFE
1		1	QMEAVNIAQTPAELYNAILVDTPLAAFFQDCISEQDLDEMNIEI
1		[IRNTLYKAYLESFYKFCTLLGGTTADAMCPILEFEADRRAFIIT
1		1	INSFGTELSKEDRAKLFPHCGRLYPEGLAQLARADDYEQVKNVA
			DYYPEYKLLFEGAGSNPGDKTLEDRFFEHEVKLNKLAFLNOFHF
1	ļ	}	GVFYAFVKLKEQECRNIVWIAECIAQRHRAKIDNYIPIF
5564	3	914	RVRRDKRAVWTARGRRRCGDSMSGGWMAQVGAWRTGALGLALLL
3364	, ,	j	LLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCRTSGLC
j)	· · · · · · · · · · · · · · · · · · ·
ţ			VPLTWRCDRDLDCSDGSDEEECRIEPCTQKGQCPPPPGLPCPCT
			GVSDCSGGTDKKLRNCSRLACLAGELRCTLSDDCIPLTWRCDGH
	i]	PDCPDSSDELGCGTNEILPEGDATTMGPPVTLESVTSLRNATTM
	+		GPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLV
	<u> </u>		TATLLLLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP
5565	993	138	RWNSPNPARAGSISRPQRAPGSVSAVAMTAAVFFGCAFIAFGPA
1	ŀ	}	LALYVFTIATEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIID
Į.			NKDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSIN
1	j		PGETAPSMRLLAYVSGLGFGIMSGVFSFVNTLSDSLGPGTVGIH
1	i		GDSPQFFLYSAFMTLVIILLHVFWGIVFFDGCEKKKWGILLIVL
i		Į.	LTHLLVSAQTFISSYYGINLASAFIILVLMGTWAFLAAGGSCRS
	Į.		LKLCLLCQDKNFLLYNQRSR
5566	2043	1232	SHIOHHGRGAOAPVKMVSWMISRAVVLVFGMLYPAYYSYKAVKT
]			KNVKEYVRWMMYWIVFALYTVIETVADQTVAWFPLYYELKIAFV
1			IWLLSPYTKGASLIYRKFLHPLLSSKEREIDDYIVQAKERGYET
			MVNFGRQGLNLAATAAVTAAVKSQGAITERLRSFSMHDLTTIQG
			DEPVGQRPYQPLPEAKKKSKPAPSESAGYGIPLKDGDEKTDEEA
1	1		EGPYSDNEMLTHKGPRRSQSMKSVKTTKGRKEVRYGSLKYKVKK
1		}	RPOVYP
	 	- 222	<u> </u>
5567	1554	233	EFLGSGVSPDLANEDGLTALHQCCIDDFREMVQQLLEAGANINA
			CDSECWTPLHAAATCGHLHLVELLIASGANLLAVNTDGNMPYDL
1			CDDEQTLDCLETAMADRGITQDSIEAARAVPELRMLDDIRSRLQ
1			AGADLHAPLDHGATLLHVAAANGFSEAAALLLEHRASLSAKDQD
1			GWEPLHAAAYWGQVPLVELLVAHGADLNAKSLMDETPLDVCGDE
1		1	EVRAKLLELKHKHDALLRAGSRGRSLLRRRTSSAGSRGKVVRRV
1			SLTQRTDLYRKQHAQEAIVWQQPPPTSPEPPEDNDDRQTGAELR
1			PPPPEEDNPEVVRPHNGRVGGSPVRHLYSKRLDRSVSYQLSPLD
1			STTPHTLVHDKAHHTLADLKRQRAAAKLQRPPPEGPESPETAEP
1	1		GLPGDTVTPQPDCGFRAGGDPPLLKLTAPAVEAPVERRPCCLLM
5568	1731	587	AEDROPASRRGAGTTAAMAASGPGCRSWCLCPEVPSATFFTALL
]	SLLVSGPRLFLLQQPLAPSGLTLKSEALRNWQVYRLVTYIFVYE
1			NPISLLCGAIIIWRFAGNFERTVGTVRHCFFTVIFAIFSAIIFL
1			SFEAVSSLSKLGEVEDARGFTPVAFAMLGVTTVRSRMRRALVFG
1	1		
			MVVPSVLVPWLLIGASWLIPQTSFLSNVCGLSIGLAYGLTYCYS
1			IDLSERVALKLDQTFPFSLMRRISVFKYVSGSSAERRAAQSRKL
1			NPVPGSYPTQSCHPHLSPSHPVSQTQHASGQKLASWPSCTPGHM
1			PTLPPYQPASGLCYVQNHFGPNPTSSSVYPASAGTSLGIQPPTP
L			VNSPGTVYSGALGTPGAAGSKESSRVPMP
5569	2	835	QTPCPLAWERGSRSEDISVPGQKPPTCSSFSGMDVGPSSLPHLG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	Į.	sequence	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion)
	sequence	 	LKLLLLLLLLPLRGQANTGCYGIPGMPGLPGAPGKDGYDGLPGP
			KGEPGIPAIPGIRGPKGQKGEPGLPGHPGKNGPMGPPGMPGVPG
			PMGIPGEPGEEGRYKQKFQSVFTVTRQTHQPPAPNSLIRFNAVL
		1	TNPQGDYDTSTGKFTCKVPGLYYFVYHASHTANLCVLLYRSGVK
	ļ	}	VVTFCGHTSKTNQVNSGGVLLRLQVGEEVWLAVNDYYDMVGIQG
			SDSVFSGFLLFPD
5570	264	946	RDRRDRGGVATSTEEPARPRAPOSRGPGPVSOTGRGRERGGGDT
}		}	MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPQGT
			PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL
1		1	DVINGTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
1		ľ	RPEBYKQKIKBYIQKYATEEALKEQEEGTGDSSSESSMSDFSED
			EAQDMEL
5571	264	946	RDRRDRGGVATSTEEPARPRAPQSRGPGPVSQTGRGRERGGGDT
]]	MSSPSPGKRRMDTDVVKLIESKHEVTILGGLNEFVVKFYGPQGT
			PYEGGVWKVRVDLPDKYPFKSPSIGFMNKIFHPNIDEASGTVCL
	Ì	l	DVINQTWTALYDLTNIFESFLPQLLAYPNPIDPLNGDAAAMYLH
		ļ	RPEEYKQKIKEYIQKYATEEALKEQEEGTGDSSSESSMSDFSED
5572	2802	2085	EAQDMEL RTDYRTGIPGRRFRVMAAGDGDVKLGTLGSGSESSNDGGSESPG
35/2	2002	2005	DAGAAAEGGGWAAAALALLTGGGEMLLNVALVALVLLGAYRLWV
)	,	ļ	RWGRRGLGAGAGAGEESPATSLPRMKKRDFSLEQLRQYDGSRNP
		}	RILLAVNGKVFDVTKGSKFYGPAGPYGIFAGRDASRGLATFCLD
ł	}	İ	KDALRDEYDDLSDLNAVQMESVREWEMOFKEKYDYVGRLLKPGE
1			EPSEYTDEEDTKDHNKOD
5573	2562	219	VPARTPNAEDOGPEARAATATPCOSGGRERAGEAAEDGVKMAAF
			SEMGVMPEIAQAVEEMDWLLPTDIQAESIPLILGGGDVLMAAET
1			GSGKTGAFSIPVIQIVYETLKDQQEGKKGKTTIKTGASVLNKWQ
			MNPYDRGSAFAIGSDGLCCQSREVKEWHGCRATKGLMKGKHYYE
1	ľ	Ì	VSCHDQGLCRVGWSTMQASLDLGTDKFGFGFGGTGKKSHNKQFD
		}	NYGEEFTMHDTIGCYLDIDKGHVKFSKNGKDLGLAFEIPPHMKN
l			QALFPACVLKNAELKFNFGEEEFKFPPKDGFVALSKAPDGYIVK
1		1	SQHSGNAQVTQTKFLPNAPKALIVEPSRELAEQTLNNIKQFKKY
1		,	IDNPKLRELLIIGGVAARDQLSVLENGVDIVVGTPGRLDDLVST
1		,	GKLNLSQVRFLVLDEADGLLSQGYSDFINRMHNQIPQVTSDGKR LQVIVCSATLHSFDVKKLSEKIMHFPTWVDLKGEDSVPDTVHHV
1		Ì	VVPVNPKTDRLWERLGKSHIRTDDVHAKDNTRPGANSPEMWSEA
j	<u> </u>	,	IKILKGEYAVRAIKEHKMDQAIIFCRTKIDCDNLEQYFIQOGGG
1		1	PDKKGHQFSCVCLHGDRKPHERKONLERFKKGDVRFLICTDVAA
1		Ì	RGIDIHGVPYVINVTLPDEKQNYVHRIGRVGRAERMGLAISLVA
1	1	}	TEKEKVWYHVCSSRGKGCYNTRLKEDGGCTIWYNEMQLLSEIEE
		1	HLNCTISQVEPDIKVPVDEFDGKVTYGQKRAAGGGSYKGHVDIL
	<u> </u>		APTVQELAALEKEAQTSFLHLGYLPNQLFRTF
5574	1731	952	NEGLEVFKEQELQPEDKGAVPEDASTERSAMASLGLQLVGYILG
}		[LLGLLGTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHS
1		1	TGITQCDIYSTLLGLPADIQAAQAMMVTSSAISSLACIISVVGM
		1	RCTVFCQESRAKDRVAVAGGVFFILGGLLGFIPVAWNLHGILRD
		ļ	FYSPLVPDSMKFEIGEALYLGIISSLFSLIAGIILCFSCSCQRN
5575	 	 _	RSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV
35/5	456	766	LLWALPCPPPTAAAVLLSSTGLMELLEKMLALTLAKADSPRTAL
			LCSAWLLTASFSAQQHKGSLQKDPLLSQACVGCLEALLDYLDAR
5576	249	2146	SPDIGRNSPHYLMFP RSWGAPWFWRMRLLRRRHMPLRLAMVGCAFVLFLFLLHRDVSSR
33,0	443	2140	EEATEKPWLKSLVSRKDHVLDLMLEAMNNLRDSMPKLQIRAPEA
			QQTLFSINQSCLPGFYTPAELKPFWERPPQDPNAPGADGKAFQK
		1	SKWTPLETQEKEEGYKKHCFNAFASDRISLQRSLGPDTRPPECV
1		1	DQKFRRCPPLATTSVIIVFHNEAWSTLLRTVYSVLHTTPAILLK
		1	EIILVDDASTEEHLKEKLEQYVKQLQVVRVVRQEERKGLITARL
		1	LGASVAQAEVLTFLDAHCECFHGWLEPLLARIABDKTVVVSPDI
	}	1	VTIDLNTFEFAKPVQRGRVHSRGNFDWSLTFGWETLPPHEKQRR
		1	KDETYPIKSPTFAGGLFSISKSYFEHIGTYDNQMEIWGGENVEM
			<u> </u>

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
}	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	}	\=possible nucleotide insertion)
}	Sequence		SFRVWQCGGQLEIIPCSVVGHVFRTKSPHTFPKGTSVIARNQVR
		l.	LAEVWMDSYKKIFYRRNLQAAKMAQEKSFGDISERLQLREQLHC
ļ		1	1
ì	}	1	HNFSWYLHNVYPEMFVPDLTPTFYGAIKNLGTNQCLDVGENNRG
		1	GKPLIMYSCHGLGGNQYFEYTTQRDLRHNIAKQLCLHVSKGALG
}	{	1	LGSCHFTGKNSQVPKDEEWBLAQDQLIRNSGSGTCLTSQDKKPA
1	1	1	MAPCNPSDPHQLWLFV
5577	3	1275	RNSDCSCGEISVHCLPWVLFILDLKVESSMFCPLKLILLPVLLD
	1		YSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTL
Ì	· ·		SPGEHAKDEYVLYYYSNLSVPIGRFQNRVHLMGDILCNDGSLLL
ĺ	ŀ		ODVORADOGTYICEIRLKGESQVFKKAVVLHVLPEEPKELMVHV
ĺ	ſ		GGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYYHKLRM
İ	Į.		_
		1	SVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESDGGNYTCS
}	1		IHLGNLVFKKTIVLHVSPEEPRTLVTPAALRPLVLGGNQLVIIV
1			GIVCATILLLPVLILIVKKTCGNKSSVNSTVLVKNTKKTNPEIK
}	1		EKPCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPV
ļ	1		WPSLRSDRNNSLEKKSGGGMPKTQQAF
5578	3	783	AVESMASPGAGRAPPELPERNCGYREVEYWDQRYQGAADSAPYD
i		Į.	WFGDFSSFRALLEPELRPEDRILVLGCGNSALSYELFLGGFPNV
Ì	ì	1	TSVDYSSVVVAAMOARYAHVPOLRWETMDVRKLDFPSASFDVVL
1			EKGTLDALLAGERDPWTVSSEGVHTVDQVLSEVSRVLVPGGRFI
l .	i	1	SMTSAAPHFRTRHYAQAYYGWSLRHATYGSGFHFHLYLMHKGGK
	1	j	LSVAQLALGAQILSPPRPPTSPCFLQDSDHEDFLSAIQL
	<u> </u>		
5579	3	1540	RNSGLARGASALARHGGGLAGGVGWDCGACASRCQGVMEGLLTR
1	[CRALPALATCSRQLSGYVPCRFHHCAPRRGRRLLLSRVFQPQNL
}		•	REDRVLSLQDKSDDLTCKSQRLMLQVGLIYPASPGCYHLLPYTV
	1		RAMEKLVRVIDQEMQAIGGQKVNMPSLSPAELWQATNRWDLMGK
1	1	1	ELLRLRDRHGKEYCLGPTHEEAITALIASQKKLSYKQLPFLLYQ
ì	1	}	VTRKFRDEPRPRFGLLRGREFYMKDMYTFDSSPEAAQQTYSLVC
1	į	1	DAYCSLFNKLGLPFVKVQADVGTIGGTVSHEFQLPVDIGEDRLA
ì	1	ì	ICPRCSFSANMETLDLSQMNCPACQGPLTKTKGIEVGHTFYLGT
1		İ	KYSSIFNAOFTNVCGKPTLAEMGCYGLGVTRILAAAIEVLSTED
		Į.	CVRWPSLLAPYQACLIPPKKGSKEQAASELIGQLYDHITEAVPQ
	1		LHGEVLLDDRTHLTIGNRLKDANKFGYPFVIIAGKRALEDPAHF
	1		1
		ļ	EVWCQNTGEVAFLTKDGVMDLLTPVQTV
5580	1681	450	ADAGTRCIPGFVVPSGAGYSAPAORGRRSSGRMRAAAAPGLTAP
İ			WRLLQCCELEAGELGMAVPAAAMGPSALGQSGPGSMAPWCSVSS
1]	1	GPSRYVLGMQELFRGHSKTREFLAHSAKVHSVAWSCDGRRLASG
1			SFDKTASVFLLEKDRLVKENNYRGHGDSVDQLCWHPSNPDLFVT
Į		1	ASGDKTIRIWDVRTTKCIATVNTKGENINICWSPDGQTIAVGNK
1		1	DDVVTFIDAKTHRSKAEEQFKFEVNEISWNNDNNMFFLTNGNGC
1		[INILSYPELKPVQSINAHPSNCICIKFDPMGKYFATGSADALVS
1			LWDVDELVCVRCFSRLDWPVRTLSFSHDGKMLASASEDHFIDIA
1	(1	EVETGDKLWEVQCESPTFTVAWHPKRPLLAFACDDKDGKYDSSR
1			EAGTVKLFGLPNDS
	+	047	GGGSGPRAPSATLLDTGESVAAVASGEDKGIAASAAAAAVFACS
5581	54	947	l .
1			CSPDPQSSTMNPVYSPVQPGAPYGNPKNMAYTGYPTAYPAAAPA
	}	1	YNPSLYPTNSPSYAPEFQFLHSAYATLLMKQAWPQNSSSCGTEG
1		1	TFHLPVDTGTENRTYQASSAAFRYTAGTPYKVPPTQSNTAPPPY
		1	SPSPNPYQTAMYPIRSAYPQQNLYAQGAYYTQPVYAAQPHVIHH
			TTVVQPNSIPSAIYPAPVAAPRTNGVAMGMVAGTTMAMSAGTLL
			TTPQHTAIGAHPVSMPTYRAQGTPAYSYVPPHW
5582	5775	2739	IITNNNNVIIPLVIAYHLSGSAQARGERSPAERLMERQKRKADI
	1		EKGLOFIOSTLPLKQEEYRAFLLKLVQNLFAEGNDLFREKDYKQ
1			ALVOYMEGLNVADYAASDQVALPRELLCKLHVNRAACYFTMGLY
	ţ		<u> </u>
	1		EKALEDSEKALGLDSESIRALFRKARALNELGRHKEAYECSSRC
1			SLALPHDESVTQLGQELAQKLGLRVRKAYKRPQELETFSLLSNG
	}		TAAGVADQGTSNGLGSIDDIETDCYVDPRGSPALLPSTPTMPLF
			PHVLDLLAPLDSSRTLPSTDSLDDFSDGDVFGPELDTLLDSLSL
1			VQGGLSGSGVPSELPQLIPVFPGGTPLLPPVVGGSIPVSSPLPP
			ASFGLVMDPSKKLAASVLDALDPPGPTLDPLDLLPYSETRLDAL
			

Designing	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Docation Corresponding	ID		E .	(A=Alanine, C=Cvsteine, D=Aspartic acid, R
Cotresponding	NO:	nucleotide	location	Glutamic Acid. F=Phenylalanine G-Glycine
LeLeucine, M-Methonine, N-Asparagine, physical amino acid acid acid acid acid acid acid acid	1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine
To first amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid amino acid aequence Security Common			to first	L=Leucine, M=Methionine, N=Asparagine.
Sestine, Trihreonine, Walline, amino acid am	ĺ			P=Proline, Q=Glutamine, R=Arginine.
amino acid sequence Codon, /-possible nucleotide deletion,		1	1	S=Serine, T=Threonine, V=Valine,
Sequence Appossible nuclectide insertion	İ			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
DEFOSTRESSILAREDE PREETINGORIEP PSGAURRE SEPENDEN TALLIUR PLANTER PRICACOLOUP OF KTOPRAGE STATEMENT TO THE CHARGE AND AND AND AND AND AND AND AND AND AND			sequence	Codon, /=possible nucleotide deletion,
TALLIANIPLAATHERKQACQLCYPKTGRRAGDYTYTEGLEHKKY RDILLGRIRSSBODYWERRIPRIPTKTSYGSYTYLCDHIKKODC KYGDNCTRAYHQEEIDWTBERKGTTANDLLEPDLGGVKRGSLT IAKLLRENGGIFFICEIGESKRYDGSVCSVALAAK HSFYNNKCHHIVRSTSLKYSKIRGPGEHFODUCHEVRYGGL REDSCHRABSFIELKYMLLQYSGWTHEDIVOSKRYGOMAH AGKASSSMAJPRTHESTSLLJOKKFVCGCCWRGCVVEPDKILK VCSAKARHCKTYKERKYMLLQYSGWTHEDIVOSKRYGOMAH AGKASSSMAJPRTHESTSLJOKKFVCGCCWRGCVVEPDKILK VCSAKARHCKTYKERKYMLLOYSGWTHEDIVOSKRYKOMAGWARH AGKASSSMAJPRTHESTSDLOKKFVCGCCWRGCVVEPDKILL CHIKAGNGRKGYVGNGSFAHSSEERDWTPHKRNKILDMQCTYV DWMLKKHNPCKGGSFTG ISBGERGUMTPHKRNKILDMQCTYV DWMLKKHNPCKGGSFTG ISBGERGUMTPHKRNKILDMQCTYV DWMLKKHNPCKGGSFTG ISBGERGUMTPHKRNKILDMQCTYV DWMLKKHNPCKGGSFTG ISBGERGUMTPHKRNKILDMQCTYV DWMLKKHNPCKGGGGKGAGGERGERFFT ISBGERGAWARPHYGGER LCDELGKGKACPGDGKCGAHGGERHENDLORFRUKALAAA KOMILOPEDDGGKYMFLLQDDDDLAGTFREYDDLOKKALAAC COKRINSKKOMOOHIGGSKHKERVFTSDEDAGGARAPEPPHGEFR RUMASKLALLKYHDDNDPDGEBFFLISOAYVLSDPYKADUVO GOGGALEGGGSGSFFSPPBHFRHWFYGGGGGMANBERBEKMY HOLSVILBDLYNGUTKKLALDANVLCEKGEGVGKKGSVEKCPL CKGKGHHHJQOLGFGMVQCQTVVLCERGGGGRTUPBCSCGG SGAKVIREKKILEVHVEKGMMGOXILFHGGDGDEPELBFGMVI LVTTSKAGEVIRHGDLACVROBENFTYAPLLSTAYDTLAVKFSASFE LKANYKLALKYHDDUNDDCEBLACOFKCTIKTLIDMT LVTTSKAGEVIRHGDLACVROBENFTYAPLLSTAYDTLAVKFSASFE LKANYKLALKYHDDUNDDCEBLEFKGUTSGAATUVLGFKCTIKTLIDMT LVTTSKAGEVIRHGDLACVROBENFTYAPLLSTAYDTLAVKFSASFE LKANYKLALKYHDDUNDDCEBCEFFLHSQAYVUJLAVKFSASFE LKANYKLALKYHDDUNDDCEBCEFFLHSQAYVUJLAVKFSASFE LKANYKLALKYHDDUNDDCEBCFFLHSGAATUVLAVKFSASFE LKANYKLALKYHDDUNDDCEBCFFLHSGAATUVLAVKFSASFE LKANYKLALKYHDDUNDDCEBCFFLHSGAATUVLAVKFSASFE CKGGROWNENGFT GARGAGGAATUVLATAGATUVLAVKFSASFE LKANYKLALKYHDDUNDDCEBCFFLHSGAGGGRAGRAGKANAV HOLSVYLEBDGDQPAAVQCQTA PROMESTARGGAATURAKTATUPHGGGGGABAERGKANAV HOLSVYLEBDGDQPAAVQCQTA LVANGAGAATURAKTATUPHGGGAATUPHGAATU		bequence		\=possible nucleotide insertion)
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DMMLKRHPGKPGESTPISSRGERKIUNTDTVANIMMRGHUNIL CORKSNSKKOWOOHIGSEKIKEKVITSISDASGMAPEPPMGERE LCDRLIGKGRACPGOKCRCHIGGEELBRILDERGVILAKARE KUMLCPRODPGKYMPILJEGEDDLAGKTBEAPAANATATTOE SEGCROGREGEDPEPPPREHRWVKETRYYDTLGVKPSASPEE IKKAYRKLAKYHIPODPGKYMPILJEGEDDLAGKTBEAPAANATATTOE IKKAYRKLAKYHIPONDOBGEEFFLISGAYEVUSDPKKROVYO GGEQALREGGSSSPSYSSIMDIFDMFFGGGGRAMBERRGKNYV HQLSVYLLEDLYNOVIKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGHHIHOJGIGFGWYQOJOTVCIEKKGGGRAMBERRGKNYV HQLSVYLLEDLYNOVIKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGHHIHOJGIGFGWYQOJOTVCIEKGGGGMARERGKNYV HQLSVYLLEDLYNOVIKKLALQKNVICHCEGEFTKITLOMRI LVITSKAGEVIKHGOLRCVRDGGMFIKARLEKGILIJQFLVIF PERHRUSLEKLAPOLBALLPPRGKVRITODMOQVELKEFCPHCON HROHREAYEEDEDGPQAGVQCTA 3 1265 SSCCKGRFGRESDRFRFPFREHKMYKETRYDILGVKPSASPEE IKKAYRKLALKYHPOKNFDEGEKFKILIGAYEVLSOPKKRDVYV QGGEGALEGGSGSPSFSSFMDIFDMFFGGGGRMABERRGKNVV HQLSVYLEDLYNOVIKKLALQKNVICKEKGEGKKASSVEKCPL CKGRGHHHIOJGIGGWVQOIOTVCIEKGQGEFINFDRICESC SGAKVIEKKI IEVUVEKGKNOVIVICKEKGEGKKASSVEKCPL CKGRGHHHIOJGIGGWVQOIOTVCIEKGQGEFINFDRICESC SGAKVIEKKI IEVUVEKGNOVIVICKEKGGDEFINFDRICESC SGAKVIEKKI IEVUVEKGNOVIVICKEKGGGEKKASSVEKCPL CKGRGHHHIOJGIGGWVQOIOTVCIEKGQGEFINFDRICESC SGAKVIEKKI IEVUVEKGNOVIVICKEKGGEKKASSVEKCPL CKGRGHHHIOJGIGGWVQOIOTVCIEKGAGEFINFDRICESC SGAKVIEKKI IEVUVEKGNOVIVICKEKGGEKKASSVEKCPL CKGRGHHHIOJGIGGWVQOIOTVCIEKGAGEFINFDRICESC SGAKVIEKKI IEVUVEKGNOVIVICKEGGEKKISVEKOPL CKREGHHIOOPROVIVITARIA IEVUVEKGNOVIVICKEGGEKKASSVEKCPL CKREGHHIOPROVIVITARIA IEVUVEKGNOVI INTARLEKGILIJOVITARIA LVITSKAGEVIKHGDLRCVRDGGFIYITARIA TARJOTESCHAPATORIA VHILITATILEMQAMMTTPOPODILLANMMKAAMICOPHERKS SVIDSFSLVANPITAGPTEEFIHAEVCYAKCLLQRAALTFLOD ENNUSFIKGGIKVRNSVOTYKELDSLOVSGOVCKGENHHPEGG VKLGVGAFNITISMPTRILIPALALIMPODRORIATILARIANI SMFGKEDHKPFGDDEVELPRAVPOLIKLIAGKSLPTEKFAIKS RRYFSSMFILEVARAMTYNDAVAVIGKGPCHANGTHINS SVIDSFSLUVMPILIPALLIELELLLIMEODORIATILALISHCORGHENS SVIDSFSLUVMPILIPALLIELELLLIMEODORIATILALISHCORGHENFS SVIDSFSLUVMPILIPALLIELELEVGFSGNKOVGLIOLGEGGG GHSFSVLCVMLLCCHTELTPUTGGTONNITEAERLLKEVILM SYNDSSTHYRIONDALLALLELEVGROEMPHFSG CKLEMMCFTYKGQMNSTYTHOLGORIANISHTYLM	1			LCIHAQNGRKCQYVGNCSFAHSPEERDMWTFMKENKILDMOOTY
SCHNSNSKKQWQHIQSEKIKEKYTISDAGWARFFPWEGFR LCDRLQKRGAGPDOKCKCHQGELMEMDLRREVHLQKHAXAR KDMLLCPRODDFGKYNFILQEDGDLAGATFEAPAAAATATTOE SSGCRGGRGFGSBOFPPPPPREKWWZETFYJUTUVFSASPER IKKAYKKLALKYHDUNDDEGEKFKLISQAYEVLSDPKRGDVYD OGGEQAIKEGGSGSPSFSSMDIFDHFGGGGRAAERRGKNVV HQLSVTLEDLYNGVTKLALQKNVICKKGGVGGKNGSVEKCPL CKGGWHIHIQQIGFGWVQQICTVCIEKKGQGEKINEKRGKVV HQLSVTLEDLYNGVTKLALQKNVICKKGGVGGKNGSVEKCPL CKGGWHIHIQQIGFGWVQQICTVCIEKKGQGEKINEKRGKSV SGAKVIEKKILEVIVEKGMCQKILFHGEGGPERLEFGDVI IVLDOKDISVPGRGHDLIMKMKIQLSEALCOFKKTIKTLONRI LVITSKAGEVIKHGDLRCVERGMFIYKARDLEGFFFKLISQAYEVLSDPKKRGUND WRGHRBAVEEDBEGPQAGVCQCTA SSCCGGGREGESDREPBPPREHKWVKETRYYDILGVKFSASFEE IKKAYEKLALKYHDUNDDEGEKFKLISQAYEVLSDPKKRUDVD OGGEQAIKEGGSGSPSFSSFMDIFDMFFGGGGRMAERRGKNVV HQLSVTLEDLINGVTKKLALQKNVICKKCGVGGKKGSVEKCPL CKGRGHHIHQGIGFGWVQQICTVCIEKCGGGRMAERRGKNVV HQLSVTLEDLINGVTKKLALQKNVICKKCGVGGKKGSVEKCPL CKGRGHHIHQGIGFGWVQQICTVCIEKCGGGRMAERRGKNVV UQLSVTLEDLINGVTKKALAQKNVICKKCGVGGKKGSVEKCPL CKGRGHHIHQGIGFGWVQQICTVCIEKCGGGRMAERRGKNVV IVLDOKONSVFGRGHDLIMKKGLISEALCFKTIKTLINRI LVITSKAGEVIKHGDLRCVEDGMFIYKAPLEKGILIQPLVIP PEKHMISLEKLIQLEALLIPPRGKVRITDMQVYLKEKFCPNEON WROHRRAVEEDBOGPQAQVQCTA SPAGTFESSIHELDQCHTALDLITNGFSEALSYLKPRTKESM YHSLTYATILEMQAMMTPPOQUILLAGNMKRAQMLCQRHERKS SVTDSFSSLWNRPTLGGTTELTAGFCVAKCLLQRAALTFLOD ENNVSPIKGGILKVRNSVOTYKLUSDLINGVAGCKGENHPHFEGG VKLGVGARNITLSMPTTLIKLLEFVUFSGRKVYGLLQLEEGAS GHSFRSVLCMULLCYHTELTVICTGTNUNTERLIKLKYPILMR YPKGAIFLFLAGRIEVIKKONIDAAIRRFECCCAQOHKQPHM CYWELMMCFTYKQOKNSYTYNGAYAICKGUCGHINTGOHM CYWELMMCFTYKQOKNSYTYNGAYAICKGUCGHNKDTHIK AEPMLEKGPENSYSDDECLVKLLKGKSLEPSKFRSMYSVSLI PAGGTPESSLIMBRTIGAATIOAKSSLENSSKSWSVSVI SHEKKERVPROBEVSUNDECLUKLLGKCLCKYLCRVQRAEBNFRS SVTDSFSSLWNRPTLGGTELHABVCYAKCLLQRAALTFLOD ENNVSPIKGGILKQAMMTPPDQTILLAGNMWGHGCHIRKS SVTDSFSSLWNRPTLGGTELHABVCYAKCLLQRAALTFLOD ENNVSPIKGTIVENSVOTYKELDSLUKSJCKYCKGENIPHFEGG VKLGVGAFNITLSMLPTRILLEFVGFSGKKVYGLLQLEEGAS GHSFSSLVCMLLCYHTLTPTLGTUNNIEGARGKILKTYTKSMY YHSLTYATILEMQAMMTSPDGCLUKLAGKSLETKFFAIKS SVTDSFSSLWRRPTLGGTTLEGFLORGKKATITYTMAATI SHEKKERVFSNDTLIPMALEBLALLKEPTURGSGRAUTHINA				DMWLKKHNPGKPGEGTPISSREGEKQIOMPTDYADIMMGYHCWI.
SSGRCORPERSDEPREPS PERRENWEST POLICYPESSEE IKKAYRKLALKYHEDINDEGEKKLISQAYEVISDEKKRUVYD OGGBOAIKSGGSGEPSES PENDIFDMFGGGGRAERGKOWV HQLSVTLEDLYNGVTKKLALKYNVICEKCEGVGGKKGSVEKCPL CKGRGHIHIQQIGPGWCQ1QTVCIECKGGGERIPKDRCESC SGAKVIREKKIISVHYGKMRGQKILFGFKITTYLDNRI LVTISKAGEVIKKGDLRCVRDEGMFYYAHLEKSILIJOPLVIF PERRINSLEKLPOLGEALLPPROKVITTDHDDQVELKEPCPNEQN WROREAVEKINGDLRCVRDEGMFYYAHLEKSILIJOPLVIF PERRINSLEKLPOLGEALLPPROKVITTDHDDQVELKEPCPNEQN WROREAVEKINGDLRCVRDEGMFYYAHLEKSILIJOPLVIF PERRINSLEKLPOLGEALLPPROKVITTDHDDQVELKEPCPNEQN WROREAVEKEDEDOPQAGVQCOTA	[ĺ		CGKNSNSKKQWQQHIQSEKHKEKVFTSDSDASGWAFRFPMGEFR
SSGCROGREGISPREPEPPRHENKYKETRYPTIGAYESSEEE IKKAYKKLAKHYHDKNPIDEGEKKKLISJOPKKRDVYD OGGOAIKSGGSGSFSSPMDIPDEGEKKKLISJOPKKRDVYD OGGOAIKSGGSGSFSSPMDIPDEGKKKLISJOPKKRDVYD OGGOAIKSGGSGSFSSPMDIPDEGKKKLISGNOWKCPL CKGRGHIHIQGIGFOMVQCTYCTECKGGGSRINFKDRCESC SGAKVIREKKIIEVHUSKOMKDGGKILFHGGSDDEPLEFGDVI IVLDOKONSVORGHGDLIMMKHOISSEALGSFKKTIKTLONRI LVITSKAGEVIKHGDLRCVRDEGNPIYKAPLEKGILIIQFLVIF PERKHIJSEKLEVQLEALLPPROKVRITDDMQVELKEFCONGON MRQHRAYEEDBDGPQAGVQCYTA SSGCRGGREGSBREPEPPRHENKYKETRYPTILGVKPSASPEE SSGCRGGREGSBSFSSPMDIPDHFFGGGGMARERGKNWV HOLSVYLEDLINGVYKKLALAKNVICEKCEGVGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQITVCIECKGGGGRINPKDRCESC SGAKVIREKKIIEVHVEKGMKCGKIKLFHGERDGPEERPGDVI IVLDOKDINSVPGRHGLINMMKNIQUSBALGGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGFLIIQFLVIF PEKHMISJEKLPQLEALLPPROKVRITDDMQVELKEFCPNEQN WROHREAVEEDBDGPQAGVQQCTA STARLENDAMMTEDPGDILLAGMMKRAGMLCQRHRRS SVIDSFSSLWARFILGGFTEEFIHADVYXAKCLLQRAALFFLQD ENNSFIKGGIKVRNSYTYKELDSLVOSKGEMIPHFEGG VKLGVGARNLTLSMLDTRILLELEFVGFSGNKDYGLLQLBEGAS GHSPRSVLCVALLLCYHTFLTFVLGTONVRIEABLIFLEFTHARK SVIDSFSSLWARFILGGFTEEFIHADVYXAKCLLQRAALFFLQD ENNSFIKGGIKVRNSYTYADLLSKENCOKSATTIMKAALL SMEGKEDHKPFGDDBVELFFRAVFGLKKLIKSLTHERFIKSM YPKGAIFLFAGRIEVIKKRIDAATRREECCCAQQHHKOPHHM CVWELMMCFTYKGQWKMSYTYADLLSKENCOKSATTIMKAALL SMEGKEDHKPFGDDBVELFFRAVFGLKKLIGALVARPALFFLGD SANBKKIKYDHYLIPNALLELALLLMEQDRRERAIKLLESAKQ NYRNYSMESRTHERIQAATIQAKSSLENSSRSMVSVSU SANBKKIKYDHYLIPNALLELALLLMEQDRRERAIKLLESAKQ VKLGVGAFNLTUSHLPTRILLEFVFGFSGNNOYGLLQLEGAS GHSFRSVLCWHLLCYHTFUTPVLGTONNIEBARKLLKPTINKSM YHGAITYATILEMQAMMTPDPODILLAGNMKRAQMLCGRRRKS SVTDSFSSLWNRPTLGGTEEFIHAEVCYAKCLLQRAALTPLQD ENNSFIKGGIKVRNSYTYKELDSLVOSSQVCKGENHPHPEGG VKLGVGAFNLTUSHLPTRILLEFVFGSGNNOYGLLQEGAS GHSFRSVLCWHLLCYHTFUTPVLGTONNIEBARKLLEFSKG SVTDSFSSLWNRPTLGQATIQAKSSLENSSRSMVSVSU SKREGEDHKPGDDBVELFRAVPGLKKLIGHGUGRHATHANTING SVTDSFSSLWANDFTLGGATTARVSTRESMCHATTYTYKARATL SMEKEBHRFSPODDBVELFRAVPGLKKLIGHGUGRHATHANTING SKREGENERSTRYSVDDECLVKLLKGLGLCKYLGGRATHANTING SKR	1			LCDRLQKGKACPDGDKCRCAHGQEELNEWLDRREVLKQKLAKAR
IKKAYKKLALKYHPDINDPEGEK KKILSPAYEVISDPKKRDVYD OGGQAIKGGSGSPFSSPMDIFDMFFGGGGRAMAFRGKNYVY HQLSVTLEDLYNGYTKKLALQKNVICEKCEGOGEKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKIIEVHVEKMDCQKLIPDMFFGGGRAMAFRGKNYVY HQLSVTLEDLYNGYTKLALQKNVICEKCEGOGERINPKDRCESC SGAKVIREKKIIEVHVEKMDCGKLIPDMFVBLKEFCPMEQN IVLDOKDHSVPGREGBLIMMMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEMPIYKAPLEKSHIIIQFLVIP PBRHWLSLEKLPQLBALLPPRQKVRITDDMDQVELKEFCPMEQN WROHREAVEEDEDOPAGVQCQTA SSCCKGGREGRSDFREPPBFRHKNVVETRYYDILGVKPSASPEE IKKAYKKLALKYHPDNPDEGEKFKLISQAYEVLSDPKKDDVJO OGGGAIKEGGGSBPFSFSPPBDFPDFDMFPGGGRMARERRGKNVV HQLSVYLEDLYNGVTKKLALQKNVICEKCEGVGGKRGSVEKCPL CKGRMHIHIQQIGPMVQQITVCIECKGGGERINPKRDCESC SGAKVIREKKIIEVHVEKGMCXQKLILHGEGGGPEELEPGDVI IVLDQKDHSVPQRRCHDLIMMMKIQLSBALCGFKKTIKTLDNRI LVITSKAGEVIKRGDLRCVYDECMPIYKAPLEKGILITQFLVIP PEKHMLSLEKLPQLBALLPPROKVRITODDDQVELKEFCPNEQN WROHEAVEEDEDGPAQVQCQTA VKGHAPAENEDEGGPAGVACQCTA 1 LPAGTFESSLHEALDQCWTALDLFLTNQFSEALSYLKPRTKESM YHSLTYATILBMQAMTTPDQDILLAGMMMKRAQMLCQRHRKS SVTIDSFSSLWNRPTLGGFTEEPEIHAEVCYALCAGRALTFLQD ENNVSPIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGARNLTLSMLPTFIILTLEFEVGFSCAQHHKOPHM CVWELMGCPTYKGQMKMSYYYADLLSKENCAGKATYITMKAATL SMFGKEDHKPFGDDEVELFRAYPGLKLKIAGKSLFTEKFAIKKS RRYFSSNPISLEVPALEMMYINNGVAVIKGEACHLOFGLEITIK AEEMLEKGPENSYSVDDECLVKLLKGLCLKYLGRQAERDFRS ISANSKIKVATHILFALLFLILLEFLYGGRONDVGLIQLEGGS VKLGVGARNLTLSMLPTFIILDLFLYGGRONDVGLIQLEGGS VKLGVGARNLTLSMLPTFIILDLFLYGGRONDVGLIQLEGGS VKLGVGARNLTLSMLPTFIILDLFLYGGRONDVGLIQLEGGS VKLGVGARNLTLSMLPTFIILDLFLYGGRONDVGLIQLEGGS VKLGVGARNLTLSMLPTFIILFALLFLILLEFUGGRONDVGLIQLEGGS VKLGVGARNLTLSMLPTFIICPTTEEIHAEVCYAKCLLQRAALTFIQD ENNVSFIKGGIKVNSYQTYKELDLLVGXCKGENHPHPEGG VKLGVGAFNLTLSMLPTFIICPTTEEIHAEVCYAKCLLQRAALTFIQD ENNVSFIKGGIKVNSYGTYKELDLLVGXCKGENHPHPEGG VKLGVGAFNLTLSMLPTFIILFFFYLGTONVBLEGAEKLKPYINR YPKGAIFLFFAGRIEVKNDCHALLGCHTFTTVFLGTONVBLEGAEKLKPYINR YPKGAIFLFAGRIEVKNDCHALLLCHAFTTVFLGTONVBLEGAEKLKPYINR YPKGAIFLFAGRIEVKLORGUKLLCCHAFTTYTYMKAPAL SMFGKEDHKPFGODEVELFRAYPGGLKKLAGKLFTTKARAL SMFGKEDHKPFGODEVELFRAYPGGLKLAGKLFTKYNGSVSL	5583		1065	KDMLLCPRDDDFGKYNFLLQEDGDLAGATPEAPAAAATATTGE
OGGROATKROGSGSPSTSSEMDIFFMFFGGGRARAERRGKNVV HQLSVTLEDLINGVTKKLALQKNV1 CRKGROVGKKGSVEKCPL CKGRGMHHIQJGFGMVQQJQTVCIECKGQGERINFKDRCESC SGAKVIREKKIIEVHVEKGMKDGQKIIFHGEGGDEFLEEPGDVI IVLDQADHSVVQRGHDLIMKMKIQLSALCGFKKTIKLDNRI LVITSKAGEVIKHGDLRCVRDBGMFIYKAPLEKGILIIQFLVIF PERHWLSLEKHPQLBALDLIMFKNKIQLSALCGFKKTIKLDNRI LVITSKAGEVIKHGDLRCVRDBGMFIYKAPLEKGILIIQFLVIF PERHWLSLEKHPQLBALDLIPPGKVKITDDHDQVELKEFCPNEQN WROHREAYSEDEDGFQAGVQCQTA SSGCEQGRPGRSDRFRFPBFRFHKMVKETRYYDILGVKFSASPEE IKKAYAKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVVD QGGCAIKSGGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV HQLSVTLEBLINGVTKKALALOKNVICEKCGGVGKKGSVGKCSVKCCL CKGRGHHHIQQIGPGMVQQIQTVCIECKGGGERINPKDRCESC SGAKVIREKKIIEVHVEKGMKDGGKILFHGEGDGPPLBFGDVI IVLDQXDHSVFQRRGHDLTMKMKXQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMFIYKAPLBKGILIIQFLVIF PERHMLSLEKLPQLEALDLPPRGVWITDMQVELKEFCPNEQN WROHREAYSEDEDDPQAGVCCTA LVATSKAGEVIKHGDLRCVRDEGMFIYKAPLBKGILIIQFLVIF PERHMLSLEKLPQLEALDLPPRGVWITDMQVELKEFCPNEQN WROHREAYSEDEDDPQAGVCCTA LVATSKAGEVIKHGDLRCVRDEGMFIYKAPLBKGILIQFLVIFT PERHMLSLEKLPQLEALDLPPRGVWITDMQVELKEFCPNEQN WROHREAYSEDEDDPQAGVCCTA LVATSKAGEVIKHGDLRCVRDEGMFIXAPLBKGILIQFLVIFT PERHMLSKEKLPQLEALDLPPRGVWITNAPLBKGLILIGFLVIFT SSTORTSSLUVARPTLGQFTEESHARVCYAKCLLQRAALTFLQD ENNVSFIKGGIKVNSYQTYKELBSJVGXCKGENHPHFEGG VKLGVGAFNITLSMLPTRILLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCVHTPLTFUTGUTGNTHEBAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHKQFHHM CYWELMMCPTYKGOMMSYFYADLLSKKLGRVQABERNPS ISANKKIKYDHYLJFNALELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRQAATIQAKSSLENSSRMVSSVSL 15AGEMLEKGPENSYSUDGECLVKLLKGLACKLLGRVGAERBENPS SYTDSFSSLVARFTIGGTEETHAEVCAKCLLGRVGAERBUFS GRIFFSSVLCVMLLLCVHTLFTFUTGTGVNTLEEAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRFFECCEAQGHKQFHHM CYWELMMCFTYKGGWKMSYFYADLLSKERCNSKATYYKKAAYL SMFGKEDHKFYNGGWFYTYGGWRSYFYADLLSKERCNSKATYYKKAAYL SMFGKEDKFFYNGGWRSFYFYDLLGKERCNSKATYYKKAAYL SMFGKEDKFFYNGGWRSFYFYDLLGKERCNSKATYTYKKAAYL SMFGKEDKFFYNGGWRSFYFYDLLGKERCNSKATYTYKKAAYL SMFGKEDKFYNGGWRGFTHM GYAVIGKOPKLIKTGGILLITK REPMLEKGPENSYSUDDECLVKLLKGLICKTCRVCPAEBEPRS ISANSKKIKYDHYLIPNALLELALLLKRGDRURGEAKLLESSKQ	1 3303	3	1265	SSGCROGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE
HQLSVTLEDLYNGVTKKLALQKNVICEKCRGVGRKGSVEKCPL CKGRGMHHIVQQIGTVCIECKGQGFKINPKDRCCSC SGARVIREKKIIEVHVEKGMKDGQKILFHGEGDQFPELEFGDVI IVLDQKDHSVPQRRGHDLIMKNKIQLSEALGGFKKTIKTLDNRI LVITSKRGVIKHGDLECVEDBGMFIVELBERGILITQFLVIF PEKHWLSLEKLPQLEALLPPRGKVRITDDHDQVELKEFCPNEQN WRGHREAVREDEDGFQAGVQCQTA SGCGCQAIRVEREDEDGFQAGVQCQTA 5584 3 1265 SSGCEQGRPGRSDRPRPPPRRHKWVKETRYYDILGVKFSASPEE IKKAYAKLALKYHPDKNPDEGSKFKLISQAYEVLSDFKKRDVYD QCGCQAIRGGGGSGSPSSPMDIFDPFGGGGGMARERGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGHHHIQOIGPGWFOXOQIQTVCIECKGGGGRINAPERGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGHHHIQOIGPGWFOXOQIQTVCIECKGGGGRINAPERGSNV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGHHHIQOIGPGWGCQTA UVITSKAGGVIKHGURCVDEGMGFIVEHGEGDGPELBFGDVI IVLDQKDHSVPQRRGHDLIMKNKIQLSEALCGFKKTIKTLDNRI LVITSKAGGVIKHGURCVDEGMGFIVEHGKGILGVLFVIF PEKHWLSLEKLPQLEALLDPRGKVRITDDMDQVELKEFCPNEQN WRGHREAVEEDEDGDQAGVQCQTA WRGHERAVEEDEDGDQAGVQCQTA YHSLTYATILEMQAMMTPDPQDILLAGNMKREAQMLCQRHRKSS SYDDSFSSLVMPTLGGFFEE HARVAKLLQKALLQKARLAFFLQD ENNVSFIKGGIKVRNSYQTYKELDSLVQSSQVCKGENHPHFEGG VKLGVGAFNLTLSMLPTTILRLLEFVGFSGNKDVGLLQLEEGGAS GHSFRSVLCVMLLLCHTFLIFTVLGTUNVIEEAEKLLKYLNRY YPKGAIFLFLAGGIEVIKGNIDAAIRRFEECCEAQGHKCFHHM CVYBELMMCFTYKGQVKMSYFYADLLSKANGKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPOLKLKIAGKSLPTEKFAIRKS RYYFSSNPISLPVPALEMMYINNGYAVIGKGPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCKKYLGRVQEAEBRNFS ISANBKKIKYDHYLIFNALLELALLLMEQDRNEARIKLLGSAKO VKLGVGAFNLTLSMLPTTILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR YPKGAIFLFLAGGIEVIKGNIDAAIRRFEECCEAQGHKQFHHM CVWELMMCFTYKGQWKMSYTYADLLSKECKLLQRAANTFLQD ENNVSFIKGGIEVRNSYGTYEELHAGKGCORMKQFHHM CVWELMGCFTYKGQWKMSYTYADLLSKECKSKATYIYMKAAYL SMFGKEDRKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RYYFSSNPISLPPPALEMMYINNGYAVIGKQPKLTGGLEDIGEAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR YPKGAIFLFLAGGIEVIKGNIDAAIRRFEECCEAQGHKQFHHM CVWELMGCFTYKGQWKMSYTYADLLSKECKSKATYIYKKAAYL SMFGKEDRFTYKGQWKMSYTYADLLSKECKSKATYIYKKAAYL SMFGKEDRFTYKGQMKMSYTYADLLSKECKSKATYIYKKAAYL SMFGKEDRFTYKGGWKMSYTYADLLSKECKCNSKATYIYKKAAYL SMF	ŀ			OCCEONTRECCECEDERGENERATION
CKGRGMHINIQQIGGGMVQQIGTCHCKGGGERINPKDRCESC SGARVIREKKIIEVNYEKGMKDGQNLIGEGDGDEPLEPGDVI IVLDQKDHSVPGRGHDLIMKWKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMFIYKAPLEKEGTIJQFLVIF PBRHWLSLEKLPQLEALLPPRGKVRITIDDMQVPELKEFCPNEGN WRQHREAYBEDEDGPQAGVQCOTA SSGCRGGRFRSBDAPREPPRRHKWYKTRYYDILGVKFSASPEE IKKAYRKLALKYHDKNPDEGEKFKLISQAYEVLSQPKKRDVYD QGGQAIKEGGSGSPSFSSPMDIFDMFFGGGRMRERGKOKVY HQLSVYLEDLINGVYKKLALQKNVICEKCEGVGGKRSVEKCPL CKGRGMHHIQQIGPGMVQQIDTVCIECKGGGERINPKDRCESC SGARVIREKKIIEVNYEKGMKDGGKIRGGDGPERIPPGDVI IVLDGKDHSVPGRRGHDLIMKMKIQLSEALCGFKYTIKTLDNRI LVTTSKAGEVIKHGDLRCVRDEGMPIYKAPLRKGGGERINPKDRCESC SGARVIREKKIIEVNYEKGMKDGGKIRDEGGDGPERIPPGDVI IVLDGKDHSVPGRRGHDLIMKMKIQLSEALCGFKYTIKTLDNRI LVTTSKAGEVIKHGDLRCVRDEGMPIYKAPLRKGILIQFLVIF PEXHILSLEKLPQLEALLPPRQKVRITDDMQCVELKEFCENEON WRQHREAYEEDEDDPQAGVQCQTA LPAGTTESSLHEALDGVATADLFEITNOFSEALSYLKPFTKESM YHSLITYATILBMQAMTEPDPODILLAGNMMKEAQMLCQRHRKS SVYDSFSSLVNRPTLGQFTEEEIHAEVCYAKLQRAALTFLQD ENNVSPIKGGIKVNSYQTYKELDSLVQSSQVKGENHPHFEGG VKLGVGARNITLSMLPTRILLELFVGFSGNBVGLLQLEEGAS GHSFRSVLCVMLLLCYHTLTTVLTGTUNNIEEBAKLLKRYINR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHKKQPHHM CYWELMWGTYKGQWKMSYFYADLLSKENCHSKATYIYMKAAYL SMFGKEDHKPFGDDEVELVKLLKGLKYLGRVGAEBENPRS ISANKKIKYDHYLIFNALLELALLLMEQDRNERAIKLLESAKQ NYKNYSMSSRTHFRIQAATHQAKSSLENSSRMVSSVSIL 15AGTPESSLUNRPTLGGTEEE HABVCYXCKLLGRAALTFLQD EMNVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHPEGG VKLGVGARNITLSMLPTRILLELEFVGFSGNBVGLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNNIEERAEKLLKYHNN YPKGGIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHKQFHHM CWYGLMMGTFTKGGWKMSYTYMLLSKACKLLGRAALTFLQD EMNVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHPEGG VKLGVGARNITLSMLPTRILLELFVGFSGNBVGLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNNIEERAEKLLKYHLNA YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQGHKQFHHM CWYGLMGTTYTKGVMKSYYYADLLSKOKKATYIYMKAAYL SMFGKEDRKPFGDDEVELFRRYYGGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIMNGYAVIGKQPKLTKAAYL SMFGKEDRKPFGDDEVELFTRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIMNGYAVIGKQPELTKLESAKQ NYKNYSMSEKSKSTHFRIQAATLOAKSLELMKSKATYIYMKAAYL SMFGKEDRKFYRGOKMSYTYADLLSKENKSKATYIYMKAAYL SMFGKEDRKFYRGOKMSYT	1			HOLSVILEDLYNGUTYYL ALOVAULI GENODOUGGING STEELEN
SGAKVIREKKI IEVIVERGMKDGGKILFIGEGDGEPELEPGDUI IVLONGNBSVFORRGHDLIMMKIN JEBALCOFKKTIKKTLONRI LVITSKAGEVIKHGDLRCVRDEMPIYKAPLEKGILTIQFLVIT PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEPCDNEON WROMREAYEEDEDGPAQAVQCOTA SSGCRQGRPGRSDRRPPPPRRHKMVXETRYYDILGVKPSASPEE IKKAYRKLALKYHDDKNPDGEGKFKKLISQAYEVLSDRKKRDVTD QGGEQAIKEGGSGSPSFSSPMDIFDMFFGGGGRMARERGKNVV HQLSVTLEDLYNGVYKKLALQKNVICEKCEGVGGKKGSVEKCPL CKGRGHNHINQOIGPGMVQOIGTVECKGGGGKGVKGSVEKCPL CKGRGHHINQOIGPGMVQOIGTVECKGGGGKGKGSVEKCPL CKGRGHHINQOIGPGMVQOIGTVECKGGGGKINFURGKEES SGAKVIREKKIEVHVEKGMKDGQKILPHGBGDGPPELEPGDVI IVLDQXDHSVPORRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLERVEDEGMPIYKAPLEKGILIGPLVIF PEKHMLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEON WROHREAVTEEDEDPGAGVQCTOTA WROHREAVTEEDEDPGAGVQCTOTA 5585 2619 915 LPAGTPESSLHBALDQCMTALDLFLTNOFSEALSYLKFRTKESM YHSLTYATILBMQAMMTFDPQOILLAGMMMKEAGMLCQRHRRKS SVTDSFSSLWRPTLGGFTEETHAGAMTHCAGAMLCQRHRRKS SVTDSFSSLWRPTLGGFTEETHAGAMTHCAGAMLCQRHRRKS GHSPSVLCVMLLLCYHTPLTRLELEFVGFSGNKDYGLDEGAS GHSPSVLCVMLLLCYHTPLTVLGTGNVNIEBAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAATRREECCEAQOHMKQFHHM CVMELMWCTTKKGGWKNSYYADLSKCMSKTNYTYTYMAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLIAGKSLPTEKFAIKKS RRYFSSNPISLPVPALEMMYINGYAVIKGOPKLTDGILBIITK AEEMLEKGPENEYSVDDECLVILLKGLCLKYLGRVQBAEENPRS SVTDSFSSLVNRPTLAGFTEETHAEVCYAKCLLQRAALTFLOD ENNVSFIKGGIKVRNSYYTYTLFRTRLELDEFSGNKDYGLIQLEGAS SVTDSFSSLVNRPTLAGFTEETHAEVCYAKCLLQRAALTFLOD ENNVSFIKGGIKVRNSYYTYTLFRTRLELDEFSGNKDYGLIQLEGAS GHSFRSVLCVMLLLCYHTFLTRLELEPGFSGNKDYGLIQLEGAS GHSFRSVLCVMLLLCYHTFLTRLELEPGFSGNKDYGLIQLEGAS GHSFRSVLCVMLLLCYHTFLTRLECFSGNKDYGLIQLEGAS GHSFRSVLCVMLLLCYHTFLTRLECFSGNKDYGLIQLEGAS GHSFRSVLCVMLLLCYHTFLTRLECFSGNKDYGLIQLEGAS GHSFRSVLCVMLLLCYHTFLTRLICHSFONKDYGLIQLEGAS GHSFRSVLCVMLLLCYHTFLTRLICHSFONKDYGLIQLEGAS GHSFRSVLCVMLLLCYHTFLTRLICHSFONKDYGLIQLEGAS GHSFRSVLCVMLLLCYHTFLTRLICHSFONKDYGLIQLEGAS GHSFRSVLCVMLLLCYHTFLTRLICHSFONKDYGLIQLEGAS GHSFRSVLCVMLLLCYHTFLTRLICHSFONKDYGLIQLEGAS GHSFRSVLCVMLLLCYHTFLTRLICHSFONKDYGLIQLEGAS GHSFRSVLCVMLLLCYHTFLTRLECCAGQHKKGPHHM CVWELMMGFTYKGGWKSTYATULTSFONKDYGLTYTTWKANYL SMFGKEDHKPFGDDEVLEFRARK	ļ			CKGRGMHIHIOOIGPGMVOOTOTVCIECKGOGEPINDKDDGGGG
IVLDQKDHSVFQRRGHDLIMMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMIYARAPLEKGILIIQFLVIF PBKHWLSLEKLPQLEALLPPRQKVRITDDMQVBLKBFCDNEQM WROHREAYBEDBDGPAGSVQCOTA SSGCRGORFGRSBRPRPPPRFHKMVKETRYYDILGVKBSASPEE IKKAYRKLALKYHPDKIPBGEGKFKLISQAYEVLSDPKKRDVYD QGGQAIKEGGSGSPSFSSPMDIFDMFFGGGGMARERGKKNVV HQUSVYTLEDLYMGVYKKLALQKNVICEKCEGVGGKKGSVKCPL CKGRGMHIHIQQIGPGMVQQIOTVCIECKGGGGGKAKGSVKCPL CKGRGMHHIQQIGPGMVQQIOTVCIECKGGGGKAKGSVKCPL CKGRGMHHIQQIGPGMVQQIOTVCIECKGGGGGKAKGSVKCPL CKGRGMHHIGQIGPGMVQQIOTVCIECKGGGGGKAKGSVKCPL CKGRGMHHIGQIGPGMVQQIOTVCIECKGGGGGKAKGSVKCPL PEKHMISLEKLYPQLEALLPPRQKNTJEMGGDEJKEFCPNEQN WROHREAYSEDBDGPQAGVQQTA 1VLDQKDHSVFQRRGHDLIMKMKIQLSEALGGFKKTIKTLDNRI LVITSKAGEVIKHGDLKCVEBGMPIYKAPLEKGILIIQFLVIF PEKHMISLEKLYPQLEALLPPRQKNTDDMQVELKEFCPNEQN WROHREAYSEDBDGPQAGVQQTA STODSFSSLVNRPTLGGFTEBEIHAEVCYAKCLLQRAALTFLQD ENNYSFIKGGIKVNSVQTYKELDSLVQSQYCKGENHPHFEGG VKLGVGAPNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTPLTFVLCTGNVNIEBAEKLLKFYINR YPRGAIFLFLAGRIEVIKKNIDAATRRFEECCEAQQHMKQFHMK CYWELMWCPTYKGQWKNSYFYADLLSKLEVLFRVGDAEENFRS ISANKKIKYDHYLIPRALLELALLLMCQDRNEEAIYLLFPRKFAIKKS RRYFSSNPISLPVPALEMMYINNGYAVIGKQPKLTDGILBITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQBAEENFRS ISANKKIKYDHYLIPRALLELALLLMCQDRNEEAIYLLFPRGS VKLGVGAPNLTLSMLPTRILLELFUGFSGNKDYGLLGLEGAS GHSFRSVLCVMLLCYHTPLTPVLGTGNVNIEBAEKLLKPYLNR YPKGAIFLYTATILBMQAMMTFPQDOILLGARALTFLQD EMWSFIKGGIKVBNSYQTYKKLDSLVQSSQYCKGENHHPEGG VKLGVGANNITLSMLPTRILLEFUGFSGNKDYGLLQLEGAS GHSFRSVLCVMLLLCYHTPLTPVLGTGNVNIEBAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFBGECCEAQCHMKQFHEM CYMELMMCFTYKCGWKMSYFYADLLSKENCNSKATIYMKANYL SMFGKEDHKPFGDDEVELFRAVFGKKLIAGKSLPTEKFAIRKS RYFSSNPISLFPVBALEMYYINGYAVIGKQPKLTDGILEITK AEEMLEKGPENEYSVDDECLIVKLIKGLCLKYLGGAEEMFRS RRYFSSNPISLFPVBALEMMYINGYAVIGKQPKLTDGILEITK AEEMLEKGPENEYSVDDECLIVKLIKGLCLKYLGGAEEMFRS ISANEKKIKYDHYLIPNALLELALLLMCORNSKATIYMKANYL SMFGKEDHKPFGDDEVELFRAVFGLKKLLESAKQ NYKNYSMESSTHFRIQAATLOKASSLENDSRSWSSVSI.				SGAKVIREKKIIEVHVEKGMKDGOKILFHGEGDOEDELEDGDUT
LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PRIMIKISLEKLPOLEALLIPPRQKVITDDMQVELKEFCPNEQN WROUREAYEEDEDGPOAGVQCQTA 3 1265 SSGCRGERGRSDRRPEPPRHEMVVETRYVDILGVKPSASPEE IKKAYRKLALKYHDRVPERBEGEKFKLISQAYEVLSDPKKDVVD QGGEQAIKEGGSGSBSTSSPMDIFDMFFGGGGRMARERGKNVV HOLSVYLEDLYNGVYKKLALQKNVICEKCEGVGGKKGSVSKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGGGERINFKDRCBES SGAKVIREKKIIEVHVEKGMKDCQKILFPRGEDGEPELBFGDVI IVLDQXDHSVPQRRSHDLIMMMIGLSEALCGFYKTIXTLDNRI LVITSKAGEVIKHGDLRCVKDEGMPIYKAPLEKGILIIQFLVIF PEKHMLSLEKLPQLEALLPPRGKVRITDDMQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA WRQHREAYEEDEDGPQAGVQCQTA 5585 2619 915 LPAGTFESSLHBALDQCMTALDLFUTNOFSEALSYLKPRTKESM YHSLTXTILIBMQAMMTPDQDOILLAGMMMKBAQMLCQRHRKS SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLQRAALTFLQD ENNVSFIKGGIKVENSYQTYKELDSLVQSSGYCKGEMHPHFEGG VKLGVGAFNLTISMLPTRIBLLEFVGFSGNKDYGLLGLEGGAS GHSFRSVLCVMLLCYHTPLTVLGTGNVNIEBAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEGCCEAQQHMKQFHM CYWELMWCFTYKGQWKNSYFYADLISKENCMSKATYIYMAAYL SMFGKEDHKPFGDDEVELFRAVFGLKLIAGKSLFTEKFAIKS RRYFSSNPISLPVPABLEMMYINGYATGKGPKLTDGLIEITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEEMFRS ISANEKKIKYDHYLINNALDLEALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAFEEIHAEVCYAKCLLQRAALTFLQD EMNVSFIKGGIKVENSYQTYKELDSLVQSSGYCKGENHPHFEGG VKLGVGANNILTSMLFTRILLEFGSGNKDYGLLQLEGGAS GHSFSVLCVMLLCYHTFLTFVLGTGNVNIEBAEKLLKPYLNR YPKGAIFLFLAGRIEVIKKNIDAAIRRFEGCCEAQQHMKQFHHM CYMELMMCFTYKGGWKMSYFYADLISGRSKMVSSVSUL LPAGTFESSLHEALDQCMTALDLAFLTRUCTGNVNIEBAEKLLKPYLNR YPKGAIFLFLAGRIEVIKKNIDAAIRRFEGCCAQQHMKQFHHM CYMELMMCFTYKGGWKMSYFYADLISGRSKMVSSVSUL SMFGKEDBKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RYFSSNPISLPVPALEMMYINNGYAVIKKDCHNSATTIYTMKAAYL SMFGKEDBKPFGDDEVELFRAVPGLKLKLIAGKSLPTEKFAIRKS RYFSSNPISLPVPALEMMYINNGYAVIKGPKLTDGAIFITM CYMELMMCFTYKGGWKMSYFYADLISGLCKLYTIGRVQEAEEMFRS ISANEKKIKYDHYLIPNALLELALLIMEODRNEAIKLLESAKQ NYKNYSBESTHFRIGALTALAMPORMEAIKLLESAKG NYKNYSBESTHFRIGALTALAMPORMEAIKLLESAKG NYKNYSBESTHFRIGAATLOKASCLENSSRSMVSSVSIL				IVLDQKDHSVFQRRGHDLIMKMKIOLSEALCGFKKTIKTLDNRI
PEKHWISLEKLPQLEALLPPRQKVRITDDMQVELKEFCPNEQN WROUREAYEEDBEDQAGWQCJT SSGCRQRPGRSDRPRPPPRRHKMVKETRYYDILGVKPSASPEE IKKAYRKLALKYHPOKNPDEGEKFKLISQAYEVLSDPKKRDVVJ QGGEQAIKEGGSSEPSSSPNDIPMFGGGGGRMARERGKNVV HQLSVTLEDLYNGVTKKLALQKNVICEKCEGVGKKGSVEKCPL CKGRGMHIHIQQIGFGMVQQIQTVCIEKCGGGERINPKDRCESS SGAKVIREKKIIEVHVEKGMKDGKILFHGEGDGEPBLBFGDVI IVLDQKDHSVFQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVTTSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIQFLVIF PEKHMLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEON WROHREAYEEDBDGPQAGVQCQTA LFAGTFESSLHEALDQCMTALDLFITNOFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDQDILLAGNMKRAGMLCQRHRKS SVTDSFSSLVNRPTLGQPTEEFIHAEVCYAKCLLQRAALTFLQD ENNVSFIKGGIKVNSYQTYKELDSLVQSSQYCKGSMHHFEGG VKLGVGAPALTLSMLPTFLIFLTFVLGTGNVMIERAEKLLKPYLNR YPKGAIFLFLAGRIEVYLGNIDAAIRFEECCEAQCHMKOFHHM CYWELMWCFTYKGWKMSYFYADLLSKENCMSKATTIYMKAAYL SMFGKEDHKPFGDDDEVELFRAVPGLKLKIGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYINNGYAVIGKQPKLTTGILEIITK AEEMLEKGPENEYSVDDECLVKLLKIGLKYLGRVQEABENPRS ISANKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSRSMVSSVSL 15586 2619 915 LPAGTFESSLHEALDQCMTALDLFLTNOFSEALSYLKPRTKESM YHSLTYATILEMQAMMTPDPQDILLAGNMKKROPMLCQRHRKS SVTDSFSSLWARPTLGQFTEEE HAEVCYAKCLLQRAALTFLQD ENNVSFIKGGIKVANGYTYKBLDSLVGSSGYCKGENHPHEGG VKLGVGAPAILTSMLPTRIFLLELFFOFSGNKDYGCLGLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVALEGARATTIYMKAAYL SMFGKEDKKPGNDAMMTPDPQDILLAGNMKKROPMLCQRHRKS SVTDSFSSLWARPTLGQFTEEE HAEVCYAKCLLQRAALTFLQD ENNVSFIKGGIKVANSYTYKBLDSLVGSSYCKGENHPHEGG VKLGVGAPNLTLSMLPTRIFLLEFFGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVALEGARATTIYMKAAYL SMFGKEDKKPGDDEVELFRAVPGLKKIKAGKLPTEKFAIRKS GYPGSSNPISLGPVALLGWHSYFYADLLSKENCNSKATYTYMKAAYL SMFGKEDKKPFGDDEVELFRAVPGLKKIKAGKLPTEKFAIRKS RYFSSNPISLGPVALLGWHSYFYADLLSKENCNSKATYTYMKAAYL SMFGKEDKKPFGDDEVELFRAVPGLKKIKAGKLPTEKFAIRKS RYFSSNPISLGPVALLGWANSYFYALLGKGRLPTEKFAIRKS PKFSSNPISLGPVALLGWANTYTORAAVICKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRQGREENFRS ISANEKKIKVDHYLINNALLELALLLMGQDRNEEAIKLLESAKQ NYKNYMSMESRTHFRIQAATCLAKSLENSSRMVSSVSL	j			LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIOFLVIF
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IKKAYRKIALKYHPDKNPDEGEKFKLISQAYEVLSDPKRDVYD QGGEQAIKEGGSGSBFSSBMDIFDMFFGGGRMARERRGKNVV HQLSVTLEDLYNGVTKKLALQKWVI CEKCEGVGGKKGSVEKCPL CKGRGHHHIQQIGPGMVQQIQTVCIECKGQGERINPKDRCESC SGAKVIREKKI IEVHVEKGMKDGQKILFHGEGDQEPELBPGDVI IVLDQKDHSVYDRGRGHDLIMKNKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMQQVELKEFCPNEQN WQQHREAYEEDBEDPQAGQVQCQTA 5585 2619 915 LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM YHSLTTATILEMQAMMTFPQDILLAGNMMKRAQMLCQRHRKS SVYDSFSSLVNRPTLGGPTEEHAEVCYAKCLLQRAALTPLQD ENNVSPIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEBGAS GHSFRSVLCVMLLLCYHFILTVGTGNVNIEBAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHMKQPHM CYWELMWCFTYKGQMKMSYFYADLLSKENCWSKATYIMKAAYL SMFGKEDHKPFGDDEVELFRAYPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYINNGVAVIGKQPKLTDGILEIITK AEEMLEKGPENESVUDDECLVKLLKGLCLKYLGRVQEREENFRS 15SANKKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLRNSSRSMVSSVSUL 14GGTPESSLVNRPTLGGFTEEFIHAEVCYAKCLLQRAALTFLQD EMNVSPIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPPTILELEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLCYHTFLTTPVLGTGNVNIEBAEKLLKPYLNR YPKGAIFLEMQAMMTDPODILLAGNMMKEAQMLCORHRKS SYTDSFSSLVNRPTLGGFTEEFIHAEVCYAKCLLQRAALTFLQD EMNVSPIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPPTILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLCYHTFLTTPVLGTGNVNIEBAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAIRFEECCEAQQHMKQFHHM CYWELMWCFTYKGQWKMSYFYADLLSKENNSKSHTYIYMKAAYL SMFGKEDHKPGDDEVELFRAVPGLKKLIAGKSLPTEKFAIRKS RRYFSSNPISLSPVPALEMMYIWNGYAVIGKQDKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQBAEENPRS ISANEKKIKYDHYLIPNALLELALLLMGDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLOGRAFLEGOREAURSLEESAKG NYKNYSMESRTHFRIQAATLOGRAFLEGOREAURSLEESAKG NYKNYSMESRTHFRIQAATLOGRAFLEGOREAURSLEESAKG NYKNYSMESRTHFRIQAATLOGRAFLEGOREAURSLEESAKG	- F 5 5 4	L		WRQHREAYEEDEDGPQAGVQCQTA
QGGEQAIKEGGSGSBFSSFMDITDMFFGGGGRMARERGGKNVV HQLSVTLEDLYNGVTKKLALQKNVI CEKCEGVGGKKGSVEKCPL CKGRGMHIHIQQIGPGMVQQIQTVCIECKGGGER INPKDRCESC SGAKVIREKKI IEVHVEKGMKDGQKILFHGEGDQFDELBEDDVI IVLDOKHSHVPQRRGHDLIMKMKQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVDEGMPIYKAPLERGILIIQFUIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WQOHREAYEEDEDGPQAGVQCQTA 5585 2619 915 LPAGTFESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMMKBAQMLCQRHRRKS SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD ENNVSTIKGGIKVRNSYQTYKELDSLVQSGVCKGENHPHFGG VKLGVGAFNLTLSMLPTRILRLEFVGFSGNKDYGLLQLBEGAS GHSFRSVLCVMLLLCYHTFLTVLCTGNVNIEBABKLLKPYLNR YPRGAIFFERGAEVIKGNGENFYRADLLSKENCWSKATYIMKAAYL SMFGKEGIEVIKGNIAATRFFEGCEAQQHMKQFHHM CYWELMMCFTYKGQWKMSYFYADLLSKENCWSKATYIMKAAYL SMFSKDDISLEVPALEMMY INGVAVIGKQPKLTDGILBIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEEMFRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEBAIKLLESAKQ NYNNYSMESRTHFRIQAATLGASLENSSRSMVSSVSL 5586 2619 915 LPAGTFESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDFQDILLAGNMMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGGFTEEIHAEVCYAKCLLQRAALTFLQD ENMVSFIKGGIKVNNSYQTYKELDSLVQSSQYCKGENHPHEGG VKLGVGAPNLTLSMLPTRILBLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTPUTGTGNVNIEBAEKLLKPYLNR YPKGAIFFLIGARIEVIKGNIDAAIRRFEECCEAQQHMKGFHHM CWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL SMFSKEDHKPFGDDEVELFRAVPGLKKLIAGKSLPTEKFAIRKS RRYFSSNPISLFVPALEMMYYMNGYAVIGKQPKLTDGILBIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS ISANEKKIKYDHYLIPRALELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFFIQAATLOKAIGKSLFTEKFAIRKS RRYFSSNPISLFVPALEMMYYMNGYAVIGKQPKLTDGILBIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS ISANEKKIKYDHYLIPRALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFFIQAATLOKASLENSSRSMYSSVSL	2284	3	1265	SSGCRQGRPGRSDRPRPPPPRRHKMVKETRYYDILGVKPSASPEE
HQLSVTLEDLYNGVTKKLLALQKNYLCEKCEGVGGKKGSVEKCPL CKGRGMHHHQQIGPGMVQQIQTVCIECKGGGERINPKDRCESC SGAKVIEKKIIEVHVEKGMKDGQKILFHGEGDQEPELEFGDUI IVLDQKOHSVPQRRGHDLIMKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEMPIYKAPLEKGILIIQFLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA LPAGTPESSLHEALDQCMTALDLEITNGFSEALSYLKPRTKESM YHSLTYATILEMQAMMTPDPQDILLAGMMKBAQMLCQRHRKS SVTDSFSSLVNRPTLGQFTPEEHAEVCYARCLLQRAALTFLQD ENNVSFIKGGIKVRNSVQTYKELDSLVQSSQYCKGENHPHFGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEBGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEBAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQPHHM CYWELMWCPTYKGQWKMSYFYADLLSKENCMSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILBIITK AEEMLEKGPENSYSVDDECLVKLLKGLCLKYLGRVQEAEBMFRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSWYSSVSL 5586 2619 915 LPAGTPESSLHEALDQCMTALDLFLTMQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRKSS SVTDSFSSLVNRPTLGGTEEEHABCVGAKCLLGRAALTFLQD ENNVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRILEFYGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVJCTGNVNIEBAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKGFHIM CYWELMWCFTYKGQWKMSYFYADLLSKENCMSKATTIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYINNGYAVIGKQPKLTDGILEITITK AEEMLEKGGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENPRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLOAKSSLENSSRMVSSVSL	1			1KKAYRKLALKYHPDKNPDEGEKFKLISQAYEVLSDPKKRDVYD
CKGRGMIHTOOIGPGMVOOIOTUCIECKGGGERINPKDRCESC GARVIREKKI EVHVEKGMKDTQCKILFHGEGDQEPELEPGDVI IVLDQKDHSVFQRRGHDLIMMKKIQLSEALGFKKTIKTLDNRI LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQPLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WRCHREAYEBDEDGPQAGVQCQTA LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGMMMKEAQMLCQRHRKKS SVYDSFSSLVMRPTLGGPTEEFHAEVCYAKCLLQRAALTFLQD ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFRLTLSMLPTRILRLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCWHLLLCYHIFTVLGTGNVNTIEBAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRFEECCEAQQHMKQFHHM CVWELMWCFTYKGQMKMSYFYADLLSKENCMSKATYIYMKAAYL SMEGKEDHKPFGDDEVELPRAVPGLKLIKJAGKSLPTEKFAIRKS RRYFSSNPISLEVPALEMMYINMGYAVIGKQPKLTDGILBIITK AEEMLEKKGPENSYSVDDECLVKLLKGLCLKYLGRVQEABENFRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSWYSSVSL LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPODILLAGNMMKEAQMLCQRHRKSS SVTDSFSSLVNRPTLGGPTEEFIHAEVCYAKCLLQRAALTFLQD ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTPLTPVLGTGNVNIEEAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRFEECCEAQQHWKQFHHM CWMELMWCFTYKGQMKMSYFYADLLSKENCMSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRS RRYFSSNPISLFVPALEMMYINNGYAVIGKQPKLTGGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENPRS ISANEKKIKYDHYLIPNALLELALLMGDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLOAKSSLENSSRWVSSVSL				QGGEQAIKEUGSGSPSFSSPMDIFDMFFGGGGRMARERRGKNVV
SGAKVIREKKI IEUHVEKGMKDOGKILFHGEGDGEPELEPGDVI IVUDOKDHSVFQRRGHDI MKMKIQLSEALCGFKKTIKTLDNRI LVITSKAGEVI KHGDLRCVRDEGMPI YKAPLEKGILI IOPLUVI P PEKHWISLEKLPOLEALLPPROKVRITDDMDQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCTTA S585 2619 915 LPAGTPESSLHEALDGCMTALDIFLTNOFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMKEAQMLCQRHRRKS SVIDSFSSLVNRPPLGGFTEEEIHAEVCYAKCLLQRAALTFLQD ENMVSFIKGGI KVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNITLSMLPTRILELLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAATRRFEECCEAQQHWKGFHHM CYWELMWCFTYKGGWKWSYFYADLLSKENCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYI WNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEBNFRS ISANEKKIKYDHYLI PNALLELALLIMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL 5586 2619 915 LPAGTPESSLHEALDQCMTALDLFTINOFSEALSYLKPRTKESM YHSLTYATILEMQAMMTPDPQDILLAGNMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD EMMVSFIKGGIKVNNSYQTYKELDSLVQSSQVCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKGFHHM CYWELMWCFTYKGQWKMSYFYADLLSKENCNSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGIKLKKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENPRS ISANEKKIKYDHYLI PNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMSSRTHFRIQAATLOAKSSLENSSRSMVSVSL	i 1			CKGPGMUTHTOOLGPGMUOOLGTAGE FORGS STREET
IVLDOKOHSVEORREHDLIMKMKIQLSEALCGFKKTIXTLDNRI LVITSKAGEVIKHGDLRCYRDEGMPIYKAPLEKGILIIQFUVIF PERHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WROHREAYEEDEDGPQAGVQCTA 558S 2619 915 LPAGTPESSLHEALDQCMTALDLFTNOFSEALSYLKFRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMKKEAQMLCQRHRKS SVTDSFSSLVNRPTLGQFTEEIHAEVCYAKCLLQRAALTFLQD ENNVSFIKGGIKVENSYQTYKELDSLVQSSQYCKGENPHFEGG VKILGVGAFNLTLSMLPFRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLCYHTFLTTVLCTGNVNIEEREKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHKQFHHM CYWELMWCFTYKGQWKMSYFYDALISKERCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKIKIAGKSLFTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEFSVDDECLVKLIKGLCLKYLGRVQEAERNFRS ISANEKKIKVDHYLIPNALLELALLIMEQDRNEEAIKLLESAKQ NYKNYSMESRTHPRIQAATLQAKSSLENSSRSMVSSVSL 5586 2619 915 LPAGTFESSLHEALDQCMTALDLFTNOFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMKKAQMLCQRHRKS SVTDSFSSLVNRPTLGGFTEEEIHAEVCYAKCLLQRAALTFLQD EMMVSFIKGGIKVRNSVQTYKELDSLVQSSQYCKGENHPHPEGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTLTPVLGTGNVNIEEAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHIM CYWELMWCFTYKGQWKMSYFYADLLSKENCNSKATYIYMKAAYL SMFGKEDHEYFGDDEVELFRAVPGLKLKAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK AEEMLEKGFENEYSVDDECLUKLLKGLCLKYLGRVQEAEENPRS ISANEKKIKYDHYLI PNALLELALLIMEQDRNEEAIKLLESAKQ NYKNYSMSSRTHFRIQAATLOAKSSLENSSRSMVSGVSL	!			SGAKVIREKKITEVHVEKGMKDGOKILEUGPGDGEDDLEBGDS
LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLEKGILIIQPLVIF PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEQN WROHREAYEEDEDGPQAGVQCTA 5585 2619 915 LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM YHSLITYATILEMQAMMTFDPQDILLAGMMMKRAQMLCQRHRRKS SVTDSFSSLVNRPTLGGFTEEEIHAEVCYAKCLLQRAALTFLQD ENNVSFIKGGIKVRNSYQTYKELDSLVQSSQVCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLBEGAS GHSFRSVLCVMLLLCYHTFLITFVLGTGNVNIEEAEKLLKPYLNR YPKGAIFLFLAGRIEVIKONIDAAIRRFEECCEAQQHWKQFHHM CYWELMWCFTYKGQWKMSYFYADLLSKENCMSKATTIYMKAAYL SMFGKEDHKPFGDDBVELFRAVPGLKKLAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWMGYAVIGKOPKLTDGILBIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL 5586 2619 915 LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM YHSLITYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGGFTEEEIHAEVCYAKCLLQRAALTFLQD EMMVSFIKGGIKVENSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTLVLGTGNVNIEEAEKKLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM CYWELMWCFTYKGQWKMSYFYADLLSKENCMSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRQCEAEENPRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMYSSVSL	1			IVLDOKDHSVFORRGHDI.IMKMKTOI.SEAL.CGEVYTTYTT DADT
PEKHWLSLEKLPPOLEALLPPROKURITDDMQVELKEFCPNEQN WRQHREAYEEDEDGPQAGVQCQTA 1	1 1			LVITSKAGEVIKHGDLRCVRDEGMPIYKAPLRKGILTOPLVTE
WROHREAYEEDEDGPOOAGVQCOTA 1 PAGTPESSLHEALDQCMTALDLFLTNOFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPODILLAGNMMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD ENNVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHMKQFHHM CVWELMMCFTYKGQWKMSYFYADLLSKENCMSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGVAVIGKQPKLTDGILBIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS ISANEKKIKYHYLIPNALLELALLLMEQDRNERAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL 5586 2619 915 LPAGTPESSLHEALDQCMTALDLFTTNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPODILLAGNMMKEAQMLCQRHRRKS SVTDSFSSLVMRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD ENNVSFIKGGIKVRNSYQTYKELDSLVQSSQYKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENPRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLOAKSSLENSSRSMVSSVSL	1			PEKHWLSLEKLPQLEALLPPRQKVRITDDMDQVELKEFCPNEON
THAUTIVATILEMQAMMTFDPQDILLTAGNMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGQFTEEETHAEVCYTAKCLLQRAALTFLQD ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLBEGAS GHSFRSVLCVMLLLCYHTPLTFVLGTGNVNIEBAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYITMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYINNGYAVIGKQPKLTUGGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLLKYLGRVQEAEENFRS ISANEKKIKYDHYLIPMALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL 5586 2619 915 LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTPDPQDILLAGNMMKEAQMLCQRHRRRS SVTDSFSSLVNRPTLGGFTEEEIHAEVCYAKCLLQRAALTFLQD ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEEAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENPRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESSTHFRIQAATLOAKSSLENSSRSMVSSVSL				WRQHREAYEEDEDGPQAGVQCQTA
YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLEGPTEESIHAEVCYAKCLLQRAALTFLQD ENMVSFIKGGIKVNNSYQTYKELDSLVQSSQYCKGENHPHFGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLBEGAS GHSFRSVLCVMLLLCYHTPLTFVLGTGNVNIEBAEKLLKPYLNR YPRGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHMKQFHHM CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSRPISLEVPALEMMYINNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEABENFRS ISANBKKIKYDHYLIPNALLELALLIMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL 5586 2619 915 LPAGTPESSLHEALDQCMTALDLIFLTNQFSEALSYLKPRTKESM YHSLTYATILEMQAMMTFDPQDILLAGNMMKEAQMLCQRHRRKS SVTDSFSSLVNRPTLGQFTEEEIHAEVCYAKCLLQRAALTFLQD ENMVSFIKGGIKVRNSYQTYKELDSLVQSSQYCKGENHPHFEGG VKLGVGAFNLTLSMLPTRILRLLEFVGFSGNKDYGLLQLEEGAS GHSFRSVLCVMLLLCYHTFLTFVLGTGNVNIEBAEKLLKPYLNR YPKGAIFLFLAGRIEVIKGNIDAAIRRFEECCEAQQHWKQFHHM CYWELMWCFTYKGQWKMSYFYADLLSKENCNSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS ISANEKKIKYDHYLIPNALLELALLIMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLOAKSSLENSSRSMVSSVSL	5585	2619	915	LPAGTPESSLHEALDQCMTALDLFLTNQFSEALSYLKPRTKESM
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CYWELMWCFTYKGQWKMSYFYADLLSKENCWSKATYIYMKAAYL SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL			1	YPKGAIFLFLAGRIEVIKGNIDA A IDD PERCORA COMMUNICATION
SMFGKEDHKPFGDDEVELFRAVPGLKLKIAGKSLPTEKFAIRKS RRYFSSNPISLPVPALEMMYY WNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENFRS ISANEKKIKYDHYLI PNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLOAKSSLENSSRSMVSSVSL			,	CYWELMWCFTYKGOWKMSYFYADI.I.SKENCWGKATYTYWWA NOT
RRYFSSNPISLPVPALEMMYIWNGYAVIGKQPKLTDGILEIITK AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENPRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLQAKSSLENSSRSMVSSVSL			İ	SMFGKEDHKPFGDDEVELFRAVPGI.KI.KIAGKSI.DTEKEATOVC
AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVQEAEENPRS ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLOAKSSLENSSRSMVSSVSL		1	1	RRYFSSNPISLPVPALEMMYIWNGYAVIGKOPKI.TDGILETTTV
ISANEKKIKYDHYLIPNALLELALLLMEQDRNEEAIKLLESAKQ NYKNYSMESRTHFRIQAATLOAKSSLENSSRSMVSSVSL			į	AEEMLEKGPENEYSVDDECLVKLLKGLCLKYLGRVOEAEENFRS
NYKNYSMESRTHFRIQAATLOAKSSLENSSRSMVSSVSL			1	ISANEKKIKYDHYLIPNALLELALLLMEODRNEEAIKLLESAKO
148 SSAVPDGAVGRPVAVAVGGPPHSCRCRPCCIMANTGUTGCTCA	5507	7760		NYKNYSMESRTHFRIQAATLOAKSSLENSSRSMVSSVSL
- COLING CONTROL OF THE CASE CONTROL OF THE CA	558/	1 \98	148	SSAVPDGAVGRPVAVAVGGPPHSCRCRPCCLMAAIGVHLGCTSA

1	1 B. 17 - 1	1 53/243	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *≈Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence	1	\=possible nucleotide insertion)
	 	 	CVAVYKDGRAGVVANDAGDRVTPAVVAYSENEEIVGLAAKOSRI
	•		RNISNTVMKVKQILGRSSSDPQAQKYIAESKCLVIEKNGKLRYE
1	l .	1	IDTGEETKFVNPEDVARLIFSKMKETAHSVLGSDANDVVITVPF
1		{	DFGEKQKNALGEAARAAGFNVLRLIHEPSAALLAYGIGQDSPTG
			KSNILVFKLGGTSLSLSVMEVNSGIYRVLSTNTDDNIGGAHFTE
	1	(TLAQYLASEFQRSFKHDVRGNARAMMKLTNSAEVAKHSLSTLGS
ļ		ļ	ANCFLDSLYEGQDFDCNVSRARFELLCSPLFNKCIEAIRGLLDQ
		1	NGFTADDINKVVLCGGSSRIPKLQQLIKDLFPAVELLNSIPPDE
İ			VIPIGAAIEAGILIGKENLLVEDSLMIECSARDILVKGVDESGA
			SRFTVLFPSGTPLPARRQHTLQAPGSISSVCLELYESDGKNSAK
	Į	ł	EETKFAQVVLQDLDKKENGLRDILAVLTMKRDGSLHVTCTDOET
	1	1	GKCEAISIEIAS
5588		589	TPPPPEOAMVAATVAAAWLLLWAAACAOOEODFYDFKAVNIRGK
מסכנ	3	203	
			LVSLEKYRGSVSLVVNVASECGFTDQHYRALQQLQRDLGPHHFN
		1	VLAFPCNQFGQQEPDSNKEIESFARRTYSVSFPMFSKIAVTGTG
		1	AHPAFKYLAQTSGKEPTWNFWKYLVAPDGKVVGAWDPTVSVEEV
	1	1	RPQITALVRKLILLKREDL
5589	1884	553	LRQAWHEGGIGQTDKERGAAALPGEEGDPTRGRSLGRASWESGS
Ì		ĺ	PRRPRSPFSSFLPRPICLSLEARPCSIEDRRNWSLIGRPGAPAS
1			GLNRSSGLWLGPDRCRPRSRCSCRVMENPSPAAALGKALCALLL
			ATLGAAGOPLGGESICSARAPAKYSITFTGKWSOTAFPKOYPLF
1	1		RPPAOWSSLLGAAHSSDYSMWRKNOYVSNGLRDFAERGEAWALM
			KEIEAAGEALOSVHAVFSAPAVPSGTGOTSAELEVORRHSLVSF
ļ	1		VVRIVPSPDWFVGVDSLDLCDGDRWREQAALDLYPYDAGTDSGF
			·-
ļ		I	TFSSPNFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARV
1			TLLRLRQSPRAFIPPAPVLPSRDNEIVDSASVPETPLDCEVSLW
1	{ ·		SSWGLCGGHCGRLGTKSRTRYVRVQPANNGSPCPELEEEAECVP
		L	DNCV
5590	72	896	LCSSGALRLLPAMVAWRSAFLVCLAFSLATLVQRGSGDFDDFNL
])	J	EDAVKETSSVKQPWDHTTTTTNRPGTTRAPAKPPGSGLDLADA
[LDDQDDGRRKPGIGGRERWNHVTTTTKRPVTTRAPANTLGNDFD
ļ			LADALDDRNDRDDGRRKPIAGGGGFSDKDLEDIVGGGEYKPDKG
1	1		KGDGRYGSNDDPGSGMVAEPGTIAGVASALAMALIGAVSSYISY
ł	1		QQKKFCFSIQQGLNADYVKGENLEAVVCEEPQVKYSTLHTQSAE
ł	ķ		PPPPPBPARI
5591	68	1494	AGSSRRAAAERLLVSAGCRSLAGRASGVLLLPAELLPGEEEAMA
2331	""	1434	
1			LRVTRNSKINAENKAKINMAGAKRVPTAPAATSKPGLRPRTALG
			DIGNKVSEQLQAKMPMKKEAKPSATGKVIDKKLPKPLEKVPMLV
			PVPVSEPVPEPEPEPEPEPVKEEKLSPEPILVDTASPSPMETSG
	1		CAPAEEDLCQAFSDVILAVNDVDAEDGADPNLCSEYVKDIYAYL
			RQLEEEQAVRPKYLLGREVTGNMRAILIDWLVQVQMKFRLLQET
1			MYMTVSIIDRFMQNNCVPKKMLQLVGVTAMFIASKYEEMYPPEI
	1	1	GDFAFVTDNTYTKHQIRQMEMKILRALNFGLGRPLPLHFLRRAS
1	1		KIGEVDVEQHTLAKYLMELTMLDYDMVHFPPSQIAAGAFCLALK
1	1		ILDNGEWTPTLQHYLSYTEESLLPVMQHLAKNAAMVNQGLTKHM
1			TVKNKYATSKHAKISTLPQLNSALVQDLAKAVAKV
5592	242	924	YGESKDWNQKDLLSALVLTTVNCLPTPIMAKSAEVKLAIFGRAG
"""	2.7.4	724	VGKSALVVRFLTKRFIWEYDPTLESTYRHOATIDDEVVSMEILD
ļ	1		· · · · · · · · · · · · · · · · · · ·
1	1		TAGQEDTIQREGHMRWGEGFVLVYDITDRGSFEEVLPLKNILDE
	1		IKKPKNVTLILVGNKADLDHSRQVSTEEGEKLATELACAFYECS
)	1		ACTGEGNITEIFYELCREVRRRRMVQGKTRRRSSTTHVKQAINK
L		1	MLTKISS
5593	3	1113	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
1	1		SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
1	1	1	DVDLNHYRIGKIEGFEVLKKVKTLCLRONLIKCIENLEELOSLR
[BLDLYDNQIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK
	1		· · · · · · · · · · · · · · · · · · ·
J	}		KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE
1	1	1	SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
1	1		ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ
·L	L	1	EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV

SEQ	Predicted	Predicted end	Amino acid recoment containing signal
	1	•	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
[amino acid	i	
1		residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ì	sequence		\=possible nucleotide insertion)
			MLALPSVRQIDATFVRF
5594	3	1113	<u> </u>
3334	1	****	HASGGRAANMAAERGAGQQQSQEMMEVDRRVESEESGDEEGKKH
1			SSGIVADLSEQSLKDGEERGEEDPEEEHELPVDMETINLDRDAE
1			DVDLNHYRIGKIEGFEVLKKVKTLCLRQNLIKCIENLEELQSLR
1	i		ELDLYDNQIKKIENLEALTELEILDISFNLLRNIEGVDKLTRLK
1	}		KLFLVNNKISKIENLSNLHQLQMLELGSNRIRAIENIDTLTNLE
ł	1		SLFLGKNKITKLQNLDALTNLTVLSMQSNRLTKIEGLQNLVNLR
1	į.	1	
1	J		ELYLSHNGIEVIEGLENNNKLTMLDIASNRIKKIENISHLTELQ
l .	l		EFWMNDNLLESWSDLDELKGARSLETVYLERNPLQKDPQYRRKV
L	<u> </u>		MLALPSVRQIDATFVRF
5595	3	1476	ARWNGRWVQVPAWPGPGCGTNASGERQRQLPRAWRPVGRTLGSE
1			PIALAWSPPLYLFPIPLPSWAVSQPTPTLGTMFADLDYDIEEDK
1			LGIPTVPGKVTLQKDAQNLIGISIGGGAQYCPCLYIVQVFDNTP
1			1
1			AALDGTVAAGDEITGVNGRSIKGKTKVEVAKMIQEVKGEVTIHY
1			NKLQADPKQGMSLDIVLKKVKHRLVENMSSGTADALGLSRAILC
l .			NDGLVKRLEELERTAELYKGMTEHTKNLLRAFYELSQTHRAFGD
i			VFSVIGVREPQPAASEAFVKFADAHRSIEKFGIRLLKTIKPMLT
1			DLNTYLNKAIPDTRLTIKKYLDVKFEYLSYCLKVKEMDDEEYSC
1			IALGEPLYRVSTGNYEYRLILRCRQEARARFSQMRKDVLEKMEL
1		!	LDQKHVQDIVFQLQRLVSTMSKYYNDCYAVLRDADVFPIEVDLA
			HTTLAYGLNQEEFTDGEEEEEEEDTAAGEPSRDTRGAAGPLDKG
ſ			GSWCDS
5596	698	219	GAVLAPSSLPAAELAAQGESQSLEDLSNTSRPTSEVYKISFIFP
1			NGDKYDGDCTRTSSGIYERNGIGIHTTPNGIVYTGSWKDDKMNG
1			FGRLEHFSGAVYEGQFKDNMFHGLGTYTFPNGAKYTGNFNENRV
1			1
			KGEGEYTHIQGTRMDVVTFHFTSCSQT
5597	3	731	ISCKMAADGQSSLPASWRSVTLTHVEYPAGDLSGHLLAYLSLSP
1			VFVIVGFVTLIIFKRELHTISFLGGLALNEGVNWLIKNVIQEPR
1			PCGGPHTAVGTKYGMPSSHSQFMWFFSVYSFLFLYLRMHQTNNA
1			RFLDLLWRHVLSLGLLAVAFLVSYSRVYLLYHTWSOVLYGGIAG
1			GLMAIAWFIFTQEVLTPLFPRIAAWPVSEFFLIRDTSLIPNVLW
1			The state of the s
F	<u> </u>	<u></u>	FEYTVTRAEARNRQRKLGTKLQ
5598	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
1			VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
1			DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG
1			EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
1			IKCALCSPHSQSLFHSPEREVLERDLVLPLLCXDYCKEFFYTCR
1			GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
1			
[1		QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
1			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
1			SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
1			NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
			ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
1			TNQPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS
1			
1			SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
1			YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG
1			HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
1	1		CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5599	326	2440	GIGPIAASFIFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCAL
1	1		
1	(VPLLGSGVPPHPPAPSPCCSGQTMLKMLSFKLLLLAVALGFFEG
1			DAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQLELLSGG
[EMLCGGFYPRLSCCLRSDSPGLGRLENKIFSVTNNTECGKLLEE
1	Į		IKCALCSPHSQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCR
1			GHIPGFLQTTADEFCFYYARKDGGLCFPDFPRKQVRGPASNYLD
Į)
1			QMEEYDKVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDGSQR
1			LFILEKEGYVKILTPEGEIFKEPYLDIHKLVQSGIKGGDERGLL
ļ			SLAFHPNYKKNGKLYVSYTTNQERWAIGPHDHILRVVEYTVSRK
1			NPHQVDLRTARVFLEVAELHRKHLGGQLLFGPDGFLYIILGDGM
ł			ITLDDMEEMDGLSDFTGSVLRLDVDTDMCNVPYSIPRSNPHFNS
!			TNOPPEVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRS
L	L	L	THAT THE THE PROPERTY OF THE P

SEO	Predicted	Predicted end	There are a factor of the same and the same
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
	† <u>-</u>		SARILQIIKGKDYESEPSLLEFKPFSNGPLVGGFVYRGCQSERL
		1	YGSYVFGDRNGNFLTLQQSPVTKQWQEKPLCLGTSGSCRGYFSG
1			HILGFGEDELGEVYILSSSKSMTQTHNGKLYKIVDPKRPLMPEE
1		Į.	
	1000	ļ	CRATVQPAQTLTSECSRLCRNGYCTPTGKCCCSPGWEGDFCRTG
5600	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE
ļ		1	EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
			SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
		1	FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
1	J	1	AVAPPAPPSSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
1		1	TFYHPTINVPPRHALKWIRPQTSE
5601	1977	1244	SLRVLSGHLMQTRDLVQPDKPASPKFIVTLDGVPSPPGYMSDQE
			EDMCFEGMKPVNQTAASNKGLRGLLHPQQLHLLSRQLEDPNGSF
			SNAEMSELSVAQKPEKLLERCKYWPACKNGDECAYHHPISPCKA
1			
1			FPNCKFAEKCLFVHPNCKYDAKCTKPDCPFTHVSRRIPVLSPKP
			AVAPPAPPSSQLCRYFPACKKMECPFYHPKHCRFNTQCTRPDC
-			TFYHPTINVPPRHALKWIRPQTSE
5602	246	766	YHTSCTVWRTAKEALENTEVPVGCLMVYNNEVVGKGRNEVNQTK
			NATRHAEMVAIDQVLDWCRQSGKSPSEVFEHTVLYVTVEPCIMC
1	1		AAALRLMKIPLVVYGCQNERFGGCGSVLNIASADLPNTGRPFQC
	1	Į.	IPGYRAEEAVEMLKTFYKQENPNAPKSKVRKKECQQILNMF
5603	1	565	FRGRTPISGGERGCAQYPIPATPARSGENRTMPGAGDGGKAPAR
	İ		WLGTGLLGLFLLPVTLSLEVSVGKATDIYAVNGTEILLPCTFSS
1			CFGFEDLHFRWTYNSSDAFKILIEGTVKNEKSDPKVTLKDDDRI
	1		TLVGSTKEKRNNISIVLRDLEFSDTGKYTCHVKNPKENNLOHHA
1		1	TIFLOVVDRRMO
	1		111 DQ V DAMANQ
5604	1	1506	EDITEDACI I KI OBUERUMOGEDDURDURGUGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
5604	1	1506	EDIFPAQLIKLQRHERVWQQEPPVRDHRSWGGSGAGGVAGREWT
5604	1	1506	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG
5604	1	1506	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG GGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ
5604	1	1506	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR
5604	1	1506	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG GGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV
5604	1	1506	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG GGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI
5604	1	1506	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQFSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE
5604	1	1506	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG GGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI
5604	1	1506	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQFSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE
5604	1	1506	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQFSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG
5604	1	1506	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL
5604	1	1506	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV
5604			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLFYPECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN
	35	1506	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGGDFG GGDFGGGDFGGGDFGGGGSFGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFFTLELQFSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLONHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVPQ
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQFSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGFGTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNNFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVPQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGFFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GDFGGGDFGGGDFGGGGSFGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFFTLELQFSLIVKVVRRRLAEKRIGYR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGFFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GDFGGGDFGGGDFGGGGSFGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFFTLELQFSLIVKVVRRRLAEKRIGYR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELQRCAQKSPRVAP GSARPWFALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQFSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVINTQVIDG
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGKKPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVINTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GDFGGGDFGGGDFGGGGSFGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFFTLELQFSLIVKVVRRRLAEKRIGYR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNNFVGLEDRKYEYLMTLHGVVNESTVCIMGHERRQTINL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRRLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGFREQ KFRLKRCGLERRVYLVEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL
5605	35	1821	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKS PRVAP GSARPWFALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPBSTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT
			DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPBLLRELQRLHVTHTVRKLHYGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFFLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTFGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK
5605	35	1821	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQFSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNNIFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESG GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPBLLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISBEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA
5605	35	1821	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQFSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNNFVGLEDRKVEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLYLLVGVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGFRREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCFGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEETCEKLKGLIQRQVOMCKRNEVMDSVRRGAQLA IEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA
5605	35	1821	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQFSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNNIFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESG GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQPLELRP GEYRVLLCVDIGETRGGGHRPBLLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISBEETCEKLKGLIQRQVQMCKRNLEVMDSVRRGAQLA
5605	35	1821	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQFSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNNFVGLEDRKVEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLYLLVGVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGFRREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCFGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEETCEKLKGLIQRQVOMCKRNEVMDSVRRGAQLA IEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA
5605	35	1821	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNNFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCPRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGKKPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLYSVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISBEETCEKLKGLIQRQVQMCKRNLEFWMDSVRRGAQLA IEECQYQFRNRRWNCSTLDSLFVFGKVVTQGTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG
5605	35	1821	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFFTLELQFSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNNFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLINL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPGGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFFLKRCGLERRVYLVEEHGSVNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWIYLAK LSSVGSISBEETCEKLKGLIQRQVMCKRNLEVMDSVRGAQLA IEECQYQFRRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTIMRVEC KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRRVG
5605	35	1821	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGSSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGMFPTLELQPSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNHFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLNL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPQGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKS PRVAP GSARPWFALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPCEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFRLKRCGLERRVYLVEEHGSVHNLSLPESTLLQAVINTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLWQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWLYLAK LSSVGSISEEETCERLKGLIQRQVQMCKRNLEFWDSVRGAQLA IEECQYQFRNRRWNCSTLDSLPVFGKVVTQGTREAAFVXAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVRERSKGASSRALMNLHNNEAGRKAILTHMRVEC KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKPDGATEVEPRRVG SSRALVPRNAQFKPHTDEDLVYLEPSPDFCBQDMRSGVLGTRGR
5605	35	1821	DQGQVALGGHYMAEGEGYFAMSEDELACSPYIPLGGDFGGDFG GGDFGGGDFGGGDFGGGGSFGGHCLDYCESPTAHCNVLNWEQVQ RLDGILSETIPIHGRGNFFTLELQFSLIVKVVRRRLAEKRIGVR DVRLNGSAASHVLHQDSGLGYKDLDLIFCADLRGEGEFQTVKDV VLDCLLDFLPEGVNKEKITPLTLKEAYVQKMVKVCNDSDRWSLI SLSNNSGKNVELKFVDSLRRQFEFSVDSFQIKLDSLLLFYECSE NPMTETFHPTIIGESVYGDFQEAFDHLCNKIIATRNPEEIRGGG LLKYCNLLVRGFRPASDEIKTLQRYMCSRFFIDFSDIGEQQRKL ESYLQNNFVGLEDRKYEYLMTLHGVVNESTVCLMGHERRQTLINL ITMLAIRVLADQNVIPNVANVTCYYQPAPYVADANFSNYYIAQV QPVFTCQQQTYSTWLPCN SQRSCFRSPSSPAPPWARCSNPDSRTGGVPVPRAWSAGGPALGL MAAPVRLGRKRPLPACPNPLFVRWLTEWRDEATRSRHRTRFVFQ KALRSLRRYPLPLRSGKEAKILQHFGDGLCRMLDERLQRHRTSG GDHAPDSPSGENSPAPGGRLAEVQDSSMPVPAQPKAGGSGSYWP ARHSGARVILLVLYREHLNPNGHHFLTKEELLQRCAQKSPRVAP GSARPWPALRSLLHRNLVLRTHQPARYSLTPEGLELAQKLAESE GLSLLNVGIGPKEPPGEETAVPGAASAELASEAGVQQQPLELRP GEYRVLLCVDIGETRGGGHRPELLRELQRLHVTHTVRKLHVGDF VWVAQETNPRDPANPGELVLDHIVERKRLDDLCSSIIDGRFREQ KFFLKRCGLERRVYLVEEHGSVNLSLPESTLLQAVTNTQVIDG FFVKRTADIKESAAYLALLTRGLQRLYQGHTLRSRPWGTPGNPE SGAMTSPNPLCSLLTFSDFNAGAIKNKAQSVREVFARQLMQVRG VSGEKAAALVDRYSTPASLLAAYDACATPKEQETLLSTIKCGRL QRNLGPALSRTLSQLYCSYGPLT GRSRCPGFGARGGTMSPRSCLRSLRLLVFAVFSAAASNWIYLAK LSSVGSISBEETCEKLKGLIQRQVMCKRNLEVMDSVRGAQLA IEECQYQFRRRWNCSTLDSLPVFGKVVTQGTREAAFVYAISSA GVAFAVTRACSSGELEKCGCDRTVHGVSPQGFQWSGCSDNIAYG VAFSQSFVDVRERSKGASSSRALMNLHNNEAGRKAILTIMRVEC KCHGVSGSCEVKTCWRAVPPFRQVGHALKEKFDGATEVEPRRVG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	1	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
\	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i			
Ī	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
5607	521	141	PPVCNPAEAMPSPGTVCSLLLLGMLWLDLAMAGSSFLSPEHQRV
	1		QQRKESKKPPAKLQPRALAGWLRPEDGGQAEGAEDELEVRFNAP
1	1		FDVGIKLSGVQYQQHSQALGKFLQDILWEEAKEAPADK
5608	2	983	WFQSPLRQADPGPPRHTLFMDFVAGAIGGVCGDAVGYPLDTVKV
		i	RIQTEPKYTGIWHCVRDTYHRBRVWGFYRGLLLPVCTVSLVSSE
			VFGTYRHCLAHICRLRFGNPDAKPTKADITLSGCASGLVRVFLT
	Į.		SPTEVAKVRLQTQTQAQKQQRRLSASGPLAVPPMCPVPPACPEP
	ì	j	KYRGPLHCLATVAREEGLCGLYKGSSALVLRDGHSFATYFLSYA
1		1	
1		i	VLCEWLSPAGHSRPDVPGVLVAGGCAGVLAWAVATPMDVIKSRL
		1	QADGQGQRRYRGLLHCMVTIVREEGPRVLFKGLVLNCCRAFPVN
	1		MVVFVAYBAVLRLARGLLT
5609	1628	304	AKGVWVLPSPPPRPGRGALVSGSGLRRGRSGTSWRPRRMNHKSK
2009	1040	307	•
1		1	KRIREAKRSARPELKDSLDWTRHNYYESFSLSPAAVADNVERAD
1		1	ALQLSVEEFVERYERPYKPVVLLNAQEGWSAQEKWTLERLKRKY
I			RNQKFKCGEDNDGYSVKMKMKYYIEYMESTRDDSPLYIFDSSYG
1			EHPKRRKLLEDYKVPKFFTDDLFQYAGEKRRPPYRWFVMGPPRS
1		1	GTGIHIDPLGTSAWNALVQGHKRWCLFPTSTPRELIKVTRDEGG
Ì			NOODEAITWFNVIYPRTQLPTWPPEFKPLEILOKPGETVFVPGG
			1
	Į.		WWHVVLNLDTTIAITQNFASSTNFPVVWHKTVRGRPKLSRKWYR
1			ILKQEHPELAVLADSVDLQESTGIASDSSSDSSSSSSSSSSDSD
Į.			SECESGSEGDGTVHRRKKRRTCSMVGNGDTTSQDDCVSKERSSS
			R
5610	54	1196	LERTPASADMAWTKYOLFLAGLMLVTGSINTLSAKWADNFMAEG
3010] 34	1190	CGGSKEHSFOHPFLOAVGMFLGEFSCLAAFYLLRCRAAGOSDSS
1			
1	1		VDPQQPFNPLLFLPPALCDMTGTSLMYVALNMTSASSFQMLRGA
	1	ſ	VIIFTGLFSVAFLGRRLVLSQWLGILATIAGLVVVGLADLLSKH
		1	DSQHKLSEVITGDLLIIMAQIIVAIQMVLEEKFVYKHNVHPLRA
			VGTEGLFGFVILSLLLVPMYYIPAGSFSGNPRGTLEDALDAFCQ
-	ì		VGQQPLIAVALLGNISSIAFFNFAGISVTKELSATTRMVLDSLR
	:		_ ==
	1	1	TVVIWALSLALGWEAFHALQILGFLILLIGTALYNGLHRPLLGR
į.	1		LSRGRPLAEESEQERLLGGTRTPINDAS
5611	2	577	FVLPNRLGIPGSTFRGPGACASSSSLAASAKPGAGGSPALAMSG
		ļ	ELSNRFQGGKAFGLLKARQERRLABINREFLCDQKYSDEENLPE
İ	l,	1	KLTAFKEKYMBFDLNNEGEIDLMSLKRMMEKLGVPKTHLEMKKM
i.	1	J	
1			ISEVTGGVSDTISYRDFVNMMLGKRSAVLKLVMMFEGKANESSP
	<u> </u>	L	KPVGPPPERDIASLP
5612	1	721	ASRDGYMDATIAPHRIPPEMPQYGEENHIFELMQAMWLCKHLNS
1			SLLTLENLILNEFSYTATEARRLYLQRKTVPSALLVQLIQERLA
1	1		EEDCIKQGWILDGIPETREQALRIQTLGITPRHVIVLSAPDTVL
1		1	
1			IERNLGKRIDPQTGEIYHTTFDWPPESEIQNRLMVPEDISELET
1			AQKLLEYHRNIVRVIPSYPKILKVISADQPCVDVFYQALTYVQS
	1		NHRTNAPFTPRVLLLGPVGS
5613	115	1279	RGVDPALRRAEKMLPLSIKDDEYKPPKFNLFGKISGWFRSILSD
1			KTSRNLFFFLCLNLSFAFVELLYGIWSNCLGLISDSFHMFFDST
1			
1			AILAGLAASVISKWRDNDAFSYGYVRAEVLAGFVNGLFLIFTAF
			FIFSEGVERALAPPDVHHERLLLVSILGFVVNLIGIFVFKHGGH
I			GHSHGSGHGHSHSLFNGALDQAHGHVDHCHSHEVKHGAAHSHDH
			AHGHGHFHSHDGPSLKETTGPSROILOGVFLHILADTLGSIGVI
1			ASAIMMONFGLMIADPICSILIAILIVVSVIPLLRESVGILMOR
1		1	· · · · · · · · · · · · · · · · · · ·
}	,	1	TPPLLENSLPQCYQRVQQLQGVYSLQEQHFWTLCSDVYVGTLKL
		1	IVAPDADARWILSQTHNIFTQAGVRQLYVQIDFAAM
5614	3	1268	LLSRNBHACPLQAGLGLTQRKPKAIRGREGRATNQGQGETQNER
		1	APWGARORLGVMAELQOLQEFEIPTGREALRGNHSALLRVADYC
1		1	EDNYVOATDKRKALEETMAFTTOALASVAYOVGNLAGHTURMLD
I		Ì	
I			LQGAALRQVEARVSTLGQMVNMHMEKVARREIGTLATVQRLPPG
			QKVIAPENLPPLTPYCRRPLNFGCLDDIGHGIKDLSTQLSRTGT
	1		LSRKSIKAPATPASATLGRPPRIPEPVHLPVVPDGRLSAASSAS
1		ţ	SLASAGSAEGVGGAPTPKGOAAPPAPPLPSSLDPPPPPAAVEVF
1			QRPPTLEELSPPPPDEELPLPLDLPPPPPPLDGDELGLPPPPPGF
ļ			1 7
L		L	GPDEPSWVPASYLEKVVTLYPYTSQKDNELSFSEGTVICVTRRY

SEQ	Predicted	Predicted end	Dring agid compet and
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
——	Dequence		SDGWCEGVSSEGTGFFPGNYVEPSC
5615	9	1558	
3313	1	1336	ALGRRRPGDPREMEAAATPAAAGAARREELDMDVMRPLINEONF
			DGTSDEEHEQELLPVQKHYQLDDQEGISFVQTLMHLLKGNIGTG
		İ	LLGLPLAIKNAGIVLGPISLVFIGIISVHCMHILVRCSHFLCLR
1			FKKSTLGYSDTVSFAMEVSPWSCLQKQAAWGRSVVDFFLVITQL
			GFCSVYIVFLAENVKQVHEGFLESKVFISNSTNSSNPCERRSVD
ţ			LRIYMLCFLPFIILLVFIRELKNLFVLSFLANVSMAVSLVIIYQ
			YVVRNMPDPHNLPIVAGWKKYPLFFGTAVFAFEGIGVVLPLENQ
1	1		MKESKRFPQALNIGMGIVTTLYVTLATLGYMCFHDEIKGSITLN
			LPQDVWLYQSVKILYSFGIFVTYSIQFYVPAEIIIPGITSKFHT
			KWKQICEFGIRSFLVSITCAGAILIPRLDIVISFVGAVSSSTLA
			LILPPLVEILTFSKEHYNIWMVLKNISIAFTGVVGFLLGTYITV
5616	1	719	EEIIYPTPKVVAGTPQSPFLNLNSTCLTSGLK
	_	'13	DDFVRCGPQSAAMGASARLLRAVIMGAPGSGKGTVSSRITTHFE
			LKHLSSGDLLRDNMLRGTEIGVLAKAFIDQGKLIPDDVMTRLAL
			HELKNLTQYSWLLDGFPRTLPQAEALDRAYQIDTVINLNVPFEV
ł			IKQRLTARWIHPASGRVYNIEFNPPKTVGIDDLTGEPLIQREDD KPETVIKRLKAYEDQTKPVLEYYQKKGVLETFSGTETNKIWPYV
			YAFLQTKVPQRSQKASVTP
5617	176	765	PWRGRGSRPRGAGAMAEEQVNRSAGLAPDCEASATAETTVSSVG
	1	703	TCEAAGKSPEPKDYDSTCVFCRIAGRQDPGTELLHCENEDLICF
			KDIKBAATUUVIJUBKUUTOMODELBYDOUBI IIING MINGUEDBICK
İ			KDIKPAATHHYLVVPKKHIGNCRTLRKDQVELVENMVTVGKTIL ERNNFTDFTNVRMGFHMPPFCSISHLHLHVLAPVDQLGFLSKLV
1			YRVNSYWFITADHLIEKLRT
5618	3	1692	YLNYINLKSENKLSGKEDLWEKLQYLWKSTLNLPEDLLRVPDES
		1032	LFLNSGGDSLKSIRLLSEIEKLVGTSVPGLLEIILSSSILEIYN
j			HILQTVVPDEDVTFRKSCATKRKLSNINGERASGTSLHQKAIMT
1			FTCHNEINAFVVLSRGSQILSLNSTRFLTKLGHCSSACPSDSVS
1			QTNIQNLKGLNSPVLIGKSKDPSCVAKVSEEGKPAIGTQKMELH
1 .			VRWRSDTGKCVDASPLVVIPTFDKSSTTVYIGSHSHRMKAVDFY
1			SGKVKWEQILGDRIESSACVSKCGNFIVVGCYNGLVYVLKSNSG
1			EKYWMFTTEDAVKSSATMDPTTGLIYIGSHDQHAYALDIYRKKC
1			VWKSKCGGTVFSSPCLNLIPHHLYFATLGGLLLAVNPATGNVIW
			KHSCGKPLFSSPQCCSQYICIGCVDGNLLCFTHFGEQVWQFSTS
			GPIFSSPCTSPSEQKIFFGSHDCFIYCCNMKGHLQWKFETTSRV
ļ			YATPFAFHNYNGSNEMLLAAASTDGKVWILESQSGQLQSVYELP
1			GEVFSSPVVLESMLIIGCRDNYVYCLDLLGGNQK .
5619	2160	1477	DSPVLPTSGNVISTAQPAQPWSAVEAALRSLGSPPGAGRGCPCP
			AQSLHSHQLAAWDPLKPSLRSYPPHLLQHPQLRSLTASSGHLGR
			RSCPQPRPLEELLRAGSSTRPQPLTSSCCGMSCMYSFLGHCSVL
			LWGTKGRGSGSPSSPGCCLHPPAQHSQDLPLVHVDVGWQPPLGP
			TVGLRPGLLGERQRGALRAGDPQCQCPLPATVREDLGVPSPWAA
	<u> </u>		ECSPPATP
5620	930	182	PLPPPTLAMFLTRSEYDRGVNTFSPEGRLFQVEYAIEAIKLGST
1			AIGIQTSEGVCLAVEKRITSPLMEPSSIEKIVEIDAHIGCAMSG
			LIADAKTLIDKARVETQNHWFTYNETMTVESVTQAVSNLALQFG
			EEDADPGAMSRPFGVALLFGGVDEKGPQLFHMDPSGTFVQCDAR
			AIGSASEGAQSSLQEVYHKSMTLKEAIKSSLIILKQVMEEKLNA
L			TNIELATVQPGQNFHMFTKEELEEVIKDI
5621	3	819	VVEFVEYTATDANVKNESLSSVQQLGIKMTVRYGKFLSLLKDGA
			ENDLTWVLKHCERFLKQQQTSIKSSLLCLQGNYAGHDWFVSSLF
			MIMLGDKEKTFQFLHQFSRLLTSAFLWLPRLHISSYLPNDTVES
] :			GIHPVYFCSTHYIEMLLKAELPLVFSAFHMSGFAPSQICLQWIT
			QCFWNYLDWIEICHYIATCVFLGPDYQVYICIAVFKHLOODILO
			HTQTQDLQVFLKEEALHGFRVSDYFEYMEILEQNYRTVLLRDMR
			NIRLOST
5622	1122	456	AASTKDAVSRKRSHSASEKSGTGTSISKRLNMNPQIRNPMKAMY
			PGTFYFQFKNLWEANDRNETWLCFTVEGIKRRSVVSWKTGVFRN
			QVDSETHCHAERCFLSWFCDDILSPNTKYQVTWYTSWSPCPDCA
			GEVAEFLARHSNVNLTIFTARLYYFQYPCYQEGLRSLSQEGVAV
	·		The state of the s

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	D-Dedeline, Managaragine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			EIMDYEDFKYCWENFVYNDNEPFKPWKGLKTNFRLLKRRLRESL
			Q
5623	3	954	FLPFFIRAPKISRNGQWLFTFTTPFPFANKALPGWEGIVPACFW
1			RKKILTPSTGTMELLQVTILFLLPSICSSNSTGVLEAANNSLVV
			TTTKPSITTPNTESLQKNVVTPTTGTTPKGTITNELLKMSLMST
			ATFLTSKDEGLKATTTDVRKNDSIISNVTVTSVTLPNAVSTLQS
			SKPKTETQSSIKTTEIPGSVLQPDASPSKTGTLTSIPVTIPENT
			SQSQVIGTEGGKNASTSATSRSYSSIILPVVIALIVITLSVFVL
		ł	VGLYRMCWKADPGTPENGNDQPQSDKESVKLLTVKTISHESGEH
			SAOGKTKN
5624	159	898	PGVAAAAGALPQYHGPAPALVSCRRELSLSAGSLQLERKRRDFT
1			SSGSRKLYFDTHALVCLLEDNGFATQQAEIIVSALVKILEANMD
1		İ	TUVVDMUTVMOORITEOOUMGOTARUVDMITV BUGBBOARA
1	1	1	IVYKDMVTKMQQEITFQQVMSQIANVKKDMIILEKSEFSALRAE
			NEKIKLELHQLKQQVMDEVIKVRTDTKLDFNLEKSRVKBLYSLN
			EKKLLELRTEIVALHAQQDRALTQTDRKIETEVAGLKTMLESHK
5625	1	2100	LDNIKYLAGSIFTCLTVALGFYRLWI
3023	1 *	1180	TIPSSAAAQRAGPPAGALEALSPGGARAHAERRGEMRATPLAAP
1]	AGSLSRKKRLELDDNLDTERPVQKRARSGPQPRLPPCLLPLSPP
1			TAPDRATAVATASRLGPYVLLEPEEGGRAYQALHCPTGTEYTCR
1			VYPVQEALAVLEPYARLPPHKHVARPTEVLAGTQLLYAFFTRTH
1		j	GDMHSLVRSRHRIPEPEAAVLFRQMATALAHCHQHGLVLRDLKL
1			CRFVFADRERKKLVLENLEDSCVLTGPDDSLWDKHACPAYVGPE
1	İ		ILSSRASYSGKAADVWSLGVALFTMLAGHYPFQDSEPVLLFGKI
			RRGAYALPAGLSAPARCLVRCLLRREPAERLTATGILLHPWLRQ
			DPMPLAPTRSHLWEAAQVVPDGLGLDEAREEEGDREVVLYG
5626	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRBLYLRVELSDVQNPAISI
			TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
-			ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
			EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN
			LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
			SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE
			IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ
			SIPIFNETGRESETLPYPVKIKVRESEFLQIYLIMIFLGLYINE
ì			RHLYKORRRYGOKKKKIH
5627	3123	2011	PPRALGSVAMENQVLTPHVYWAQRHRELYLRVELSDVQNPAISI
			TENVLHFKAQGHGAKGDNVYEFHLEFLDLVKPEPVYKLTQRQVN
l			ITVQKKVSQWWERLTKQEKRPLFLAPDFDRWLDESDAEMELRAK
l			
			EEERLNKLRLESEGSPETLTNLRKGYLFMYNLVQFLGFSWIFVN
			LTVRFCILGKESFYDTFHTVADMMYFCQMLAVVETINAAIGVTT
1			SPVLPSLIQLLGRNFILFIIFGTMEEMQNKAVVFFVFYLWSAIE
1			IFRYSFYMLTCIDMDWKVLTWLRYTLWIPLYPLGCLAEAVSVIQ
1			SIPIFNETGRFSFTLPYPVKIKVRFSFFLQIYLIMIFLGLYINF
5628	75	1,55	RHLYKQRRRRYGQKKKKIH
3020	75	1455	VAGAMASKCLKAGFSSGSLKSPGGASGGSTRVSAMYSSSPCKLP
1			SLSPVARSFSACSVGLGRSSYRATSCLPALCLPAGGFATSYSGG
1			GGWFGEGILTGNEKETMQSLNDRLAGYLEKVRQLEQENASLESR
]]		IREWCEQQVPYMCPDYQSYFRTIEELQKKTLCSKAENARLVVEI
			DNAKLAADDFRTKYETEVSLRQLVESDINGLRRILDDLTLCKSD
			LEAQVESLKEELLCLKKNHEEEVNSLRCQLGDRLNVEVDAAPPV
			DLNRVLEEMRCQYETLVENNRRDAEDWLDTQSEELNQQVVSSSE
]		QLQSCQAEIIELRRTVNALEIELQAQHSMRDALESTLAETEARY
			SSQLAQMQCMITNVEAQLAEIRADLERQNQEYQVLLDVRARLEC:
			EINTYRGLLESEDSKLPCNPCAPDYSPSKSCLPCLPAASCGPSA
	<u> </u>		ARTNCSARPICVPCPGGRF
5629	2287	938	GRPRSSSDNRNFLRERAGLSSAAVQTRIGNSAASRRSPAARPPV
			PAPPALPRGRPGTEGSTSLSAPAVLVVAVAVVVVVVSAVAWAMA
			NYIHVPPGSPEVPKLNVTVQDQEEHRCREGALSLLQHLRPHWDP
	[QEVTLQLFTDGITNKLIGCYVGNTMEDVVLVRIYGNKTELLVDR
			DBEVKSFRVLQAHGCAPQLYCTFNNGLCYEFIQGEALDPKHVCN
	ļ J		PAIFRLIARQLAKIHAIHAHNGWIPKSNLWLKMGKYFSLIPTGF
	<u> </u>		

SEO	Predicted	Dwadi shad sad	
ID	beginning	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1.0.	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W-Trophon V-Tunci- V Til
i	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	sequence	bequence	Codon, /=possible nucleotide deletion,
		 	\=possible nucleotide insertion)
1			ADEDINKRFLSDIPSSQILQEEMTWMKEILSNLGSPVVLCHNDL
1			LCKNIIYNEKQGDVQFIDYEYSGYNYLAYDIGNHFNEFAGVSDV
į			DYSLYPDRELQSQWLRAYLEAYKEFKGFGTEVTEKEVEILFIQV
ł			NQFALASHFFWGLWALIQAKYSTIEFDFLGYAIVRFNQYFKMKP EVTALKVPE
5630	1194	278	
	1	270	GFWAIAQTCAHHLPPGSPWLVPASPWRLPEMSSFGYRTLTVALF
			TLICCPGSDEKVFEVHVRPKKLAVEPKGSLEVNCSTTCNQPEVG
			GLETSLDKILLDEQAQWKHYLVSNISHDTVLQCHFTCSGKQESM
			NSNVSVYQPPRQVILTLQPTLVAVGKSFTIECRVPTVEPLDSLT
		1	LFLFRGNETLHYETFGKAAPAPQBATATFNSTADREDGHRNFSC
1			LAVLDLMSRGGNIFHKHSAPKMLEIYEPVSDSQMVIIVTVVSVL
5631	1053	290	LSLFVTSVLLCFIFGQHLRQQRMGTYGVRAAWRRLPQAFRP
	1	230	SRVDDFVRPEPSRAEPSRSGRRRPARRAATMSVFGKLFGAGGGK
			AGKGGPTPQEAIQRLRDTEEMLSKKQEFLEKKIEQELTAAKKHG
1	1		TKNKRAALQALKRKKRYEKQLAQIDGTLSTIBFQREALBNANTN
i	1		TEVLKNMGYAAKAMKAAHDNMDIDKVDELMQDIADQQELAEEIS
			TAISKPVGFGBEFDEDELMAELEELEQEELDKNLLEISGPETVP
5632	3	952	LPNVPSIALPSKPAKKKEEEDDDMKELENWAGSM
3332		352	VVLGWSPPRRLWWGSLGAAQRPAVPVSGLARSLHVETRRPHRRA
1			SVRVARGRLGVWAQPQPLLPRPVGSRREMQPPGPPPAYAPTNGD
			FTFVSSADAEDLSGSIASPDVKLNLGGDFIKESTATTFLRQRGY
1			GWLLEVEDDDPEDNKPLLEELDIDLKDIYYKIRCVLMPMPSLGF
1			NRQVVRDNPDFWGPLAVVLFFSMISLYGQFRVVSWIITIWIFGS
1			LTIFLLARVLGGEVAYGQVLGVIGYSLLPLIVIAPVLLVVGSFE
			VVSTLIKLFGVFWAAYSAASLLVGEEFKTKKPLLIYPIFLLYIY
5633	771	460	FLSLYTGV
3033	//1	460	QGCSKTMSVGRPFYRSSEFMEQLLSSHLHQVPFFCCFTVVCLCN
			CLFENSVSKLYMLCFNFFMSIFFYSLSITKLNLIYLWGLSYQSL
5634	1446	855	LLLLLSGHRPWGSSMV
3031	1440	855	PRATGRIRSRAAASRPRAGAGASGAEPRSGRERSRLSGRRAPAM
			ARNTLSSRFRRVDIDEFDENKFVDEQBEAAAAAEPGPDPSEVD
1			GLLRQGDMLRAFHAALRNSPVNTKNQAVKERAQGVVLKVLTNFK
i l			SSEIEQAVQSLDRNGVDLLMKYIYKGFEKPTENSSAVLLQWHEK
5635	3	043	ALAVGGLGSIIRVLTARKTV
1 3033	3	. 943	DRGPRSTATDTGRARVSFWRFPLDPGVKNSNVQISGEKRRFRTL
1			RSLFHPFPVTRSGAPRAVLVGSSWPAKMVAPAVKVARGWSGLAL
[GVRRAVLQLPGLTQVRWSRYSPEFKDPLIDKEYYRKPVEELTEE
			EKYVRELKKTQLIKAAPAGKTSSVFEDPVISKFTNMMMIGGNKV
			LARSLMIQTLEAVKRKQFEKYHAASAEEQATIERNPYTIFHQAL
			KNCEPMIGLVPILKGGRFYQVPVPLPDRRRRFLAMKWMITECRD
		٠	KKHQRTLMPEKLSHKLLEAFHNQGPVIKRKHDLHKMAEANRALA
5636	2253	1345	HYRWW
0000	2433	1143	LEDTICQHPPAEKKLYLYHRKLREVERNGIPRLPKDVFMDTHQG
			LTDVRAKVTGFSEGVVDSVKGGFSSFSQATHSAAGAVVSKPREI
]	ļ	ASLIRNKFGSADNIPNLKDSLEEGQVDDAGKALGVISNFQSSPK
	ļ		YGSEEDCSSATSGSVGANSTTGGIAVGASSSKTNTLDMOSSGFD
	ľ	İ	ALLHEIQEIRETQARLEESFETLKEHYQRDYSLIMQTLOEERYR
	1		CERLEEQLINDLTELHQNEILINLKQELASMEEKIAYQSYERARDI
	1		QEALEACQTRISKMELQQQQQQVVQLEGLENATARNLLGKLINI
	1		LLAVMAVLLVFVSTVANCVVPLMKTRNRTFSTLFLVVFIAFLWK
J			HWDALFSYVERFFSSPR
5637	948	2532	MSFCGARANAKMMAAYNGGTSAAAAGHHHHHHHHLPHLPPPHLH
			HHHHPQHHLHPGSAAAVHPVQQHTSSAAAAAAAAAAAAAMLNPG
		Ì	QQQPYFPSPAPGQAPGPAAAAPAQVQAAAAATVKAHHHQHSHHP
	1	ŀ	QQQLDIEPDRPIGYGAFGVVWSVTDPRDGKRVALKKMPNVFONL
]			VSCKRVFRELKMLCFFKHDNVLSALDILQPPHIDYFEBIYVVTE
	1	1	LMQSDLHKIIVSPQPLSSDHVKVFLYQILRGLKYLHSAGILHRD
			IKPGNLLVNSNCVLKICDFGLARVEELDESRHMTQEVVTQYYRA
	ļ		PEILMGSRHYSNAIDIWSVGCIFAELLGRRILFQAQSPIQQLDL
L			ITDLLGTPSLEAMRTACEGAKAHILRGPHKQPSLPVLYTLSSOA
			7

Degianing nucleotide location corresponding control coation corresponding cofired mino acid mi	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No. nucleotide			l .	
location cofreeponding to first amino acid maino acid cesidue of amino acid amino acid amino acid sequence seq	1			
Lequine, M-Methionine, N-Asparagine, Pepcine, Q-Glutamine, R-Asparagine, Pepcine, Q-Glutamine, R-Asparagine, Pepcine, Q-Glutamine, R-Asparagine, Pepcine, Q-Glutamine, R-Asparagine, Pepcine, Q-Glutamine, R-Asparagine, Pepcine, Q-Glutamine, R-Asparagine, Pepcine, Q-Glutamine, R-Asparagine, Pepcine, Q-Glutamine, R-Asparagine, Pepcine, Q-Glutamine, R-Asparagine, Pepcine, Q-Glutamine, R-Asparagine, Pepcine, Q-Glutamine, R-Asparagine, Pepcine, Q-Glutamine, R-Asparagine, Pepcine, Q-Glutamine, R-Asparagine, Pepcine, Q-Government, Pepcine, R-Asparagine, Pepcine, R-Asparagine, Pepcine, R-Asparagine, Pepcine, R-Asparagine, Pepcine, R-Asparagine, Pepcine, R-Asparagine, Pepcine, R-Asparagine, Pepcine, R-Asparagine, R-Asparagine, Pepcine, R-Asparagine, R-Asp	1.0.		1.	
to first amin acid residue of amino acid amino acid sequence sequence sequence amino acid sequence seq				
amino acid residue of amino acid sequence Sequence Codon, /=possible nucleotide deletion, _>possible nucleotide insertion) THEAVELLCHRUFDPYKRISKADLAMPYLDEGELTYTTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDEGELTYTTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDEGELTYTTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDEGELTYTTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDEGELTYTTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDEGELTYTTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDEGELTYTTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDEGELTYTTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDEGELTYTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDEGELTYTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDEGELTYTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDEGELTYTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDEGELTYTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDGGELTYTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDGGELTYTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDGGELTYTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDGGELTYTCHK THEAVELLCHRUFDPYKRISKADLAMPYLDGGELTYTCHKADLAMPICHT THEAVELLCHRUFDPYKRISKAPLANSONGALLTHOLY THEAVELLCHRUFDPYKRISKAPLANSONGANCAPLAND THEAVELLCHRUFDPYKRISKAPLANDHTVOLICALSKANAVANANANANANANANANANANANANANANANANANA			1	
residue of amino acid sequence (Codon, *possible nucleotide deletion, \			1 '	
amino acid sequence Codon, /=possible nucleotide insertion) THEAVELLCENCYPEPPYREISAKDIARHEYLDEGELEVETCHICA Logography-Terrorysispley-Three propriets and the control of	ŀ			1
Sequence			1	
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IEKVHRGCVIANVVSGSTGILSVIGVMLAPFTAGLSLSITAAGV GLGIASATAGIASSIVENTYTRSAELTASRLTATSTDQLEALRD ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW RYVPINVVETLRTRGAPTRIVRKVARRNLGKATSGVLVVLDVVNL VQDSLDLHKGEKSESAELLRQWAQELEENLNELTHIHQSLKAG 5645 537 799 VQSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPLNSASSQVPTL YLCLQNSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSD AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFBELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ 5647 288 800 GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH	1	1	[KKVSPVHLKILLTSDEAWKRFVRVAELPREEADALYEALKNLTP
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GLGIASATAGIASSIVENTYTRSAELTASRLTATSTDQLEALRD ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW RYVPINVVETLRTRGAPTRIVRKVARNLGKATSGVLVVLDVVNL VQDSLDLHKGEKSESABLLRQWAQELEENLNELTHIHQSLKAG 5645 537 799 VQSVRDLKRLSPTDPPGDSRRDVTREDPVTGPLNSASSQVPTL YLCLQNSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSD 5646 3745 3328 AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFBELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ 5647 288 800 GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH	1	1	1	IEKVHRGCVIANVVSGSTGILSVIGVMLAPFTAGLSLSITAAGV
ILHDITPNVLSFALDFDEATKMIANDVHTLRRSKATVGRPLIAW RYVPINVVETLRTRGAPTRIVRKVARNLGKATSGVLVVLDVVNL VQDSLDLHKGEKSESABLLRQWAQELEENLNELTHIHQSLKAG 5645 537 799 VQSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPLNSASSQVPTL YLCLQNSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSD 5646 3745 3328 AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFBELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ 5647 288 800 GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH			1	GLGIASATAGIASSIVENTYTRSAELTASRLTATSTDOLEALRD
RYVPINVVETLRTRGAPTRIVRKVARNLGKATSGVLVVLDVVNL VQDSLDLHKGEKSESABLLRQWAQELEENLNELTHIHQSLKAG 5645 537 799 VQSVRDLKRLSPTDPPGDSGNRDVTREDPVTGPINSASSQVPTL YLCLQNSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSD 5646 3745 3328 AEQYGTSPHLLPTMLLSSCLPPANVTKAATPPPLVLSLTTADP AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFBELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ 5647 288 800 GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH	1			
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YLCLQNSLLGHSSVEDARATMELYQISQRIRARRGLPRLAVSD 5646 3745 3328 AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFEELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ 5647 288 800 GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH	5645	537	799	
5646 3745 3328 AEQYGTSPHLLPTMLLSSCLPPANVTTKAATPPPLVLSLTTADP AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFEELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ 5647 288 800 GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH	-7			1 ' 7 1
AGKPAPCRVTLTLLRASIPATKRASFLSSFIKMFFBELEYILGF LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ 5647 288 800 GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH	5646	3745	3226	
LSLLKFHVHVSVYSAICHFQKEGTGNSRSFTCTPELFPRLQTHL RAEGGAQ 5647 288 800 GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH	5575	3/#3	3320	1 -7
RAEGGAQ 5647 288 800 GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH	1		1	1
5647 288 800 GVIMATSELSCEVSEENCERREAFWAEWKDLTLSTRPEEGCSLH				
		1 222		
EEDTQRHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQEYQLPY	5647	288	800	1
				EEDTQRHETYHQQGQCQVLVQRSPWLMMRMGILGRGLQEYQLPY

SEO	Predicted	Predicted end	I Design and a second assets a second assets a second assets a second assets a second assets a second assets a
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
Į	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			QRVLPLPIFTPAKMGATKEEREDTPIQLQELLALETALGGQCVD
			RQEVAEITKQLPPVVPVSKPGALRRSLSRSMSOEAORG
5648	7	1518	VLSELCGRHEALREVGAEWPPPTCSPNICSGLOOAGNTDWSLTM
1			APQSLPSSRMAPLGMLLGLLMAACFTFCLSHONLKEFALTNDRK
1			SSTKETERKETKAEEELDAEVLEVFHPTHEWOALOPGOAVPAGS
	•		HVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTNTYTSODLKS
			ALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVV
1	ļ		IETDMQIMVRLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQD
			LLSFGGLQVVINGLNSTEPLVKEYAAFVLGAAFSSNPKVQVEAI
İ			BGGALQKLLVILATEQPLTAKKKVLFALCSLLRHFPYAQRQFLK
			LGGLQVLRTLVQEKGTEVLAVRVVTLLYDLVTEKMFAEEEAELT
			QEMSPEKLQQYRQVHLLPGLWEQGWCEITVHLLALPEHDAREKV
			LQTLGVLLTTCRDRYRQDPQLGRTLASLQAEYQVLASLELQDGE DEGYFQELLGSVNSLLKELR
5649	1172	3006	MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL
			KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
			MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR
1			TLRLEKLGHPALSQEEGKSALEDQGSNPSSSNSSQDSLHKGAKR
1 1			KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMQEPM
1 1			VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAQWDGPTVVSWL
i			ELWVGMPAWYVAACRANVKSGAIMSALSDTEIOREIGISNALHR
			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHEEMETLETSTK
1 1			TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPOYRSYPMECLV
İ			DARMLDHLTKKDLRVHLKMVDSFHRTSLOYGIMCLKRLNYDRKE
ļ			LEKRREESQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
			HGALLALDENFDHNTLALILQIPTQNTQARQVMEREFNNLLALG
			TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD
5650	1172	3006	MLQEQLDAINEEIRMIQEEKESTELRAEEIETRVTSGSMEALNL
1 1			KQLRKRGSIPTSLTDLSLASASPPLSGRSTPKLTSRSAAQDLDR
			MGVMTLPSDLRKHRRKLLSPVSREENREDKATIKCETSPPSSPR
			TLRLEKLGHPALSQEEGKSALEDOGSNPSSSNSSODSLHKGAKR
1 1			KGIKSSIGRLFGKKEKGRLIQLSRDGATGHVLLTDSEFSMOEPM
1			VPAKLGTQAEKDRRLKKKHQLLEDARRKGMPFAOWDGPTVVSWI.
1			ELWVGMPAWYVAACRANVKSGAIMSALSDTEIOREIGISNALHR
1 1			LKLRLAIQEMVSLTSPSAPPTSRTSSGNVWVTHREMETLETSTK
1	1	[TDSEEGSWAQTLAYGDMNHEWIGNEWLPSLGLPQYRSYFMECLV
		İ	DARMLDHLTKKDLRVHLKMVDSFHRTSLQYGIMCLKRLNYDRKE
			LEKRREBSQHEIKDVLVWTNDQVVHWVQSIGLRDYAGNLHESGV
			HGALLALDENFOHNTLALILQIPTQNTQARQVMEREFNNLLALG
1			TDRKLDDGDDKVFRRAPSWRKRFRPREHHGRGGMLSASAETLPA GERVSTLGTLOPPRADDRYMMENUSWHY SEGMLSASAETLPA
5651	646	1869	GFRVSTLGTLQPPPAPPKKIMPEAHSHYLYGHMLSAFRD ARQGQRQPWG*EARAKGPASESPRV*EGSGWEGPASP*TPGSTL
		·	AWGEGAGIR*ASGLTAAGAASAAAA/PPPTRGGPAPAGCGRAPP
1 1			WPAPLRVPTHGRAPAPRSRAAPRAPALSHGTAAAALSPASPAGP
1 1		į	ADP*LPGHSSQSPPRG*RWGRSRSAPAPAHPEHPAPAGSASASQ
1 1			QTPGWPGSCCLAQGWQAEPLGAPGAEDG\PVPPQRGFPLGTLGS
i l		İ	PAGSWAGLAGYG*AGAPGTQATAPRAAGQTPVAAAPNCRV*GSA
1			PALHRAPAAADPGSPLQAPPRAWASPAAAGPGLSSSDYCGGLGA
1 1	1	1	GWRAGISPELLGAAGLSDNWARCPGPGPAE*GGOPGCRTTPASA
		1	CMPSPPVEGSLGLSRKGHGDLPSQAR*GWHECRRARHLVPLPRL
ECEO	725		LGPRGRTGRPSSPS
5652	735	343	HHKKYQHIHQKSFSCPEPACGKSFNFKKHLKEHMKLHSDTRDYI
	j		CEFCARSFRTSSNLVIHRRIHTGEKPLQCEICGFTCROKASLNW
5653	66		HQRKHAETVAALRFPCEFCGKRFEKPDSVAAHRSKSHPALLLA
	00	- ,	RGRLQSRGRLTLGLVLLLLDILGARQHGQRVSHGWKGGFLTAPL
			CFPQPCQPGTRRGRRRSLKEATEPQLAMAEEFVTLKDVGMDFTL
			GDWEQLGLEQGDTFWDTALDNCQDLFLLDPPRPNLTSHPDGSED
	1	l l	I PRI ACCORDAMORDIMENTO
	1	1	LEPLAGGSPEATSPDVTETKNSPLMEDFFEEGFSQEI/SRDVIQ GWLLELQFRRSLYRGHLVR*FARRSRKSSEV*YCHQRGKSHGMQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ŀ		to first	
	corresponding to first		L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ĭ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
	1		ES*IKERTQSCVHRFHGRRFHG\DNVSEKTLTPAKSKEYRGEFF
			SYSDHSQQDSVQEGEKPYQCSECGKSFSGSYRLTQHWITHTREK
		1	PTVHQECEQGFDRKASHSGYPKTHTGYKFYVCNEYGTPFSQSTY
			LWHQKTHAGEKPCKSQDSDHPPSHDTQSGEHQKTHTDSKSYNCN
			ECGKAFTRIFHLTRHQKIHTRKRYECSKCQATFNLRKHLIOHOK
			THAANV
5654	3	598	
3654	3	598	TLPLFPGRRFRGWRRCGAVAARKNSTGGNVSINQRRDSVRMSAL
			NWKPFVYGGLASITAECGTFPIDLTKTRFQIQGQTNDAKFKEII
	}	}	YRGMLHALVRIGREEGLKALYSG*VGLHAFLCHCSLFHMGIDFR
1			PRLHRSQVKSLRCV*KEQIA**/MFSLLISTLISKYIYYAADVL
1			EKLFYYIQVQTDNNKKICLFKNI
5655	2	867	RPPGIRAPROLHPAAGRRPDASARPRFRPTVLLHDPFQLSFPPP
			PLSYPSVFPAVARVLPQRSGDYRAAGMPQLSGGGGGGGGDPELC
		1	ATDEMIPFKDEGDPQ\REKIFAEIVNPEEEGDLADIKSSLVNES
		}	EIIPASNGHEVARQAQTSQEPYHDKAREHPDDGKHPDGGLYNKG
		} •	PSYSSYSGYIMMPNMNNDPYMSNGSLSPPIPRTSNKVPVVQPSH
	1	1	AVHPLTPLITYSDEHFSPGSHPSHIPSDVNSKQGMSRHPPAPDI
		1	PTFYPLSPGGGGQITPPLGWQGQP
5656	228	1066	
3636	228	1000	PRRVPPLPEFASGPGAAFFHSGRLQRSLTKDSAGCFSQCRSRAM
Ì		1	LVLRSGLTKALASRTLAPQVCSSFATGPRQYDGTFYEFRTYYLK
į			PSNMNAFMENLKKNIHLRTSYSELVGFWSVBFGGRTNKVFHIWK
1			YDNFPHRAEVRKALANCKEWQEQSIIPNLARIDKQETEITYLIP
1	1	ì	WSKLQKPPKEGVYELAVFQMKPGGPALWGDAFERAINAHVNLGY
i	1	1	TKVVGVFHTEYGELNRVHVLWWNESADSRAAVRHKSHEDPISWG
l		ļ	GVRESVNYL\VSQQNM
5657	105	1052	GQRLQSPRVQMPVQPPSKDTEEMEAEGDSAAEMNGEEEESEEER
1			SGSQTESEESSEMDDEDYERRRSECVSEMLDLEKOFSELKEKL
			FRERLSQLRLRLEEVGAERAPEYTEPLGGLQRSLKIRIOVAGIY
			KGFCLDVIRNKYECELQGAKQHLESEKLLLYDTLQGELQERIQR
1	Į.		LEEDRQSLDLSSEWWDDKLHARGSSRSWDSLPPSKRKKAPLVSG
			PYIVYMLQEIDILEDWTAIKKARAAVSPQKRKSD\DLDPAVHSQ
1	1		
		l	GDPQSSWHCTQDSRLPPADRRTHRPLRVCPARLLWCCWALPLHL
			ALVWTPPL
5658	2346	3541	TERRVYNPWPEPDPD\CIQEDPWNLPNSIKTLVDNIQRYVEDGK
			NQLLLALLKCTDTELQLRRDAIFCQALVAAVCTFSEQLLAALGY
		1	RYNNNGEYEESSRDASRKWLEQVAATGVLLHCQSLLSPATVKEE
		!	RTMLEDIWVTLSELDNVTFSFKQLDENYVANTNVFYHIEGSRQA
		1	LKVIFYLDSYHFSKLPSRLEGGASLRLHTALFTKVLENVEGLPS
			PGSQAAEDLQQDINAQSLEKVQQYYRKLRAFYLERSNLPTDAST
		l .	TAVKIDQLIRPINALDELCRLMKSFVHPKPGAAGSVGAGLIPIS
Ì		1	SELCYRLGACOMVMCGTGMQRSTLSVSLEQAAILARSHGLLPKC
			IMQATDIMRKQGPRVEILAKNLRVKDOMPOGAPRLYRLCOPKMN
			GDL
5659	2	696	WKRSGEVSPKGELGAWRGNSGRPKIIGRAAEAENEDRTLGRLLP
1 3333	-	050	
			GNERSQPRSPLRLLAPQLKAEAAADKGLAPVPPPFSSGHSGPC\
]	EREGEGQRGRGRSRRGAHLELKPSPGLRAGAPTDRGRGGPABVA
			AAGGRRMVQKESQATLEERESELSSNPAASAGASLEPPAAPAPG
i			EDNPAGAGG\AAVAGAAGGARRFLCGVVEGFYGRPWVMEQRKEL
			FRRLQKWELNTYL
5660	229	853	PVTMWAFSELPMPLLINLIVSLLGFVATVTLIPAFRGHFIAARL
			CGQDLNKTSRQQIPESQGVISGAVFLIILFCFIPFPFLNCFVKE
			QRKAFPHHEFVALIGALLAICCMIFLGFADDVLNLRWRHKLLLP
			TAASLPLLMVYFTNFGNTTIVVPKPFRPILGLHLDLGR*SYHCC
		{	PYGTYFREPFLVLHILLQVFLFCLCVFPDPFW
5661	2	473	LNLYPSPCGGIPKLPGLPREAAAALGASFLAEAPLPVTVRGSGL
2001		"/3	
			AGMAVTCDPKAFLSICFVTLVFLQLPLASICQN*GTDSCASRGK
			ADFDVTGPHAPILAMAGGHVELQCQLFPNISAEDMELRWYRCQP
			SLAVHMHERGMDMDGEQKWQYRGRT
5662	2	1318	LRKEGRCRRGSNRGVWAAPAEGLGGRGMLGVRCLLRSVRFCSSA
L	L		PFPKHKPSAKLSVRDALGAQNASGERIKIQGWIRSVRSQKEVLF

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ĺ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
İ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
- }	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	'	\=possible nucleotide insertion)
			LHVNDGSSLESLQVVADSGLDSRELTFGSSVEVQGQLIKSPSKR
			QNVELKAEKIKVIGNCDAKDFPIKYKERHPLEYLRQYPHFRCRT
			NVLGSILRIRSEATAAIHSFFKDSGFVHIHTPIITSNDSEGAGB
			LFQLEPSGKLKVPEENPFNVPAFLTVSGQLHLEVMSGAFTQVFT
1			FGPTFRAENSQSRRHLAEFYMIEAEISFVDSLQDLMQVIEELFK
1			ATTMMVLSKCPEDVELCHKFIAPGQKDRL*HMLKNNFLIISYTE
		ĺ	AVEILKQASQNFTFTPEWGADLRTEHEKYLVKHCGNIPVFVINY
			PLTLKPFYMRDNEDGPQELEGSVA*HSLGLMILLSIVVIGQP
5663	119	698	PADIGRSTAKTPGPPRSLEMDDPRYGMCPLKGASGCPGAERSLL
			VQSYFEKGPLTFRDVAIEFSLEEWQCLDSAQQGLYRKVMLENYR
		1	NLVFLGIALTKPDLITCLEQGKBPWNIKRHEMVAKPPVICSHFP
			QDLWAEQDIKDSFQEAILKKYGKYGHANFQLQKGCKSVDECKVH
	<u></u>		KEHDNKLNQCLIPKKKK
5664	118	572	SLSMESNHKSGDGLSGTOKEAALRALVORTGYSLVORNGORKYG
			GPPPGWDAAPPERGCEIFIGKLPRDLFEDELIPLCEKIGKIYEM
			RMMMDFNGNNRGYAFVTFSNKVEAKNAIKQLNNYEIRNGRLLGV
		i	CASVDNCRLFVGGIPKTKK
5665	347	702	VVQHLIILLHCERTSPAMITSELPVLQDSTNETTAHSDAGSELE
1			ETEVKGKRKRGRPGRPPSTNKKPRKSPGEKSRIEAGIRGAGRGR
			ANGHPQQNGEGEPVTLFEVVKLGKSAMQRC
5666	213	540	VSCLPTSCKMITLNNODOPVPFNSSHPDEVKIAALVEVCCTETT
			GLFVNITALWVFSCTTKKRTTVTIYMMNVALVDLIFIMTLPFRM
			FYYAKDEWPFGEYFCQILGA
5667	1	695	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP
			SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFITGLARSKGER
			VLDACSSEATHVVMEETSAEEAVSWOERRMAAAPPGCTDDALLD
1			ISWLTESLGAGQPVPVECRHRLEVAGPSKGPLSPAWMDAVACOR
			PTPLTHHNTGLSEALEILAEAAGFEGSEGRLLTFCRAASVLKAI.
F. C. C.			PSPVTTLSQLQ
5668	691	894	CSFLFCIPDLFLQFLLGRKEEEAVLVGGEWSPSLDGLDPQADPQ
5669			VLVRTAIRCAQAQTGIDLSGCTKW
3669	407	1	DSGAPEGLSPLMSTQEGLSMHAHPQAYTPFIYLHARKRRGEIGD
i i			ADSRENDRYAHKSAQLYFLYFVCWIFODVYVFTIKEKNUEFEDE
			ARGAPTKYSGSPIGSPTTTPPTRPPSFNLHPAPHLLASMOLOKI
5670			NSQ
3670	3	373	SSECLTMAWIPLLLPLLILCTVSVASYELAQPSSVSVSPGQTAK
	1		ITCSGDVLAKKYARWFQOKPGOAPVI.VIVKDTRPDCGIDEBECC
5671	202		STSGTTVTLTISGAQVEDRADYFCYSATDNFLWVF
30/1	280	524	KFPPKKTPPHLGMESAITLWOFLLOLLLDOKHRHLICWTSNDGF
5672			FKLLKAKKVAKLWGLRKNKTNMNYDKLSRALRLLFMT
3012	2	557	FVPATPDPGVWLPPSRDPAMAKRSSLYIRIVEGKNI.DAKDITCC
	i		SDPYCIVKVDNEPIIRTATVWKTLCPFWGEEYOVHI.ppTFHAVA
			FYVMDEDALSRDDVIGKVCLTRDTIASHPKGKFSLDSHTGLDSD
			WPPSHSETSPLGSVWSPAQGKPFLLSPEAGATFCTPGLCSAACS
5673	307		QAMPPPAD
30/3	327	696	ITVADQISHWSAGRIKNRTRIPECIHSSAATTLAGPHTMEGESV
			KLSSQTLIQAGDDEKNQRTITVNPAHMGKAFKVMNELBSKOLLC
5674	17		DVMIVAEDVEIEAHRVVLAACSPYFCAMFTGDMS
JU / 12	17	984	GGGSMEGESTSAVLSGFVLGALAFQHLNTDSDTEGFLLGEVKGE
ļ			AKNSITDSQMDDVEVVYTIDIOKYIPCYOLFSFVNSSGFVNFO2
			LKKILSNVKKNVVGWYKFRRHSDOIMTFRERLLHKNLOEHRSNO
			DLVFLLLTPSIITESCSTHRLEHSLYKPOKGLFHRVPLVVANLG
			MSEQLGYKTVSGSCMSTGFSRAVOTHSSKFFEEDGSLKEVHKIN
			EMYASLQEELKSICKKVEDSEQAVDKLVKDVNRLKRETEKRDGA
			QIQAAREKNIQKDPQENIFLCQALRTFFPNSEFLHSCVMSLKID
5675			MFLKVAVTTTTISM
30/5	80	753	EGSRRGPTRLARLSARAGRLHFPPGFSSRLIHFRGVSECRRPPG
1		ľ	KSGVPVSAPGSDGKWWEERPGMFSLMASCCGWFKRWREPVRKUT
	1	ł	LLMVGLDNAGKTATAKGIQGBYPEDVAPTVGFSKINLROGKFEV
			TIFDLGGGIRIRGIWKNYYAESYGVIFVVDSSDEERMEETKEAM

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
MO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid		S=Serine, T=Threonine, V=Valine,
		residue of	
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SEMLRHPRISGKPILVLANKQDKEGALGEADVIECLSLEKLVNE
		1	HKCL
5676	2	930	FVSSPPPRPVQPARPGGFGLSGRRSLLCQVASTPAHVGVMRSPV
	1	1	RDLARNDGEESTDRTPLLPGAPRAEAAPVCCSARYNLAILAFFG
			FFIVYALRVNLSVALVDMVDSNTTLEDNRTSKACPEHSAPIKVH
			HNOTGKKYOWDAETOGWILGSFFYGYIITQIPGGYVASKIGGKM
			LLGFGILGTAVLTLFTPIAADLGVGPLIVLRALEGLGEGVTFPA
			MHAMWSSWAPPLERSKLLSISYAGAQLGTVISLPLSGIICYYMN
	1		WTYVFYFFGTIGIFWFLLWIWLVSDTPQKHKRISHYEKEYILSS
			1
		ļ	L
5677	1	1028	PPRDGFLELRRLSVPLCSGPCPLTSLSRQGERSGGHLVAAARAA
			VTAETHPLPLLAPLAVCQSVKSPAACQVRPRPRAVALPAALGGP
			GRSLPGLTAATMSSFSESALEKKLSELSNSQQSVQTLSLWLIHH
			RKHAGPIVSVWHRELRKAKSNRKLTFLYLANDVIQNSKRKGPEF
			TREFESVLVDAFSHVAREADEGCKKPLERLLNIWQERSVYGGEF
	1		IQQLKLSMEDSKSPPPKATEEKKSLKRTFQQIQEEEDDDYPGSY.
			SPQDPSAGPLLTEELIKALQDLENAASGDATVRQKIASLPQEVQ
			DVSLLEKITDKEAAERLSKTVDEACLRNRGPGTS
5678	3	593	SSSPSSTPSLPLPFYLLLGOLRLQLLWGTAHLSGAGEAAPCPG
	_	1	GSGRTAAPRTRADPAAQSLMIMNKMKNFKRRFSLSVPRTETIER
İ			SLAEFTEOFNOLHNRRNENLOLGPLGRDPPQECSTFSPTDSGER
			PGQLSPGVQFQRRQNQRRFSMEVRASGALPRQVAGCTHKGVHRR
		1	AAALQPDFDVSKRLSLPMDI
			LNSRVDDFVAVPGAIMDEDYYGSAAEWGDEADGGQQEDDSGEGE
5679	2	623	1
ĺ			DDAEVQQECLHKFSTRDYIMEPSIFNTLKRYFQAGGSPENVIQL
		1	LSENYTAVAQTVNLLAEWLIQTGVEPVQVQETVENHLKSLLIKH
			FDPRKADSIFTEEGETPAWLEQMIAHTTWRDLFYKLABAHPDCL
			MLNFTVKVGRVLELRRKVFMNVYFWLLVCFL
5680	258	592	RRLTSTSEKLONRNSHTPLESLIHPOPSYKGFGIMFGKKKKKIE
	İ		ISGPSNFEHRVHTGFDPQEQKFTGLPQQWHSLLADTANRPKPMV
'		1	DPSCITPIQLAPMKTIVRGNKPC
5681	45	869	LLCAKTLGVRTKESQAEGYNRSGINNHQAEDPRFCPSFCWMRSA
		ļ	RQTRPQRLRKEAARPPTPGSCPGGTGMDGKKCSVWMFLPLVFTL
]	FTSAGLWIVYFIAVEDDKILPLNSAERKPGVKHAPYISIAGDDP
			PASCVFSQVMNMAAFLALVVAVLRFIQLKPKVLNPWLNISGLVA
	1		LCLASFGMTLLGNFQLTNDEEIHNVGTSLTFGFGTLTCWIQAAL
			TLKVNIKNEGRRVGIPRVILSASITLCVGPLLHPHGPKHPHVCS
1			OGPVGPGHVL
5682	39	622	PSRSCLGTMRKWRHREVNLPEVTQQDAVCPAPIPSPGLSAQTGL
2002		022	OKIWGTIHCOVCPGAPAWPGSPWHEEMGLLLLVPLLLLPGSYGL
	1		PFYNGFYYSNSANDONLGNGHGKDLLNGVKLVVETPEETLFTYO
	1		GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLVAIG
1		1	
			LRHRSFGDYQGRVHLRQD
5683	89	778	GSCGATALITRCLAWSVLISRLAMATYTCITCRVAFRDADMQRA
	}		HYKTDWHRYNLRRKVASMAPVTAEGFQERVRAQRAVAEEESKGS
-	1	1	ATYCTVCSKKFASFNAYENHLKSRRHVELEKKAVQAVNRKVEMM
		1	NEKNLEKGLGVDSVDKDAMNAAIQQAIKAQPSMSPKKAPPAPAK
	1		EARNVVAVGTGGRGTHDRDPSEKPPRLQWFEQQAKKLAKHSEDD
	1		SEDEEHDLC
5684	195	677	TWCFRGYLGPRVIMKALDEPPYLTVGTDVSAKYRGAFCEAKIKT
		1	AKRLVKVKVTFRHDSSTVEVQDDHIKGPLKVGAIVEVKNLDGAY
Ì			QEAVINKLTDASWYTVVFDDGDEKTLRRSSLCLKGERHFAESET
1	1		LDOLPLTNPEHFGTPVIGKKTNRGRRYE
5685	779	1262	LLLOOPVVHCFLLFPPFRFSHHMIPGPPGPHTTGIPHPAIVTPQ
2082	1/3	1404	VKOEHPHTDSDLMHVKPOHEORKEQEPKRPHIKKPLNAFMLYMK
	1		
			EMRANVVAECTLKESAAINQILGRRWHALSREEQAKYYELARKE
			RQLHMQLYPGWSARDNYVSPSSIPVALHS
5686	128	1181	CTWWQVNITLLDINDNHPTWKDAPYYINLVEMTPPDSDVTTVVA
			VDPDLGENGTLVYSIQPPNKFYSLNSTTGKIRTTHAMLDRENPD
1		1	PHEAELMRKIVVSVTDCGRPPLKATSSATVFVNLLDLNDNDPTF
			PHEAELMRKIVVSVTDCGRPPLKATSSATVFVNLLDLNDNDPTF

Seginaling	CEC	Predicted	D==4?=b=4 ==4	Amino acid segment containing signal peptide
Not	SEQ		Predicted end	
cortesponding to first amino acid amino ac	1		4	
to first amino acid residue of amino acid amino acid sequence Poption Poption Poption Poption Poption	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid residue of amino acid amino acid amino acid sequence S-Serie, T-Threonine, V=Valine, W-Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, V=possible nucleotide deletion, V=possible nucleotide insertion) ONLEPTARVINGVISIOLEGICIGALINGVISIPHIPVOMP RMPFLINSSSGVVVTTTELDRER: AEYQLEVVASDAGTPTKSST STLTIHIVLDNOPETPTFPAPTYNOVSSDEDYNSGSGMS-AARN NDVGLNARLSYFTIGGNVDGKFSVGYRDAVVETVVSLORETTAA YNLLEALDINGPVGKHRYDTAYTVTVTVJDORKSPTILGGS-AARN NDVGLNARLSYFTIGGNVDGKFSVGYRDAVVETVVSLORETTAA YNLLEALDINGPVGKHRYDTAYTVTVTVJDORKSPTILGGS- SCHAMPSTASSE, ALMOGRAVGHVVADAVGAVGTVGTVSTDORTTAA YNLLEALDINGPVGKHRYDTAYTVTVTVJDORKSPTILGGS- SCHAMPSTASSE, ALMOGRAVGHVVADAGGACHLAKOSSTOPATSPELLCP- YAAPAADSCOPHENSAGRAA GCDGGAAAVGHLVVADAGGACHLAKOSSTOPATSPELLCP- YAAPAADSCOPHENSAGRAA GCDGGAAAVGHVLVVADAGGACHLAKOSSTOPATSPELLCP- YAAPAADSCOPHENSAGRAA SSFPANISSCM.RGIPPPSGGFLCPGRAAGPVPITTHGORGGOP VLDI TURKDLETANTATKTTERMSTGGAAPEVQUOTVWNS/CLYDSRKLFF SFRINGSCM.RGIPPPSGGFLCPGRAAGPVPITTHGORGGOP VLDI TURKDLETANTATKTTERMSTGGAAPEVQUOTVWNS/CLYDSRKLFF SFRINGSCM.RGIPPPSGGFLCPGRAAGPVPITTHGORGGOP VLDI TURKDLETANTATKTTERMSTGGAAPEVQUOTVWNS/CLYDSRKLFF SFRINGSCM.RGIPPPSGGFLCPGRAAGPVPITTHGORGGOP VLDI TURKDLETANTATKTTERMSTGGAAPEVQUOTVMS/CLYDSRKLFF SFRINGSCM.RGIPPSGGFLCPGAARAGPVPITTHGORGGOP TURKDLETANTATKTTERMSTGGAAPEVQUOTVMS/CLYDSRKLFF SFRINGSCM.RGIPPSGGFLCPGAARAGPVPITTHGORGGOP TURKDLETANTATKTTERMSTGGAAPEVQUOTVMS/CLYDSRKLFF SFRINGSCM.RGIPPSGGFLTSHAGGGGT-SAGCARAFGAAPEA TURKDLETANTATKTTERMSTGGAAPEVQUOTVMS/CLIDAGPSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid sequence S-Serine, T-Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide insertion) ORLEPTARVINGYSIDELGING/VSYRMPVGKP RMPFLINSSSGVVVTTTELDRER: AEVQLWVASDAGTPTKSST STATIHUMUNDETPTPAPYNVNVSVSBUDYNGKSPHGAY-ARN NDVGLNARLSYFTIGGNVDGKFSVGVAIDLEGLING/VSYRMPVGKP RMPFLINSSSGVVVTTTELDRER: AEVQLWVASDAGTPTKSST STATIHUMUNDETPTPAPYNVNVSVSBUDYNGKSPHGAY-ARN NDVGLNARLSYFTIGGNVDGKFSVGVAIDLEGLING/VSYRMPVGKP RMPFLINSSSGVVVTTTELDRER: AEVQLWVASDAGTPTKSST STATIHUMUNDETPTPAPYNVNVSVSBUDYNGKSPHGAY-ARN NDVGLNARLSYFTIGGNVDGKFSVGTRDAVVTTVGLORETTAA VMLLEADINGPVGKENTGTATVVTVTVLOUNGKPHILGSSSG STATIHUMUNDETPTPAPYTFFPAPYTFFPAPYTFFPAPYTFFPAPY SCRUMPSTASSE/ANGGVGLVANGFANGAGTAGTS SCRUMPSTASSE/ANGGVGLVANGFANGAGTAGTS SCRUMPSTASSE/ANGGVGLVANGFANGAGTAGTS FPHLTGGPGNYSSEAKLPNSTSCLALAGTGGAGT-ATASAGTS SPHANGSCHLRGIPPAGSGFLCORARGEPVPITTHGGGGGP VLDI	1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
amino acid residue of amino acid sequence whospetpophan, Y=7yrosine, X-uknkovm, Y=5top (Codon, /=possible nucleotide deletion, Codon, /=possible nucleotide deletion). Noterhapper	Į.		amino acid	
residue of anino acid sequence codon, /=possible nucleotide deletion. Vapossible nucleotide deletion. Vapossible nucleotide deletion. Vapossible nucleotide insertion) ONLEPTARVIGETRANCYTYCVAIDLESSIGNUSYEMPUCHP PROPERTY ONLESSIGNUSYEMPUCHP PROPERTY ONLESSIGNUSYEMPUCHP PROPERTY ONLESSIGNUSYEMPUCHP PROPERTY ONLESSIGNUSYEMPUCHP PROPERTY ONLESSIGNUSYEMPUCHP PROPERTY ONLESSIGNUSYEMPUCHP PROPERTY ONLESSIGNUSYEMPUCHP PROPERTY ONLESSIGNUSYEMPUCHP PROPERTY ONLESSIGNUSYEMPUCHP PROPERTY ONLESSIGNUSYEMPUCHP PROPERTY ONLESSIGNUSYEMPUCHP PROPERTY ONLESSIGNUSYEMPUCHP PROPERTY ONLESSION ON THE PROPERTY OF THE PROPERTY ON THE PROPERTY OF THE PROPERTY ON THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPE	i	I		
### and acid sequence Codon, /=possible nucleotide deletion,				
Sequence N=possible nucleotide insertion		1		
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S689 1504	1		1	LRVEKTFAITYLKNFTVKVDFSLLGEIPLISMAAILKLWIMKID
TWA/RKPIGTWTATKPTHRAG**CGABEYOPPOPCEGPRSTSRG GEG*GRAVGPGREIGKEGSLPFLGPKALGF**SASCQAFFEGAH GSTARKPAPATPGTRHPRTMETREVAGWPAGPRSOFMOCHHIS PGEHRPSG\SPLPACPPRAWPKAGAVASATGTO*PQLPGSRGKQ KLPFTREPPLLQAGWAVKPPWSEAKEALGQAGRPSGCMDSSAS\ POTTEGGRGSLBWGLPLLGPHHDV**RSDRLG**PP**GPOGGGGH GAPSTPGPOGEAW**LPQQTSRPKPGPQAY**PG\GSPGLQCPCK EL**RVPPGSLGPSTQCMYEPTDKHS\GGADAGLEVSTAGSRSTT GQELKGPLDAGGHAPGAPSASSSHR**GG**BEARAGGRRGST**A SSKIEGGRPROPTSDALDAUPSGARSA*GPPSPTDFTLPMR/P GSPPPA**ASAGRKGTVSTLGGGLL 5690 1424 58 PSPFAGVCAAPAPLPLLALARRDRRPCSPGABAAPWOTGGPAID CAMRTSVSALRRGATG*APCSSGABAAPWOTGGPAID OGAWRTSVSALRRGATG*APCSSGABAAPWOTGGPAIDO**DGAWATGWAFAPAPLPLLALARRDRRPCSPGABAAPWOTGGPAID OGAWRTSVSALRRGATG*APCSSGABAAPWOTGGPAIDO**DGAWATGWAFAPAPLPLALARRDRRPCSPGABAAPWOTGGPAID OGAWRTSVSALRRGATG*APCSSGABAAPWOTGGPAIDO**DGAWAGASHARHLGORLPGGHANGASHARHLGORLPGGHANGAGGRQODPEP DGLRHRGHGAASHARHLGORLPGGHANRUVRRDPOAPPGGPAP GHAAALPERTRGVAEPPAWAHAGSDAWRAGR*SQRT*ERARPH PTFQGRAGS\GGPGGGPVRPFGAGRGAHAGGGRQDPEP GNSVR**LLLMP/GVA**HGTSPFLJGBCGGGOMDSGADLPGTP KG**SHPAPTKST**SMEARKSYWNIPHR\DBGRQGVXINCLRVGG SEMWGPYSAPRPGTVFLSSFLSSPASEEN\PEUSSSFNTPFPBA 5691 107 550 ISNDEPGYNIEGWAKRGKLVELPYTVKGMDVSFSGILSFIED VARRMLATGECTPEDLCFSLQYMO**KTGTSSG*RSTPLTYPPPAG GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG CVCVYULESVPLSYS GDAPLIFSPYLSLTGNCGFAMLVEITERAMAH\CGSPGGPSLWG CVCVYULESVPLSYS TQAWTFAKENDRKGSVKRALEHLHLERGPPT**RGSHPL\QSVPCTQK PSIFSSYPI/GlLGQSGGEPGPVGGQOPVRRPEOPSCGFASMPL TSRSVPPGGALPPDSLSTTRKOLPPSTAHVRDSGKKLEVPSO RLNLPVMGATRSNLQPPRKVAVPGPTR**RQDGSKQDFSSKPLQS VPGLASTQQTLTTADSGGFGBATRAGLPGVETMGNGVD ALTVIVPKGTTHANGDPGGSNLVSTARDLESSRFSGNTEDQAP *QAGPSSLRPP\SGRT**APEWPKATGGSRCGGLSAPPWPPPAA RGE/PGSAPSHAP/PNS PRSGTTRP/PGPSSRVLYSPILTNSER ARGE/PGSAPSHAP/PNS PRSGTTRP/PGPSSRVLYSPILTNSER SLAESGLSWFSESBEKAPKLEXPDGGSLKKERRSTTVLTSPERQ PGALYWRSSRPPLWFPLRCCTWVSGFKDDNPULRFF SLAESGLSWFSESBEKAPKLEXPDGGSLKKRERPES CDDSKGGELKKPISLGHPGSLKKKRTPTAATLSPAK KVAGKPECKATDKIGKLAVKNTGLQRSSDAGRBDSJAKPPSG CDDSKGGELKKPISLGHPGSLKKKTTLTTDSER SLAESGLWFSESBEKAPKLEXPDGGSLKKERPETSTURTSPAC SLAESGLWFSESBEKAPKLEXPDGG				DGYIPAVF
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SLAESGLSWFSESEBKAPKKLEYDSGSLKMEPGTSKWRRERPES CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG	2634	3	1228	
CDDSSKGGELKKPISLGHPGSLKKGKTPFVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG				QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
CDDSSKGGELKKPISLGHPGSLKKGKTPFVAVTSPITHTAQSAL KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG				SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
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		l		ALINCOLOGICAL LATGIAL AND LOCAL TOTAL CANDOLOGY

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	1	Giutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Godon / Tanadala Maria M
1		Bedgeuce	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
i	l		VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
1	1	1	PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
	1		DEVENT AET DEEDT DAMA KORUKDERT DAMA KORUKDERT
	l		PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
			DTTQCI
5695	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
			QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
ļ			SLAESGLSWFSESBEKAPKKLEYDSGSLKMEPGTSKWRRERPES
1		_	CDDCCCCCEI VVDICI CUDGCI VVCVCDDIN IMCDITATA
İ			CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
1	}	Į.	KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
	1		IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
1			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
1	1		VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
t			PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
1			DEATER ARE DESIGNATION OF THE PROPERTY AND ASSESSMENT AND ASSESSMENT ASSESSME
1		1	PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
<u> </u>		<u> </u>	DTTQCI
5696	3	1338	GSKEPARSLHRRGSGHKSSAGKWGSVTLSTAGALG*KQLHQ*WT
ł	1	ł	QRCL\NNLSSEEFNASSSLNSLPSTPTASRRNSTIVLRTDSEKR
1	1		SLAESGLSWFSESEEKAPKKLEYDSGSLKMEPGTSKWRRERPES
	1		CDDSSKGGELKKPISLGHPGSLKKGKTPPVAVTSPITHTAQSAL
	1		
			KVAGKPEGKATDKGKLAVKNTGLQRSSSDAGRDRLSDAKKPPSG
		l	IARPSTSGSFGYKKPPPATGTATVMQTGGSATLSKIQKSSGIPV
1			KPVNGRKTSLDVSNSAEPGFLAPGARSNIQYRSLPRPAKSSSMS
	į –		VTGGRGGPRPVSSSIDPSLLSTKQGGLTPSRLKEPTKVASGRTT
] .		PAPVNQTDREKEKAKAKAVALDSDNISLKSIGSPESTPKNQASH
		l	DTATEL ACI DEBUT DAMA COMUNDOS AND DISPLOYED
			PTATKLAELPPTPLRATAKSFVKPPSLANLDKVNSNSLDLPSSS
			DTTQCI
5697	1147	47	PSEALSPPACPSAPAPRRSIISRLFGTSPATEAAPPPPEPVPAA
1			QGPATVQSVEDFVPDDRLDRSFLEDTTPARDEKKVGAKAAQQDS
1			DSDGEALGGNPMVAGFQDDVDLEDQPRGSPPLPAGPVPSQDITL
			SSEEEAEVAAPTKGPAPAPQQCSEPETKWSSIPASKPRRGTAPT
1	j		
1		•	RTAAPPWPGGVSVRTGPEKRSSTRPPAEMEPGKGEQASSSESDP
	l		EGPIAAQMLSFVMDDPDFESEGSDTQRRADDFPVRDDPSDVTDE
			DEGPAEPPPPPKLPLPAFRLKNDSDLFGLGLEEAGPKESSEEGK
+			EGKTPSKENKKKKKKGKEEEEKAAKKKSKHKKSKDKEEGKEERR
ŀ			RRQQRPPRSRBRTAA
5698	2	666	GAEAAEPQEDLPPLSQSSRFFQEQQKMNKSLGPVSFKDVAVDFT
[-		OFFWOOLD PROCESS TO STAND THE STANDARD TO
1			QEEWQQLDPEQKITYRDVMLENYSNLVSVGYHIIKPDVISKLEQ
]			GEEPWIVEGEFLLQSYPDEVWQTDDLIERIQEEENKPSRQTVFI
1			ETLI*R/ERGNVPGNTFDVETNPVPSRKIAYTHSLCNSCER\GF
			NASSEYISSDGRYARMKADECSGCGKSLLHIKLEKTHPGDQAYE
			FNO
5699	2	1448	RVRQPPGLWVRRTVPAMQCPAGLSRVPGVAG/DPSLPSFRGPRD
	-	7440	EARLIDON TOWN THE THE TOWN THE
			EAAHRGTIQTARHTRKLYVQGPASGPPLPRVSTQVAI*DEKPLA
			RPS/GRTNAPFPQGQKPAGKAAPGPAAAGRVAMR\PGHPGLLAS
1			DSQRSSSKGSGWETPVPWS*AQPGWVSGLLLLGDPSGPGSL*RS
1			TWLVGGARGPEGSGVRGSGWPSGCSDIGWALAGWNHS+HLDPNT
			WTQKWTGE/SPAPGEEG\VAPAPRGPTAEHGHCELTTESQYSNN
[VDILPONDECAL DEDDOCHARACTER TRANSPORTED TO THE TENTE TO T
			VPILFQNPSGALRSRRTEPAGWVPPTRHE*DDG*TAAPASGGAP
			VSTPTWAGTP/LNASLGPTDPQGKPGCRPPCALPKPAGPERSA*
, ,			GGSLGCR/SMLPASSGPPPAPGPRRLAAGAHTSASARCPPAAAA
ţ			GWQPRRPGFAGRAALPGPPHPPSS*RELGGLPGPGW*TLDPLPA
ļ			HPAHPPGSAPPWGALGGWAAARASLPWSPSLCLSFPAVTPVAGL
5700	633	F 6 7	FPPGRG
2,00	923	597	NGHKGVWEINIY*RRSNIHKNSKSESHLNQDHSFPPPTPNSARS
			KLHSTGTAKNTGLPLSGAPRQRAVFSGRTICQEFSSCLQCAYLD
			E*CSIASSLIKAILRVSVLSE
5701	59	410	IFEKICSDTQEFISPEINPQICSWLIFDKGAK/NHATGKDSLFN
	·		KMCMKMMI CACD+WDDCDADADADADATAGAK WWWIGKDSTKM
	1		KWSWKNWLSTCR*MRPGPYFTPYTKINSK*IK/DANIRCETVKL
Ll			LEENTGENLHDTGLGNVFLDMTPKTQPTKQK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	Talanda M. Mathianda N. Kabysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
			P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ţ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
5702	3	1517	ETFVDPSQCGGIPSDSPHPVITPSRASESSASSDGPHPVITPSR
			ASESSASSDGPHPVITPSRASESSASSDGLHPVITPSRASESSA
1	1		SSDGPHPVITPSRASESSASSDGPHPVITPSRASESSASSDGLH
1			
1			PVITPSRASESSASSDGPHPVITPSWSPGSDVTLLARALVTVTN
			IEVINCSITEIETTTSSIPGASDTDLIPTEGVKASSTSDPPALP
	l	· •	DSTEAKPHITEVTASAETLSTAGTTESAAPHATVGTPLPTNSAT
İ			EREVTAPGATTLSGALVTVSRNPLEETSALSVETPSYVKVSGAA
İ			PVSIEAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETLTMDI
			TTKGPFPTSRDPLPSVPPTTTNSSRGTNSTLAKITTSAKTTMKP
İ			PTATPTTARTRPTT\A*VQVKMEVSSSCG*VWLPRKTSLTPEWQ
1		ļ	KG*CSSSTGNSTPTRLTSRSPYCVSGEANG/PSAAARHVPYAKR
1	1		GCCP*PGPPPTDCSCVTVLRGTQKVPMKGSMSKPLTPDVATGPS
1	1		LTSTGVYVWGGASPVPRGVLGLTLAHVLCFSKEKT
5703	14	1117	
3,03	1 14	111/	HHKDSRSQGLPRTQECARPELRPLLCPRALWPVTRLSYRCPWQA
	1		PKAGIGTKAKPSESHLKLHPGWPSLDRQGEPATLGTGTGHCSDS
	1		RILRWHP*HTAAR*PRWRRLPSSHRWTRHLGVLRVQDKS**VSL
	1		DPSCRPRFLRTC**YGMRSVASSSNPPPGWSGPGASVFPARPVS
			ALPTGPRCW*APRGRTRQPCGWPRLSSPHATADWGPGCPLSPSR
	}		GSWETAPGS*WCPWL*AARWTGWRTASGASAGLGRAADRPSAWA
			RRVAGLLPGQGLTVRR*H*TAGAPASVRSSQGATRSPAPGGDQC
			ACGRGPGSC*HPPPWPVSPSSPVPCPSGR*HLRGPLLSAARPRA
	ł		AGWPRHSPHDTQTPEP
5704	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
		502	
1			SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE
	J .		QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
			KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
			SPQP
5705	23	562	GDYEFDSPYWDDISQAAKDLVTRLMEVEQDQRITAEEAISHEWI
1			SGNAASDKNIKDGVCAQIEKNFARAKWKKAVRVTTLMKRLRAPE
1			QSSTAAAQSASATDTATPGAAGGATAAAASGATSAPEGDAARAA
			KSDNVAPRRP*LPPQPQMEVPPQPLMAVSPQPPMEASLQPLMGE
			SPQP
5706	1161	610	QLGRFXAQDTVAIRKVKEVFGTGAMRHVVILFTHKED*GGQALD
			DYVANTDNCSLKDLVRECERRYCAFNNWGSVEEQRQQQAELLAV
			IERLGREREGSFHSNDLFLDAQLLQRTGAGACQEDYRQYQAKVE
	į		WQVEKHKQELRENESNWAYKALLRVKHLMLLHYEIFVFLLLCSI
ļ,	i		
5707	28	600	LFFIIFLF
] 3,0,	40	609	GSPAPTPGPRRPGRGTPSPGTRHHQGRAEPEPDAPERAPLRR*
			MFAIQPGLAEGGQFLGDPPPGLCQPELQPDSNSNFMASAKDANE
		•	NWHGMPGRVEPILRRSSSESPSDNQAFQAPGSPEEGVRSPPEGA
			EIPGAEPEKMGGAGTVCSPLEDNGYASSSLSIDSRSSSPEPACG
			TPRGPGPPDPLLPSVAQA
5708	44	1925	SFSWEETISPCFPKMPAEPWWLSPVSLGAAGWPGQPRPYLDLPA
			QASVSRPHDRA+GEAVSLSLSSGDVCGHTDGGGAGSDPQAKPKP
			PRCPFTAMPSPRTKQKVRNKVCLLIAIRYSDIPSDVSKAP\GPA
			GNPHDRSSTAA+LHRRAGAGSLCLSASLLPPSFSLGAPGAPSPL
			RVSPASGGPRKEGRQGSGG+AGGGGP\ARTHADLPCVGFVCSPP
}			
			LLK+SDSPVKQLPA\SGQGSGAGMPPVGSSDILRPRPTSVSGTG
			RAAG*CSWQPAACCTPRSQ*WAVARSPSRCSRW*RQSGR*RG*S
			SRRRRGP*AAGRSTPAVP*PCS*GGAGRRAYACRTGWGYAPSR*
	i		LEPSGPTSGSAL*TWASHSTGA**SRLCGTAGTGPLCSQSSRS*
			AG*RCCCTAASPCGGSGPSHPGSPSAHCLSWSGGRTQPRAPSAH
			GRGRAMGSRCVCTCTGLPCPGIPLSGASPGGSGETGAGRSHTLK
ļ			AARSRLSPRPGSGSRGSY*SHNDNWGTWPAPPSAGHLLVGG*NS
			QRTSSDH*YTGTRRPWAGPGTRCSTAPSRAAPPVSRCRPPPPPP
[PPRPPRLPAAAS/SGGASGSPAASCSCSCRAPAKPASS/GEAPA
			PPPRPEPPPPPARRP
5709	2	2031	
	*	2031	ITLCPLPQTEKCLNVVTEAATPLGIYLKARVEAGGLKELEISWG
			LHQIVVRWGAVVMRAGMGGCRCWGVMAPFAPR/NALSFLVNDCS
	<u> </u>		LIHNNVCMAAVFVDRAGEWKLGGLDYMYSAQGNGGGPPRKGIPE
			· · · —

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location		H=Histidine, I=Isoleucine, K=Lysine,
1	1	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence]	\=possible nucleotide insertion)
			LEQYDPPELADSSGRVVREKRSADMWRLGCLIWEVFNGPLPRAA
ì		i	ALRNPGKIPKTLVPHYCELVGANPKVRPNPARFLONCRAPGGFM
1			SNRFVETNLFLEEIQIKEPAEKQKFFQELSKSLDAFPEDFCRHK
		1	VLPQLLTAFEFGNAGAVVLTPLFKVGKFLSAEEYOOKIIPVVVK
	!		MFSSTDRAMRIRLLQQMEQFIQYLDEPTVNTQIFPHVVHGFLDT
1	i		NPAIREQTVKSMLLLAPKLNEANLNVELMKHFARLQAKDEQGPI
1	l .	İ	
ì	i	1	RCNTTVCLGKIGSYLSASTRHRVLTSAFSRATRDPFAPSRVAGV
			LGFAATHNLYSMNDCAQKILPVLCGLTVDPBKSVRDQAFKAIRS
			FLSKLESVSEDPTQLEEVEKDVHAASSPGMGGAAASWAGWAVTG
	ŀ	[VSSLTSKLIRSHPTTAPTETNIPQRPTPEGVPAPAPTPVPATPT
1			TSGHWETQEEDKDTAEDSSTADRWDDEDWGSLEQEAESVLAQQD
1	1		DWSTGGQVSRASQVS\TPTTNPPNPQSPTGAAGK\RGLLGTGLA
			GAKLPGATS*RYTAGQRV
5710	1	562	IPGSTISCEVELMARMAKTIDSFTQNQTRLVVIIDGLDACEQDK
	1		VLQMLDTVRVLFSKGPFIAIFASDPHIIIKAINQNLNSVPSGFK
		1	\LNGHDYMRNIVHLPVFLNSRGL/RQ/LQENFS*LQQQMETFHA
		1	QILQGYRKMLTEEFHRTALGR*QNLVARQPSIDG*DAIGFELYV
			CIAIOFNTNKDDAT
5711	1526	1130	RRHPFQWTTVTQEAFSHHDVAFTSTPVLFYPDSAQPFIVKSESS
] 3/11	1 1320	1 1130	SQIAKAVLSQQRPSLFHECAFHFFS*SLQRHTINLDQGIF*LLM
		į.	
	l		LSEBRQHLFESS/IWTTPHNLK*/FEIHEHLGSHEGHWTLFFLL
ļ		<u> </u>	QIL
5712	3	1391	GRKLFQSLDISERLKFLLTLDCVDDTLIVLAEBHGCLDIIKELP
			ETVIDLLNKCLTFHPSKRPTPDELMKDKVFSEVSPLYTPFTKPA
İ			SLFSSSLRCADLTLPEDISQLCKDINNDYLAERSIEEVYYLWCL
1		1	AGGDLEKELVNKEIIRSKPPICTLPNFLFEDGESFGQGRDRSS/
		Ì	TFR+YHWDIVVMPAKK+IERCWGRSILPITLKMTSLILPYSNSN
			NELSAAATLPLIIREKDTEYQLNRIILFDRLLKAYPYKKNQIWK
		1	EARVDIPPLMRGLTWAALLGVEGAIHAKYDAIDKDTPIPTDROI
			EVDIPRCHQYDELLSSPEGHAKFRRVLKAWVVSHPDLVYWOGLD
į		i	SLCAPFLYLNFNNEALVYACMSAFIPKYLYNFFLKDNSHVIQEY
ĺ			LTVFSQMIAFHDPELSNHLNEIGFIPDLYAIPWFLTMFTHVFPL
			HKIFHLW\DTLLLGEFLFPILYWE
5713	634	284	
5/13	634	284	PVCAVPVDRWPVLPREDQEGQQL*AKLPRDFRR*FQILGPMEGH
	1	j	TACRCSRRGAQVQHLPREDIRAAE*DPHLREVWPGLPTSSATSP
			*RAVLTSPCSHLGSADAASSHWLCGVSFH
5714	212	613	WGLGLGPTMSSLGGGSQDAGGSSSSTNGSGGSGSSGPKAGAAD
			KSAVVAAAAPASVADDTPPPERRNKSGIISEPLNKSLRRSRPLS
	1		HYSSFGSSGGSGGSMMGGESADKATAAAAAASLLANGHDLAAA
		1	MA
5715	131	1979	ESASQQKRSKCLILTLKLELSGSAPKKTSARPGSSLWLPPHSQE
	ļ		QTPPASKLQGGGGLQTGWGLHPVPVTAASPLPRWCLFGAVAK\
			GLPGP*LCPSGAA/GGLQRGPGLSPLGAAGKVSCLHPPSMVBNN
			DSTCHEHHEGILAARVTPVP\SGKPGRVLKPPGRVCRPPHPAAS
		1	PRPPGS/SDLDGPRPQMHLRAFPAAHGGPVNTPHGGEEKTFMSS
			QIRRKETKPL*RKTPAG\NNYQSNSIPVSQSPQLTVDLLPSAGR
			TQAPSGRGDAGKPTPGHG\LPKASVILTPNCPCSLAGGQ*PPGL
			1
		1	YPKTPKQRRWRRPL/LLGPSQ*GSRQSTC*EV\GALGEPVRIPG
			L*PDLSCILSNGSKHRREGLSFPRSLGPGRRGPAGLQSLGCSPT
			PKNTACHSSGHVALQAGHDSARDVGSGHVALQAGHDSTQDVGRP
1		}	VWRWIPLE*LGLSRETGQATRRGLVWISPGRAAAACVACAQALE
		1	EGPLRLPGQDRGAQPCSHCPGRAAGQPBPGAGAPCRE/GG*DPT
			GLT/GVPGTDPKRGGRKPGQSGQETQGPTVWSGPESPLQPKP*E
			RQE/VGAGASSGVGLSRGRAGGPSSAWEVAAMLLLLRHGSHSEL
			TDLTEAQTSQH
5716	1711	1370	RVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEHTD
1	- ·	1	*LPK*GPGYIOHFHCDSNILCILYNISFNLFSYSF*GVARYAC*
1.			RCPLVL*SGFFTIIVGGYSCCMPLKT
5717	44	1489	LPTEALRESEWVSEYGKCGPRGLVPEGESTSPLPSSVDTEDSLD
1 3/1	***	1403	
L	L	1	EGPGALVLESDLLLGQDLEFEEEEEEEEGDGNSDQLMGFERDSE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	1	\=possible nucleotide insertion)
			GDSLGARPGLPYGLSDDESGGGRALSAESEVEEPARGPGEARGE
			RPGPACQLCGGPTGEGPCCGAGGPGGGPLLPPRLLYSCRLCTFV
1			SHYSSHLKRHMQTHSGEKPFRCGRCPYASAQLVNLTRHTRTHTG
			EKPYRCPHCPFACSSLGNLRRHQRTHAGPPTPPCPTCGFRCCTP
		1	RPARPPSPTEQEGAVPRRPEDALLLPDLSLHVPPGGASFLPDCG
			Q\CGVKGRASAGLDQNHCQS/SLFPWTCRGCGQELEEGEGSRLG
ļ			AAMCGRCMRGEAGGGASGGPQGPSDKGFACSLCPFATHYPNHLA
1			
1		1	RHMKTHSGEKPFRCARCPYASAHLDNLKRHQRVHTGBKPYKCPL
F73.0	100		CPYACGNLANLKRHGRIHSGDKPFRCSLCNYSCNQSMNLIRHM
5718	120	284	VAHALSLPAESYGNDVSMTHPQLPPTQLAWDLCRTCLPLSYNFT
L			S**STADPLHL
5719	48	428	ELNNGPFQMPLCNGGNLAVTGSWADRSPLHEAASQGRLLALRTL
1		1	LSQGYNVNAVTLDHVTPLHEACLGDHVACARTLLEAGANVNAIT
		1	IDGVTPLFNACSQGSPSCAELLLEYGAKAQP\ESCLPSP
5720	i	1051	LQAFRNASEVPMVLVGTQDAISAA\NPRVYRRTSRARKLSTDLK
			\RCT\YYE\TCGGTYGLQMWSVSFQDVAQKVVAL\RKKQQ\LAI
		1	GPCK\SLPN\SPSH\SAVSAASIPARAPINQGHE\SGGGSAFSD
i			Y\SSSVPSTPSISQRELRIETIAASSTPTPIRKQSKRRSNIFTS
	1		RKGADP\DREKKAAGCKVDSIGSGRAIPIKQGILLKRSGKSLNK
ł	1		EWKKKYVTLCDNGLLTYHPSLHDYMQNIHGKEIDLLRTTVKVPG
1	{	1	
		ł	KRLPRATPATAPGTSPRANGLSVERSNTQLGGGTGAPHSASSAS
			LHSERPLSSSAWAGPRPEGLHQRSCSVSSADQWSEATTSLPPGM
			QHPASG
5721	97	492	RHSSPCCSLRRTERSSNAAVST/TTVQQFKRFIENYRRHIGCVA
		1	VFYAIAGGLFLERAYYYAFAAHHTGITDTTRVGIILSRGTAASI
			SFMFSYILLTMCRNLITFLRETFLNRYVPFDAAVDFHRLIASTA
5722	88	1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
	1	1	GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP
1			QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR
J			GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG
1			GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPAPA
	i		PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
			RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
		ĺ	KSSTREIPEMI
5723	88	1043	VALDVLAGSSPGGGMAGALLGPRVHGIRAVLRVARGGVQAPGAP
			GSLGVSHAAAPPARPQGAAQSPHRGRRHGGGGAGLPPPRSPRFP
			QESVPASTSTARGPRRVSRRLPPQHPGPRGRRRRPGAGVGAPRR
			GRARGQAGLLGRQGQGGRGAERERAALQARRGRRPGPEPDQSCG
	1		GRPRRAAAAPGRAPADPQPPAPRPAPAPDVRPPADAPAPAPA
ļ	1		PPPPPHLGALTAGSGEERQSQPRAETLRLGRGAPLP\PRAERGG
		1	RPKQAEQQQ\PKRPTPPARGPQSSGDPAMLPQRAGLRTGGLAGT
	ļ		KSSTREIPEMI
5724	3	1841	FTNEAPPAPLPDASASPLSPHRRAKSLDRRSTEPSVTPDLLNFK
	1		KGWLTKQYEDGQWKKHWFALADQSLRYYRDSVABEAADLDGBID
] .	LSACYDVTEYPVQRNYGFQIHTKEGEFTLSAMTSGIRRNWIQTI
	†	1	MKHVHPTTAPDVTSSLPEEKNKSSCSFETCPRPTEKQEAELGEP
	1	1	DPEQKRSRARE\RRREGRSKTFDWAEFRPIQQALAQERVGGVGP
1			ADTH\DPWRPEAEHGELERERARRREERRKRFGMLDATDGPGTE
			DAALRMEVDRSPGLPMSDLKTHNVHVEIEQRWHQVETTPLREEK
	1	1	QVPIAPVHLSSEDGGDRLSTHELTSLLEKELEQSOKEASDLLEO
			NRLLQDQLRVALGREQSAREGYVLQATCERGFAAMEETHOKKIE
}			DLQRQHQRELEKLREEKDRLLAEETAATISAIEAMKNAHREEME
			RELEKSQRSQISSVNSDVEALRRQYLEBLQSVQRELEVLSEOYS
}		}	
			QKCLENAHLAQALEAERQALRQCQRENQELNAHNQELNNRLAAE
1	1	}	ITRLRTLLTGDGGGEATGSPLAQGKDAYELEVPSGARPCLTQLC
			TQEPQGSAAWPLSYRVVGGTDLRQQESQGPGRSKSPEGGEEQ
5725	3	1049	VNGHSEETSQSPNRTEPHDSDCSVDLGISKSTEDLSPQKSGPVG
	1		SVVKSHSITNMEIGGLKIYDILSDN\DLSSHLQPLK/FTSAVDG
	1		KNIVRSKAATLLYDQPLQVFTGSSSSSDLISGTKAIFKFDSNHN
L			PE/GAKYNKRPHKWAHNLHLKYMVLHSIISNTVAV\RSQRHFVA

Deginning incleation corresponding or fire to first amino acid amino acid amino acid amino acid sequence of residue of residue of amino acid sequence of residue of resi	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
Sociation Corresponding		t .		(A-Alapine C-Ousteins D-Assaulti Brid D
Cortesponding	1		Y .	Glutamic Acid F-Dhonylalanina G Cluster
Leucine, M-Methionine, N-Asparagine, Popular damino acid amino acid sequence acid sequence acid sequ	"""	1		U. Wietidine T. Tankaraine, G-Glycine,
to first amino acid residue of shino acid amino acid amino acid amino acid sequence		•		Introducing, Mathining, Kabysine,
amino acid residue of amino acid sequence Sequence				Debeddine, Memethionine, Neasparagine,
residue of anino acid sequence (Codon, '-possible nucleotide deletion, '-voposible nucleotide deletion, '-voposible nucleotide deletion,' '-voposible nucleotide deletion,' '-voposible nucleotide insertion)	1	1		P=Proline, Q=Glutamine, R=Arginine,
Sequence Codon, /-possible nucleotide deletion,	1	1		S=Serine, T=Threonine, V=Valine,
Sequence				W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
LGTKSPNBFOOFSSSAPS/UDGRAO/INGSYAKJISANNNFSHIBN NYRANTAYHHIGHGUPARHEEMMAI SINDRIJ PANTSTIORGS SVSSTASVNIJOPGSTRRAQI PEGDYLSYREFISAGRTPPMWFG SQRPLSARTYS IDGPANSRFQSARPS INSI PERTMSVSDFYNYS TSP 5726 2 486 SRSISMWINSGIPASSHSSKLFYTOGFSGCVELLHGEPLAAD TRMAGVTPCILAPLEAGLEPPSGGVITL/BSVGAILGESRAG GSSGGSGEPPLSSSPQLRADLEGATLPOVIGLEEVRPLAVT GLIPHLIGAATPYLOLOVTEKOVLLEADDG GSSGGSGPPLSSSPQLRADLEGATLPOVIGLEEVRPLAVT GLIPHLIGAATPYLOLOVTEKOVLLEADDG TRMAGVTSTPNNSSKRSSLPRGS 5727 21 221 RPILITIKESTERIPARTYATEVTIKAKSTINEDGASCEVLTVKKK AGAVTSTPNNSSKRSSLPRGS GRAGGAGGAG/LFGGTSFAGAAGGFGVORPRGSG/LFG GRAGGAGGAG/LFGGTSFAGAAGGFGVORPRGSG/LFG GRAGGAGGAG/LFGGTSFAGAAGGFGVORPRGSG/LFG GRAGGAGGAG/LFGGTSFAGAAGGFGVORPRGSG/LFG GRAGGAGGAG/LFGGTSFAGAAGGFGVORPRGSG/LFG GRAGGAGGAG/LFGGTSFAGAAGGFGVORPRGSG/LFG GRAGGAGGAG/LFGGTSFAGAAGGFGVORPRGSG/LFG GRAGGAGGAG/LFGGTCFAGAFAGAAGGFGVORPRGSG/LFG GRAGGAGGAG/LFGGTCFAGAFAGAAGGFGVORPRGSG/LFG GRAGGAGGAG/LFGGTCFAGAFAGAAGGFGVORPRGSG/LFGG GGPAGGAGGAG/LFGGTCFAGAFAGAAGGFGVORPRGSG/LFGG GGPAGGAGGAG/LFGGTCFAGAFAGAAGGFGVORPRGSG-GFGGTAGAAGAGGAGA/LFGGTCFAGAFAGAAGAGAGAGAGAGA/LFGGTCFAGAFAGAAGAGAGAGAGAGAGAA/LFGGTCFAGAAGAGAGAGAGAAGA/LFGGTCFAGAAGAAGAAGAGAGAGAAGAAGAAGAAGAAGAAGAAGA			sequence	Codon, /=possible nucleotide deletion,
NVRANTAYHLHORLOPARHGEMMAISENDRLIPAVTESTIQAGE SVSSTSAVNIG,DOSDRARQIPSONISYERPISAGAETPOMMOS SQRPLSARTYS DOSPASSRERQI PEGOTYSYREPISAGAETPOMMOS SQRPLSARTYS DOSPASSRES PINEIPERTMSVSDFNYSR TSP 5726 2 486 SRSLSHWHNSGLPSSISSKLTYTOGSSCVERLE-HERBICASD COSPGGSGEOPLESSPODLDADLCATLEPONGELEVER, LAVOUR CLIPHIQASTPPHILOLOVTEKOVLLARDOS GLIPHIQASTPPHILOLOVTEKOVLLARDOS 5727 21 221 PEILILKETER, PRATITYAREVITA AND COSPGGSCEOPLESSPODLDADLCATLEPONGELEVER, LAVOUR CLIPHIQASTPPHILOLOVTEKOVLLARDOS GRANDATEN DE LANDACAR PURILARDOS CEVILTYKKK AGANTSTENNIS SURPSIS LANDACA GARVETENNIS SURPSIS LANDACA GARVETENNIS SURPSIS LANDACA GARVETENNIS SURPSIS LANDACA GARVETENNIS SURPSIS LANDACA GARVETENNIS SURPSIS LANDACA GARVETENNIS SURPSIS LANDACA GARVETENNIS SURPSIS LANDACA GARVETENNIS SURPSIS LANDACA GARVETENNIS SURPSIS LANDACA GARVETENNIS SURPSIS LANDACA GARVETENNIS COMPANIS AND COMPANIS COM	L	sequence		\=possible nucleotide insertion)
SVSSTASVNIGPOSTRRAQIPSOVILSYREFISACRIPPMWS SQRPLSARTYSIDOPMSREGORARPSINEIPERTMSVSDPYNYS TSP 5726 2 486 SRSILSHWINSGLPASSHSSKLFYTVGFSGCVYELRHGRPLAD TRIAGGTPCILOPLEAGLPPCSGCVITL/RSVOADIGGSEAG CGSPGGGEDPLSSGGLPTLOPUGELEVRPLAVT GLIPHLGQASTPPVLLGATLPDVGLELEVRPLAVT ALIPHLGQASTPPVLLGATLPDVGLELEVRPLAVT LILHERTERLPHATYAEVINAGKSTHNEDGASCEVLTVKK AGAVTSTPNRISSKRRSLPNGE 5728 2 877 GTRRGGFSPRGRARGGSGGIRAGGANAGGFGVOPGRGSG/LPG NARRGONFORGABLSPRULSLEPROLAGESCVLTVKK AGAVTSTPNRISSKRRSLPNGE GRAGGGIBAGGANGGFGVOPGRGSG/LPG NARRGONFORGABLSPRULSLEPROLAGESCOLFORGASCPLPAVE GRAGGGIBAGGANGGANGGGFGVOPGRGSG/LPG NARRGONFORGABLSPRULSLEPROLAGESCOLFORGASCPLPAVE GRAGGGIBAGGANGAGGANGGARGGANGGAPGVOPGRGSG/LPG GGRAGGGIBAGGANGAGGANGGARGGANGAGAPGADFPAVE GRAGGGIBAGGANGAGARGGANGAGAPGAGAPGAPAVE GRAGGGIBAGGANGAGARGAGAPGAGAPGAGAPGAGAPAVE GRAGGGIBAGGANGAGARGAGAPGAGAPGAGAPGAPAVE GRAGGGIBAGGANGAACAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	ļ			LQTKSPNRPCQFSSSAPS/VDQRAQ/INQSYAKHSANMNFSNHN
SQRPLSARTYSIDGPNASRPGSARPSINEIPERTMSVSDPNYSR			İ	NVRANTAYHLHQRLGPARHGEMWAISPNDRLIPAVTRSTIQRQS
SQRPLSARTYSIDGPNASRPGSARPSINEIPERTMSVSDPNYSR	i			SVSSTASVNLGDPGSTRRAQIPEGDYLSYREFHSAGRTPPMMPG
S726 2 486 SRSISWWINGILPROSCUTEL/RIGRPLAAP TRWAGVTPCILGPLEAGLPPOSCOVITL/ESVGAGIDQDSEA OGSGGGGGGGGGTESPSSPOLPAGTATPOVALERWPLAAV GLIFHLGGATTPPVIJOLOVTEKOVLIRADDO SPILLIKETRELSSSPSOLPAGNETSSTEVLDEAGT TRYAGVTSCHIRGSSTEVLDAGT GLIFHLGGATTPPVIJOLOVTEKOVLIRADDO SPILLIKETRELSSSSPOLPAGTATAGRAAGGPSCEVLTVKKK AGAVTSTENINSKRISSLPNOE STORY GREEN CONTROL SPILLIKETRELSKRISSLPNOE GERMAGGATSPARAGGAAGGPOVQPRGSG/LPG NAIRAGVNPGRGPASPFWIJOLIPHDIMPPTDEHAGAPDPPAVE GR. PANAGRPPWPVSOVLOSROVCOPLYSTSSBADFG/SGGISPGGGGACAGGAG/LPGCRAAAGGPOPAVE GR. PANAGRPPWPVSOVLOSROVCOPLYSTSSBADFG/SGGISPGGGGACAGGAG/LPGCRAAAGGPOSGGISPGGGGGACAGGAGA/LPGCRAAAGGPOPAVE GR. PANAGRPPWPVSOVLOSROVCOPLYSTSSADFG/SGGISPGGGGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG				SQRPLSARTYSIDGPNASRPQSARPSINEIPERTMSVSDFNYSR
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STATE	ŀ			OGSPGGSGEGPPLSSPSOPLPADI.PGATI.PDVGI.FI.FVPDI.AUT
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NAIRAGVNPGGPASPFWDLSLUMDLWPPTDHAPGADPPPAWS GR\PMAGGPPPWPWGSGVGLSEWCQPLYSTAGG/SGGLSPSQ GGP\AGGACGDAG/LogCCPsapwragsrpaascpdwipgpqglwl HRNPTS/GPPSQIGGGAEQGDGVADAGQICCKW/GABPPAGE EPPQVPEAGEDAVPABEGPGGTFETQADAGGRAIDFAEG FPPQVPEAGEDAVPABEGPGGTFETQADAGGRAIDFAEG KGSPRIADPQDLPAGQWSLAPPFPPVAAVITSNK AGGARSVLTQLGHHFAGYGGAHWWNQQDAALGRATDSKEPPGGL CPDVLWRTGRTLHGGGTTTPRLILMDLKGSLSSLKEEGGLYRDK KGSPRIADPQDLPAGQWSLAPPFPPVAAVITSNK KSIPNGKGSSPLPPTTPKLTLMDLKGSLSSLKEEGGLYRDK KSIPNGKGSSPLPPTTPKPLIPTBASTRVMGDFLRVHLHPRSI CMIQKYNHDGBAGRLEAPGQGSVLKEPKYPELGALFYVEE CDTLQGPGILCDLHGDFSGVGAKAAELLQDEYSGRGITTWGLLP GPYHRGBAGRITYRLLNTAFGLVHLTAHSSLVCPLSLGGSLGLR PEPPVSFFYLHYDATLPPHCSATLATALTGSLYPCHSYBRIC GPYHRGBAGRITYRLLNTAFGLVHLTAHSSLVCPLSLGGSLGLR PEPPVSFFYLHYDATLPPHCSATLATALTGSLYPCTSYPES MYHLLADMLSFCGKKVVTAGAIIPFPLAGGSLDDGSLAMFGGAT PWTFLSACGSESGTGGFAGSVVLRGIDRAFGLYFOCHAFF PWTSSACGSPGTSTGGFAGSVVLRGIDRAFGLYFOCHAFF PWTSSACGSPSGTGGFAGSVVLRGIDRAFGLYFOCHAFF PWTSSACGSPSGTGGFAGSVVLRGIDRAFGLYFOCHAFF PWTSSACGSPSGTGGFAGSVVLRGIDRAFGLYFOCHAFF SCSPPGWLADLGSKGAAVEGPGGFAGFHEDLWAT KISTEGFFERPRFFENGGFLKSPGGEDCFGCGGGSSTY*AQ GSSSREKGGQASWNFLLKVA GSSREKGGGASWNFLLKVA GSSREKGGGAGSWNFLLKVA SSREKGGLTRAFATAGAKFLATARTKLATANI UN LLGTKEQAHRAFATAGAKFLATARTKLATANI UN LLGTKEQAHRATALANFRCGGRKODPGFIKKYGGIGWYLDEKNIAA QVSTHILDFEVTALHTVVEFTCREAGELSLPVVGSQLVGLVPLK ALLDAA ACQUSMWVTRNAMYFANDFPRMKREGLYVVGGGWYLDEKNIAA QVSTHILDFEVTALHTVVEFTCREAGELSLPVVGSQLVGLVPLK ALLDAA ACQUSMWVTRNAMYFANDFPRMKREGLYVVGTGWYLDEKNIAA QVSTHWVTRNAMYFANDFPRMKREGLYVVGTGRWYLDEKNIAA QVSTHWVTRNAMYFANDFPRMKREGLYVVGTGRENKSAYM ACQUSMWVTRNAMYFANDFPRMKREGLYVVGTGREKNAMPATFFTUFFUT GSLFLMMLLTAAITSGFRGVLMSSLOTSLFRRFLATAFEVLS SMCGEGGFPOAGVVKPONLAULDLVGLVGLDSHGAAMFURSY GSULLSABEPOKLFWELDRSVVKEHPPRPEYQSPFLQSAQFLFG HYYFDYLGNLLALANLUSICVELUDDVULAPERDBILGILIUN VFIVYTLLEMLLKVPALGREGVLSVFENVEGGTSCCLDSGRIGATHSAYM ACQUSMWVTRNAMYFALDRGRVJSSFRGAGGGTSCCLDFAGTGTSLILGH VFIVYTLUEMLLKVPALGREGTSSCPLVDLTVLLIVLISIS TLVCTTCHTOHGGGRRW/SLSPROGGTSCCLDFAGTGTSLILGH YPVFPWLTNYSEBELDLTLPORFDLSKPILOTARTUFLISIGT YPVFPWLTNYSEBELDLTLPORFDLSKPILOTARTUFLAGR	5729		077	
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HRNPTS/GPPSGIGBGAEGQBGDXUADAGCIQCKN/GAEDPPAED EPPOVPEAGEDADADAGCTPSTOADQVERRPEAHLAEGGA KGSPRILADPQDLPAGQMSLAPPFPPVAAVIRSNK AGGARSVLTLGLGHFAGFVGAHWMQQDAALGRADSKEPFGEL CPPOVLWTGRTHHAGGTYTPRILIMDLKGSLSSLKEEGGLYRDK CLDAATAMGGKILTHKEELYPKNPYLQDFLSAEGVLSSDGWRW KSIPNKKGSSPLPTATTPKPLIPTEAS CMIQKYNHIGGBAGRLEAPFQGESVLKEPKYQEBLEDRLHFYVEE CDYLQGFQILCDLHOGFSGVGAKAAELLQDEYSGGSITMGLLP GPHRGEAGRNIYRLLANTAFGLVHITAHSSLVCPLSLSGSIGGR GPHRGEAGRNIYRLLANTAFGLVHITAHSSLVCPLSLSGSIGGR GPHRGEAGRNIYRLLANTAFGLVHITAHSSLVCPLSLSGSIGGR GPHRGEAGRNIYRLLANTAFGLVHITAHSSLVCPLSLSGSIGGR GPHRGEAGRNIYRLLANTAFGLVHITAHSSLVCPLSLSGSIGGR GPHRGEAGRNIYRLLANTAGALIPPHAPQSSLPDSIMM/GGAT GWHALACATGGEFILAQVILOQOPGWMSSSHLLLTPGRVAPPYPHLFS SCSPPGMVLLOGSPKGAAVESVPVPG KKPQAFARETCVECQKTVYPMERLLANQOVFHISCFRCSYCNNK KLSGTYASLHGRIYCKYPHROLIPKSKONYDEGFGRPHKDLWAT KISTGFMERPRHFENQGFPLKSONYDEGFGRPHKDLWAT KISTGFMERPRHFENQGFPLKSONYDEGFGRPHKDLWAT KISTGFMERPRHFENQGFPLKSONYDEGFGRPHKDLWAT KISTGFMERPRHFENQGFPLKSONYDEGFGRPHKDLWAT KISTGFMERPRHFENQGFPLKNYDLGFSKONYDEGFGRPHKDLWAT KISTGFMERPRHFENQGFPLKNYNLENYRNLESVGLTSKDSWYMK KROGRGKQRKQBMFPLRYY FSPSSCQSPRRKSGANPHKHRVENYNLESVGLTSKDSWYMK KPGRGKGKQRRQBMFPLRYY PFSSSCQSPRRKSRRRAHTVTVLVCGTSFSFSLFLVLCGLEF FPSELCOLOQADWADPFGSSFVENGATATGARKFLIARN LN LLGTKRQAHRIALMLERQGRGKQDGGRLKKVQGIGWYLDEKNLA QVSTNLLDFEVTALHTVYEETCREAGELSLPVUSQLVGLVPLK ALLDAA QVSTNLLDFEVTALHTVYETCREAGELSLPVUSQLVGLVPLK ALLDAA GSLFLMNLLTALITYSGFRGYLMYNLIFFTENTYNDEN GSLFLMNLLTALITYSGFRGYLMYNLIFFTENTYNDEN GSLFLMNLLTALITYSGFRGYLMYNLIFREDADDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFGGLTSVLGNARNSL GSULSABEFQKLFNELDRSVVKHHPPREYGSFPLQSAGFLING HYYFDYLGNLTALANUSCUCPULJALDHARDDDFILGILNC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFGGLTSVLGLINC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFGGLTSVLGLINC VFIVYYLLEMLLKVFALGLRGYLSYPSNVFGGLTSVLGLINC VFIPCVARANNFDQATVKAAYSLPRVGGGTSCGLFQARRISL ATPROLVKY,SSNNTORMORREISNFFEYLHFINTTAGRTVYNDLN ATPROLVKY,SSNNTOR		1		GR\PWAGGRPPWPVSGVLGSRVCGPLYSTSPAGPG/SGGLSPSQ
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ST329 1 1525 ARGAREVILLQUETRAGPYONANINANK		1		HKNPTS/GPPSQIGEGAEQGDEGVADAPQIQCKN/GAEDPPAED
1 1525 AGGAREVLTLGLGHFAGFVGAHRWBQQDAALGRATDSKEPFGEL CPDVLYRTGRTLHQGETYTPRLILMDLKGSLSSLKERGGUYRK GLDAALAMGGKLTHKEELYPRNYLQDFLSAEGVLSDGWRW KS IPNGKGSSPLPTATTPKPLITTASIRWBSDFLWSLHFRSI CMIQKYNHGEGAGGLBAFGQGSVLKERGGWRWK KS IPNGKGSSPLPTATTPKPLITTASIRWBSDFLWSLHFRSI CMIQKYNHGEGAGGLBAFGQGSVLKAERDLQDFLSGRGITWGLLP GPYHRGBAQRILAFGGGSVLKAERDLQDFLSGRGITWGLLP GPYHRGBAQRILAFGGWSVLKAERDLTDVTCS\YRLCSSPUS MYHL\ADMLSPCGKKVVTAGAIIPPPLAPGGSIPDSLMQFGGAT PWFPLSAGCSPSGTRGFAGSVVLKGIPGHTSQGTFGTPPPGA LHACTTGEFILAQVLQQDPGWMSSSHLLLTPCRVAPPPPHLFS SCSPPGMVLDGSPKGAVESVPVFO KKFPQAFARFTCVECQKTVYPMERLLANQQVFHISCFRCSYCNK LSLGTYASLHGRIYCKPHYNQLFKSKGMYDGFGGRPKKDLWAT KIETGFFMERFRFRFERGSVVLKGIPGHTSQFTGCATGATGATGATGATGATGATGATGATGATGATGATGATGA	1			
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SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	1	1	1
Į.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1			
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
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	1		
		i	PGEPGLLVAPVSQQSPFLGYAGGPELAQGKLLKDVFRPGDVFFN
1	Į.	1	TRDLLVCDDQGFLRFHDRTGDPFRWKGENVATTEVAEVFEALDF
	1	1	LQEVNVYGVTV
			
5740	265	231	PAYWLKVPTLCLESKTDLREKASHVSAQLQGEVRGLAGALWM*A
l			YVYERVYN*NISRMVHALEQKRHPAGLSSSMALQLNPCLGMLMA
	1		LOSELHKLYDEETOSWVSGSACGGYP
		+	1
5741	1	650	PRKTMRRGVLMTLLQQSAMTLPLWIGKPGDRPPPLCGAIPASGD
	1		YVARPGDKVAARVKAVDGDEQWILAEVVSYSHATNKYEVDDIDE
			EGKERHTLSRRRVIPLPQWKANPETDPEALFQKEQLVLALYPQT
1	1		
			TCFYRALIHAPPQRPQDDYSVLFEDTSYADGYSPPLNVAQRYVV
			ACKEPKKK*CRLADSPSPNDTGQDSRGRAGIKHIPPLKKK
5742	2	362	TOSVKEILKRNPNVNLTDKDGNTALMIASKEGHTEIVODLLDAG
] 3,772	1 -	1	1 7
1			TYVNIPDRSGDTVLIGAVRGGHVEIVRALLQKYADIDIRGQDNK
t	j	1	TALYWAVEKGNATMVRDILQCNPDTEICTKDG
5743	2	415	GKTPEGIDAIEEIEIDLEETEREISPQENGLEEVKPLGEMOTDL
3/43		1 112	-
1			KATGREISPREKTPEVIDATEEIDKDLEETGRREISPEENGPEE
			VKPVDEMETDLKTTGREGSSREKTREVIDAABVIETDLEETERE
1	1	1	ISPQE
	+		·
5744	3	703	TRRTTTTSPTTTROMTTTPAALPTTVVTTPDLTTGTPLOMTTIA
}		1	VFTTANTCLSLTPSTLPEEATGLLTPEPSKEGPILTAESETVLP
1		1	SDSWSSAESTSADTVLLTSKESKVWDLPSTSHVSMWKTSDSVSS
		į.	
	1	1	PQPGASDTAVPEQNKTTKTGQMDGIPMSMKNEMPISQLLMIIAP
ļ	1	1	SLGFVLFALFVAFLLRGKLMETYCSQKHTRLDYIGDSKNVLNDV
i	1	1	QHGREDEDGLFTL
E745	1400	599	GKSRFVNLMKHSKKTYDSFQDELEDYIKVQKARGLEPKTCFRKM
5745	1400) 599	
1	1	1	KGDYLETCGYKGEVNSRPTYRMFDQRLPSETIQTYPRSCNIPQT
			1
1			VENRLPOWLPAHDSRLRLDSLSYCOFTRDCFSEKPVPLNFNOOF
			VENRLPQWLPAHDSRLRLDSLSYCQFTRDCFSEKPVPLNFNQQE
			YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR
			YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR
			YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPBEGR EKSEEBRSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI
			YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPBEGR EKSEEBRSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF
5746	3	821	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPBEGR EKSEEBRSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI
5746	3	821	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPBEGR EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES
5746	3	821	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE
5746	3	821	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP
5746	3	821	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE
5746	3	821	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT
5746	3	821	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER
5746	3	821	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQEEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPERSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA
5746	3	821	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER
			YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPERSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV
5746	3	821	YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG
			YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPPPPPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG PSPRGKGYSSNYRRSPERPTGDLRERIKNKRQDVDTEPQKRNTE
			YICGSHGVEHRVYKHFSSDNSTSTHQASHKQIHQKRKRHPEEGR EKSEERSKHKRKKSCEEIDLDKHKSIQRKKTEVEIETVHVSTE KLKNRKEKKSRDVVSKKEERKRTKKKKEQGQERTEEEMLWDQSI LGF SFASGRLTPSSPAFDGELDLQRYSNGPAVSAWSLGMGAVSWSES RAGERRFPCPVCGKRFRFNSILALHLRTHQPERPRSPAARLLLE LEERALLREARLGRARSSGGMQATPATEGLARPQAPSSSAFRCP YCKGKFRTSAERERHLHILHRPWKCGLCSFGSSQBEELLHHSLT AHGAPERPLAATSAAPPPQPQPQPPPQPEPRSVPQPEPEPQPER EATPTPAPAAPEEPPAPPEFRCQVCGQSFTQSWFLKGHMRKHKA SFDHACPV DRHVETLCIHFLGPSTGSTAKTGGRNWLKTGNCLYGNTCRFVHG

C-070	1 6 1 1 1 1		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequence	
	Bequence	-	\=possible nucleotide insertion)
	1		SDNGDINYDYVHELSLEMKRQKIQRELMKLEQENMEKREEIIIK
ì			KEVSPEVVRSKLSPSPSLRKSSKSPKRKSSPKSSSASKKDRKTS
ſ	1		AVSSPLLDQQRNSKTNQSKKKGPRTPSPPPPIPEDIALGKKYKB
			KYKVKDRIEEKTRDGKDRGRDFERQREKRDKPRSTSPAGQHHSP
	1	ļ	ISSRHHSSSSQSGSSIQRHSPSPRRKRTPSPSYQRTLTPPLRRS
	i		ASPYPSHSLSSPQRKQSPPRHRSPMREKGRHDHERTSQSHDRRH
		1	ERREDTRGKRDREKDSREEREYEQDQSSSRDHRDDREPRDGRDR
	1		RE
5748	934	473	
3,40	334	3/3	SEGPQVFYKGLAPTLIAIFPYAGLQFSCYSSLKHLYKWAIPAEG
	1	}	KKNENLQNLLCGSGAGVISKTLTYPLDLFKKRLQVGGFEHARAA
		1	FGQVRRYKGLMDCAKQVLQKEGALGFFKGLSPSLLKAALSTGFM
			FFSYEFFCNVFHCMNRTASQR
5749	552	1	GFPVDPRVRGSTLSLAERPKGMIRSGSFRDPTDDVHGSVLSLAS
			SASSTYSSAEERMQSEQIRKLRRELESSQEKVATLTSQLSANAN
1			LVAAFEQSLVNMTSRLRHLAETAEEKDTELLDLRETIDFLKKKN
			SEAQAVIQGALNASETTPKELRIKRQNSSDSISSLNSITSHSSI
			GSSKDADA
5750	22	866	IFISICLWNAHLCFLLLPKDCIDQVMKLQNLPVDDSGRYLAIQF
			III PHA VIET VIVENDUA VOOLDTA VOOLOTA CON CONTRACTOR
			HLEWAYVFLYYYEYRKAKDQLDIAKDISQLQIDLTGALGKRTRF
			QENYVAQLILDVRREGDVLSNCEFTPAPTPQEHLTKNLELNDDT
1		ĺ	ILNDIKLADCEQFQMPDLCAEEIAIILGICTNFQKNNPVHTLTE
	1		VELLAFTSCLLSQPKFWAIQTSALILRTKLEKGSTRRVERAMRQ
			TCALADQFEDKTTSVLERLKIFYCCQVPPHWAIQRQLASLLFEL
			GCTSSALQIFEKLEMWE
5751	3	751	SCGSALRAWRCGAAALATFPAPALPGLMYRALYAFRSAEPNALA
l			FAAGETFLVLERSSAHWWLAARARSGETGYVPPAYLRRLOGLEO
			DVLQAIDRAIEAVHNTAMRDGGKYSLEQRGVLQKLIHHRKETLS
			RRGPSASSVAVMTSSTSDHHLDAAAARQPNGVCRAGFERQHSLP
			SSEHLGADGGLFQIPLPSSQIPPQPRRAAPTTPPPPVKRRDREA
ł			
5752	3	471	LMASGSGGHNTMPSGGNSVSSGSSVSSCI
3/32	3	4/1	GPVCGVGLSVAWAGPWRGPVHSVGGGGRAALHGAELPCLSGAAT
			VEREMELRHKNEMLRVETBARARAKAERENADIIREQIRLKASE
	1		HRQTVLESIRTAGTLFGEGFRAFVTDRDKVTATVNIFIKQGWQV
	,		AERQHVGASWSPRSCPCRLCTAL
5753	34	483	DDSXAIPGGVQAPFGAVRNIYTPRTGHRIRKLDQIQSGGNYVAG
			GQEAFKKLNYLDIGEIKKRPMEVVNTEVKPVIHSRINVSARFRK
	-		PLQEPCTIFLIANGDLINPASRLLIPRKTLNQWDHVLQMVTEKI
	1		TLRSGAVHRLYTLEGRLV
5754	14	331	TLVHVVEPAGEHAEAIASREQEVLQGWKELLSACEDARLHVSST
1]		
			ADALRFHSQVRDLLSWMDGIASQIGAADKPRCPSSLLGLPASPW
5755	-	000	WPTPATPSPLTAPFSME
3/33	3	888	LGDQFYKEAIEHCRSYNSRLCAERSVRLPFLDSQTGVAQNNCYI
			WMEKRHRGPGLAPGQLYTYPARCWRKKRRLHPPEDPKLRLLEIK
			PEVELPLKKDGFTSESTTLEALLRGEGVEKKVDAREEESIQEIQ
			RVLENDENVEEGNEEEDLEEDIPKRKNRTRGRARGSAGGRRRHD
}			AASQEDHDKPYVCDICGKRYKNRPGLSYHYAHTHLASEEGDEAQ
1	1		DQETRSPPNHRNENHRPQKGPDGTVIPNNYCDFCLGGSNMNKKS
			GRPEELVSCADCGRSAHLGGBGRKEKEAAA
5756	3	621	SSKLQALFAHPLYNVPEEPPLLGAEDSLLASQEALRYYRRKVAR
			WNRRHKMYREQMNLTSLDPPLQLRLEASWVQFHLGINRHGLYSR
]		SSPVVSKLLQDMRHFPTISADYSQDEKALLGACDCTQIVKPSGV
	1		HLKLVLRFSDFGKAMFKPMRQQRDEETPVDFFYFIDFQRHNAEI
			AAFHLDRILDFRRVPPTVGRIVNVTKEIL
5757	3	473	YKDALLLPDNHRQVVFENGTLKLTDVQKGMDEGEYLCSVLIQPQ
	[LSISQSVHVAVKVPPLIQPFEFPPASIGQLLYIPCVVSSGDMPI
			RITWRKDGQVIISGSGVTIESKEFMSSLQISSVSLKHNGNYTCI
]		ASNAAATVSRERQLIVRVPPRFVV
5758	1	474	FRRGAGAERGEHREGERGAAGMGEFKVHRVRFFNYVPSGIRCVA
	-	-/=	l i
			YNNQSNRLAVSRTDGTVEIYNLSANYFQEKFFPGHESRATEALC
L	لــــــــــــــــــــــــــــــــــــ		WAEGORLFSAGLNGBIMEYDLQALNIKYAMDAFGGPIWSMAASP

	5: 31 3	D	Amino acid segment containing signal peptide
ו עב	Predicted	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	beginning		
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of.	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 - · ·	\=possible nucleotide insertion)
			SGSQLLVGCEDGSVKLFQITPDKIPV
		1240	GNAAFAGOGVVYETFHMSDLPSYTTNGTVHVVVNNQIGFTTDPR
5759	2	1240	
1			MARSSPYPTDVARVVNAPIFHVNADDPBAVIYVCSVAAEWRNTF
Į.			NKDVGADLVCYRRRGHNEMDBPMFTQPLMYKQIHRQVPVLKKYA
		-	DKLIAEGTVTLQEFEEEIAKYDRICEEAYGRSKDKKILHIKHWL
l l			DSPWPGFFNVDGEPKSMTCPATGIPEDMLTHIGSVASSVPLEDF
1			KIHTGLSRILRGRADMTKNRTVDWALAEYMAFGSLLKEGIHVRL
ļ			NGQDVERGTFSHRHHVLHDQEVDRRTCVPMNHLWPDQAPYTVCN
			SSLSEYGVLGFELGYAMASPNALVLWEAQFGDFHNTAQCIIDQF
- 1			ISTGQAKWVRHNGIVLLLPHGMEGMGPEHSSARPERFLQMSNDD
- !			SDAYPAFTKDFEVSQL
		1001	
5760	1	1221	VRDITSDSLSLSWTVPEGQFDHFLVQFKNGDGQPKAVRVPGHED
1		1	GVTISGLEPDHKYKMNLYGFHGGQRVGPVSAVGLTAPGKDEEMA
]		1	PASTEPPTPEPPIKPRLEELTVTDATPDSLSLSWTVPEGQFDHF
			LVQYKNGDGQPKATRVPGHEDRVTISGLEPDNKYKMNLYGFHGG
			QRVGPVSAIGVTAAEEETPTPTEPSMEAPEPPEEPLLGELTVTG
			SSPDSLSLSWTVPQGRFDSFTVQYKDRDGRPQVVRVGGEESEVT
ı İ			VGGLEPGRKYKMHLYGLHEGRRVGPVSTVGVTAPQEDVDETPSP
		1	TEPGTEAPEPPEEPLLGELTVTGSSPDSLSLSWTVPQGRFDSFT
			VOYKDRDGRPOAVRVGGOESKVTVRGLEPGRKYKMHLYGLHEGR
			RLGPVSAIGVT
5761	3	1275	SCDMAEAAALVWIRGPGFGCKAVRCASGRCTVRDFIHRHCQDQN
3/61		12/3	VPVENFFVKCNGALINTSDTVQHGAVYSLEPRLCGGKGGFGSML
		1	<u> </u>
1			RALGAQIEKTTNREACRDLSGRRLRDVNHEKAMAEWVKQQAERE
			AEKEQKRLERLQRKLVEPKHCFTSPDYQQQCHEMAERLEDSVLK
		İ	GMQAASSKMVSAEISENRKRQWPTKSQTDRGASAGKRRCFWLGM
		ļ	EGLETAEGSNSESSDDDSEEAPSTSGMGFHAPKIGSNGVEMAAK
		i	FPSGSQRARVVNTDHGSPEQLQIPVTDSGRHILEDSCAELGESK
!!		1	EHMESRMVTETEETQEKKAESKEPIBEEPTGAGLNKDKETEERT
1		ł	DGERVAEVAPEERENVAVAKLQESQPGNAVIDKETIDLLAFTSV
			AELELLGLEKLKCELMALGLKCGGTLQ
5762	2	344	GSTGOTPLHSQGGGGGGGGGRRTTPRGMPKEKYEPPDPRRMYTI
3,62	_	1 3	MSSEBAANGKKSHWABLEISGKVRSLSASLWSLTHLTALHLSDN
		1	SLSRIPSDIAKLHNLVYLDLSSNKIR
5763	3	429	LDKDTGLIMLIARLDYELIQRFTLTIIARDGGGEETTGRVRINV
			LDVNDNVPTFQKDAYVGALRENEPSVTQLVRLRATDEDSPPNNQ
		1	ITYSIVSASAFGSYFDISLYEGYGVISVSRPLDYEQISNGLIYL
ļ			TVMAMDAGN
5764	19	441	VCARACGEMRQLLRPIDRQRYDENEDLSDVEEIVSVRGFSLEEK
}		1	LRSQLYQGDFVHAMEGKDFNYEYVQREALRVPLIFREKDGLGIK
1 1	1		MPDPDFTVRDVKLLVGSRRLVDVMDVNTQKGTEMSMSQFVRYYE
1			TPEAQRDKL
5765	3	825	OKILRLNNSHOPPTSSSNSKDCGGPASSGAGATAALADGLKFAS
2,02]	043	, -
ļ I			VQASAPQGNSHKETSKSKVKRSKTSKDANKSLPSAALYGIPEIS
1			STGKRQEVQGRPGEATGMNSALGQSVSSGGSGNPNSNSTSTSTS
	1		AATAGAGSCGKSKEEKPGKSQSSRGAKRDKDAGKSRKDKHDLLQ
			GHQNGSGSQAPSGGHLYGFGAKSNGGGASPFHCGGTGSGSVAAA
			GEVSKSAPDSGLMGNSMLVKKBEEEEESHRRIKKLKTEKVDPLF
	Į.		TVPAPPPHV
; !	1608	663	SGLFSVDPASSQAMELSDVTLIEGVGNEVMVVAGVVVLILALVL
5766		1	AWLSTYVADSGSNOLLGAIVSAGDTSVLHLGHVDHLVAGQGNPE
5766		i	PTELPHPSEGNDEKAEEAGEGRGDSTGEAGAGGGVEPSLEHLLD
5766			
5766			
5766			IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND
5766			IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL
5766			IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG
5766			IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL
5766			IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR
5766	2	892	IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV
	2	892	IQGLPKRQAGAGSSSPEAPLRSEDSTCLPPSPGLITVRLKFLND TEELAVARPEDTVGALKSKYFPGQESQMKLIYQGRLLQDPARTL RSLNITDNCVIHCHRSPPGSAVPGPSASLAPSATEPPSLGVNVG SLMVPVFVVLLGVVWYFRINYRQFFTAPATVSLVGVTVFFSFLV FGMYGR

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	1	H=Histidine, I=Isoleucine, K=Lysine,
	1	corresponding	
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	1		P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			HIDEFFTLNSTPSRSAYDEPHLLVNIEKQKLELEKRRLDIEAER
			LQVEKERLQIEKERLRHLDMBHERLQLEKERLQIEREKLRLQIV
			NSEKPSLENELGQGEKSMLQPQDIETEKLKLERERLQLEKDRLQ
			FLKFESEKLQIEKERLQVEKDRLRIQKEGHLQ
5768	3	476	SSRSRLSVSVSPPPPGIVELGPPFAWEFCSRLGSAVTSQRAGPA
	1		AAMVAKDYPFYLTVKRANCSLELPPASGPAKDAEEPSNKRVKPL
			SRVTSLANLIPPVKATPLKRFSQTLQRSISFRSESRPDILAPRP
1			WSRNAAPSSTKRRDSKLWSETFDVC
5769	38	667	TKTKKGVKEKATDQSVKAFAEHCPELQYVGFMGCSVTSKGVIHL
3,05	, 30	007	
			TKLRNLSSLDLRHITELDNETAMEIVKRCKNLISLNLCLNWIIN
1			DRCVEVIAKEGQNLKELYLVSCKITDYALIAIGRYSMTIETVDV
1	1	1	GWCKEITDQGATLIAQSSKSLRYLGLMRCDKVNEVTVEQLVQQY
			PHITFSTVLQDCKRTLERAYQMGWTPNMSAASS
5770	1	484	DSRRYDVKTRKWSFLLEEHSKLIAKVRCLPQVQLDPLPTTLTLA
	1		FASQLKKTSLSLTPDVPEADLSBVDPKLVSNLMPFQRAGVNFAI
1	1		AKGGRLLLADDMGLGKTIQAICIAAFYRKEWPLLVVVPSSVRFT
	L		WEQAFLRWLPSLSPDCINVVVTGKDRLTA
5771	168	741	GLLPSACLRARSWREASEGPSSRACSNGSQDTFEACYSGTSTPS
			FHGSHCSGSDHSSLGLEQLQDYMVTLRSKLGPLEIQQFAMLLRE
			YRLGLPIQDYCTGLLKLYGDRRKFLLLGMRPFIPDQDIGYFEGF
			LEGVGIREGGILTDSFGRIKRSMSSTSASAVRSYDGAAQRPEAQ
1	ĺ		AFHRLLADITHDIE
5772	148	383	EFNLALVSPSHPQIKAEDDQPLPGVLLSLSGGLFRSNLLTQDNG
			ILTFSNLVTCSAIYHLPVFPEREPGCSMRDLRVA
5773	2	723	PRVRSKHNFCFMEMNTRLQVEHPVTEMITGTDLVEWQLRIAAGE
1	-	1	KIPLSQEEITLQGHAFEARIYAEDPSNNFMPVAGPLVHLSTPRA
1		1	DPSTRIETGVRQGDEVSVHYDPMIAKLVVWAADRQAALTKLRYS
		Į.	
1			LROYNIVGLHTNIDFLLNLSGHPEFEAGNVHTDFIPOHHKQLLL
1			SRKAAAKESLCQAALGLILKEKAMTDTFTLQAHDQFSPFSSSG
5774			RRLNISYTRNMTLKDGKNSK
5//4	· 2	592	FVEEENIRVVRCGGSELNFRRAVFSADSKYIFCVSGDFVKVYST
1			VTEECVHILHGHRNLVTGIQLNPNNHLQLYSCSLDGTIKLWDYI
1			DGILIKTFIVGCKLHALFTLAQAEDSVFVIVNKEKPDIFQLVSV
1			KLPKSSSQEVBAKELSFVLDYINQSPKCIAFGNEGVYVAAVREF
			YLSVYFFKKETTSRVTLSSS
5775	3	538	SSGCCDPAAPSSLAEAATMPVSKCPKKSESLWKGWDRKAQRNGL
			RSQVYAVNGDYYVGEWKDNVKHGKGTQVWKKKGAIYEGDWKFGK
			RDGYGTLSLPDQQTGKCRRVYSGWWKGDKKSGYGIQFFGPKEYY
			EGDWCGSQRSGWGRMYYSNGDIYEGQWENDKPNGEGMLRLSQNP
1			RP
5776	2	484	RLPQDCVCQNLSESLGTLCPSKGLLFVPPDIDRRTVELRLGGNF
			IIHISRQDFANMTGLVDLTLSRNTISHIQPFSFLDLESLRSLHL
1			DSNRLPSLGEDTLRGLVNLQHLIVNNNOLGGIADEAFEDFLLTL
			EDLDLSYNNLHGPAVGLRGDAWVQPSTS
5777	2	949	GQDPEPGQDLFQPEREVDPSWGRGREPRLGKLRFQNDHLSVLKQ
1			VKKLEQALKDGSAGLDPQLPGTCYSPHCPPDKAEAGSTLPENLG
1			GGSGSEVSQRVHPSDLEGREPTPELVEDRKGSCRRPWDRSLENV
1	1		
	ļ	1	YRGSEGSPTKPFINPLPKPRRTFKHAGEGDKDGKPGIGFRKEKR
1			NLPPLPSLPPPPLPSSPPPSSVNRRLWTGRQKSSADHRKSYEFE
	İ	1	DLLQSSSESSRVDWYAQTKLGLTRTLSEENVYEDILDPPMKENP
	1		YEDIELHGRCLGKKCVLNFPASPTSSIPDTLTKQSLSKPAFFRQ
L	<u> </u>		NSERRNV
5778	1	1210	QRRQSVSRLLLPVFLLEPPAEPGLEPPPEEEGGEPAGVAEEPGS
	1	1	GGPCWLQLEEVPGPGPLGGGGPLRSPSSYSSDELSPGEPLTSPP
1			WAPLGAPERPEHLLNRVLERLAGGATRDSAASDILLDDIVLTHS
			LFLPTEKFLQELHQYFVRAGGMEGPEGLGRKQACLAMLLHFLDT
			YQGLLQEEEGAGHIIKDLYLLIMKDESLYQGLREDTLRLHQLVE
	1		TVELKIPEENQPPSKQVKPLFRHFRRIDSCLQTRVAFRGSDEIF
			CRVYMPDHSYVTIRSRLSASVQDILGSVTEKLQYSEEPAGREDS
			LILVAVSSSGEKVLLQPTEDCVFTALGINSHLFACTRDSYEALV
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Deginning location corresponding to first amino acid coation corresponding to first amino acid caidue of caidue of amino acid caidue of amino acid caidue of amino	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Iocation Iocation			nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid P-
Corresponding to first amin acid acid amin aci	NO:		1	Glutamic Acid, F=Phenylalanine G=Glycine
amino acid residue of amino acid residue of amino acid sequence #TYPOTOMIN, *TYPOTOMINO, ** #				H=Histidine, I=Isoleucine, K=Lysine
amino acid residue of amino acid amino acid sequence Se				L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence			1	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence Codom: /-post-in-levic-line /-butchise deletion;				S=Serine, T=Threonine, V=Valine,
Sequence Veposeible mucleotide imertion Differiorpotrinkreprovabilitarrepreventelipe Differiorpotrinkreprovabilitarrepreventelipe EAVQUIRKISADVRADVANICTPHUNASANKAVKCAEVITPLI EAVQUIRKISADVRADVANICTPHUNASANKAVKCAEVITPLI EAVQUIRKISADVRADVANICTPHUNASANKAVKCAEVITPLI EAVQUIRKISADVRADVANICTPHUNASANKAVKCAEVITPLI EAVQUIRKISADVRADVANICTPHUNASANKAVKCAEVITPLI EAVQUIRKISADVRADVANICTPHUNASANKAVKCAEVITPLI EAVQUIRKISADVRADVANICTPHUNASANKAVKCAEVITPLI EAVQUIRKISADVRADVANICTPHUNASANKAVKCAEVITPLI EAVALATAVISGAPTRAGICLELVANGADVNIQSKO SPLEMTAVISGAPTRAGICLELVANGADVNIQSKO ELLINTIITISADTAKCGIHSMPFHIRAAANCHHCIETIVTTGANV EILINTIITISADTAKCGIHSMPFHIRAAANCHHCIETIVTTGANV ERIDMERTAHIYAAANCHHCIETIVTTGANV ERIDMERTAHIYAAANCHHCIETIVTTGANV ERIDMERTAHIYAAANCHHCIETIVTTGANV ERIDMERTAHIYAAANCHHCIETIVTTGANV ERIDMERTAHIYAAANCHHCIETIVTTGANV ERITCHERTAHAANCHHCIETIVTTGANV ERITCHERTAHAANCHHCIETIVTTGANV ERITCHERTAHAANCHHCIETIVTTGANV ERITCHERTAHAANCHHCIETIVTTGANV ERITCHERTAHAANCHHCIETIVTTGANV DERTERTAGICLAESTEPRAVEDENISERICHEN ERITCHERTAHAANCHCHCELLLI S781 19 941 RISILGEHPREPREASGOCLPVFVTGHOERAVGGGRAGGAGA KKIMNYINGADOSPICSPOINTENP ERITCHERTAHAANCHCHCERTAHAANCHCHELL ERITCHERTAHAANCHCHCHCHCHCHCHCHCHCHCHCHCHCHCHCHCHC		1		Codon (-nossible nucleation) x=Unknown, *=Stop
PLPEZIONS REDTETHIN VERDEV NAHLTAFHNEL PROVIDED	1	sequence		\=possible nucleotide incontinul
5779 138 1671 BAYOULIMISADVAREDINMOTPLIVAAANKAVKCAEVITPLL SVAVSDROGGTALIHBALINGTVEMVILLIKAGANTARDIKKOR ALIMAAYMGHUVAULINGASVICOKKOYTULIAAASINOJ NVVORILIKIJOVE IDE INVVORTALIHACYNOODAVUNEL JOVA NVORONNOFT JURAAASTHOLEELLIVINGODAVUNEL JOVA SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO SPLIMTAVIGRETESOTLI ONGGE EDCVOKOONTOGKOO EDATLESSEL ONGGE EDCTIVARIOESENGERGE EATLESSEL ONGGE EDCTIVARIOESENGERGE EATLESSEL ONGGE EDCTIVARIOESENGERGE EXPRELICATIVA EETSVIKUSSIPPYGAVEPEASSEL ONGGE ENCONTRICATIVA EETSVIKUSSIPPYGAVEPEASSEL ONGGE ENCONTRICATIVA SELECTORICA ONG ENCONTRICATIVA SELECTORICA ONG ENCONTRICATIVA OPPOSTOR	-		 	PLPEEIOVSPGDTETHRVEDEDVANUI TARINGE PROMITE POLI
SVINVEDRAGORTALIHHAALINGHUWINLLIAKANINAPDIKKOR ALHWAAIWGILDVVALLIIMGABVICODKKGYTELHAALSONG NUVEHLINIGSELDIVVQORTALIKACYNOGUVORLIDVG NUQHNINGFTELHEFAASTIGALCLELLVINGADUNIGSKOG SPLEMHAVIGGRISGTULONGGOTHHAVARVG ELLIITLITEGADTAKCGIIHMFPHHAALAMSDCCKILLSS CKYSTVSLESBEHVLSAGFEIDTPKGFGRICHAAAAGGWYEC KLLGSSGAPHKKDKGGRIFHAAAACHRIKCIETLVTTAAWY ETDDWGRTALHYAAADDHRNKTIIGHABDISERERERELKEE EATLCLSFLLONDANDSIRDKGGYNSIHVAAAAVGHROCLELLI RINGSFEEDSGAAADDHRNKTIIGAADDHSERERERELKEE EATLCLSFLLONDANDSIRDKGYNSIHVAAAAVGHROCLELLI RINGSFEEDSGAAADDHRNKTIIGAADDHSERERERELKEE EATLCLSFLLONDANDSIRDHAAAAVGHROCLELLI RINGSFEEDSGAADDHSKRITIIGAADDHSERERERELKEE EATLCLSFLLONDANDSIRDHAWAAYGHROCLELLI RINGSFEEDSGAADDHSKRITIIGAADDHSERERERELKEE EATLCLSFLLONDANDSIRDHAWAAYGHROCLELLI RINGSFEEDSGAADDHSKRITIIGAADDHSERERERELKEE EATLCLSFLLONDANDSIRDHAWAAYGHROCLELLI RINGSFEEDSGAADDHSKRITIIGAADGGGGAA FRINGSFEEDSGAADDHSKRITIIGAADGGGGAADGAACHAAAAAAAAAAAAAAAAAAAAAAAA			ĺ	DYVFHGE
SVINVSDROGRTALHHAALINGHVENVILLIKAGANINAPDIKUSH ALHMAAYMGHLUVALLINHGASVICOKKGYTELHAALASANO NVVHILIKIGVEIDEINVYGRTALHIACYNGDAVNINGEKDG SPLHHTAVHGRFTESGTLIONGGEIDCYDKOGHTPHIVAARVG SPLHHTAVHGRFTESGTLIONGGEIDCYDKOGHTPHIVAARVG ELLINTLITEGGATAKCGIEMBPHIJALALMANDCEKILLAS CKYSIVSLESHEHULSAGFEIDTPDKFGRTCLHAAAAGGNVCCKLLAS CKYSIVSLESHEHULSAGFEIDTPDKFGRTCLHAAAAGGNVCCK KLLOSSGADPHKKKOKGSTPHAVAAAACHHCIETSTVTTGANVI ETDDMGRTALHYAAASDMDRNKTILGANAHDNSEELERARELEE CATLCLEFLLOMDHOSITRUKGGYDHAAAAGGNVCCLELLIG TUSGFEESDGATKSPLHLAVSEMP 5780 154 624 OFFEVITCIDFKGPDVRIVSEEPELTTVAEVDENGEREELELI RTNSGPEESDGATKSPLHLAVSEMP 625 OFFEVITCIDFKGPDVRIVSEEPELTTVAEVDENGEREELELI RTNSGPEESDGATKSPLHLAVSEMP FRANKVAGANGVANPPBEAGTGCLEVESTVIGHUGERAVGGRGGGA KKGLMV LGANOGSPLGSPSSLLADN KKGLMV LGANOGSPLGSPSSLLADN KKGLMV LGANOGSPLGSPSSLLADN KKGLMV LGANOGSPLGSPSSLLADN KKGLMV LGANOGSPLGSPSSLLADN VAPRATGGG-THOPLATVSPKAGGGGRGGAAHGROG OAPCRAGPTRKVAVABRPSED-GPE VOEBFRREVERSPELG VAPRATGGG-THOPLALVSP, VGGDRFENDARDLAGGRY OKSHITVTCKSPRQKEDESFRPQARFREKGGGANGHPPPEGEARAGGG CROALFPGG*ROGPRGRRF/PTGARSSHPAKAKGCGGPFKIRW NIMD 5782 5782 5782 5782 5782 5782 5782 5782 5782 5784 5784 5784 5785 6786 6787 6787 6787 6787 6787 678	5779	138	1671	EAVQVLIKHSADVNARDKNWQTPLHVAAANKAVKCARVIIPLLS
ALMMAYNGILDVALLINIGAEVTCOKKGYTPLHAAASING NVVEHLINIGVEIDE INYVENTALHIACYNGUVELIDUG NVQENNIGFTPLHFAAASTHGALCLELLVUNGADVINIGOS SPLHMTAVHGFTRSGYLLJONGGS IDCUNKORSTPLHVAARYG SPLHMTAVHGFTRSGYLLJONGG IDCUNKORSTPLHVAARYG SPLHMTAVHGFTRSGYLLJONGGS IDCUNKORSTPLHVAARYG ELLINTLITEGADTAKGJISSPPLHHAAAMGNYGCCEKLLSS OKYSTVSLFSHRHVLSAGFEIDT DPKPGTRCLHAAAGAGVEC KLUGSSGADFHKKDKCGTPLHVAAANCHFICLETI-VTTGANVU ETDDWGRTALHVAAASDMORSTLIANGSHD EATLCLEFLLONDANDS IDDKGYNS IHVAAAYGHROCLELLI RTNSGFEEDSGATYSPLHLAUSSMP 5780 154 624 0FFFVTTCDFFGDPVRLYSSEPPLTTVAEVDESNGEEKSEPV EATLCLEFLLONDANDS IDDKGYNS IHVAAAYGHROCLELLI RTNSGFEEDSGATYSPLHLAUSSMP DLATTEPPSAVOJCLAESTRPRTVTECOMER IRRHOCACKEE KKULAVIGASDSPLOS PSULRDIN DLATTEPPSAVOJCLAESTRPRTVTECOMER IRRHOCACKEE KKULAVIGASDSPLOS PSULRDIN DLATTEPPSAVOJCLAESTRPRTVTECOMER IRRHOCACKEE KKULAVIGASDSPLOS PSULRDIN OPPREVISCH FOR VOR VOR VOR VOR VOR VOR VOR VOR VOR V	1			SVNVSDRGGRTALHHAALNGHVEMVNLLLAKGANINAFDKKDRR
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ELLINTLITEGADTAKCG HEMPFLEHAALMANISDCCRILLES OKKSTVISLENBHULSAGFEIDT PDKPRGTCLIBAAGGNVEC KLLQSSGADPHKKDKGGTPLHYAAANCHFICLETLUTTAAGGNVEC KLLQSSGADPHKKDKGGTPLHYAAANCHFICLETLUTTAAGGNVEC KLLQSSGADPHKKDKGGTPLHYAAANCHFICLETLUTTAAGGNVEC EATLCLEFLLGNDANPS IDKEGYNS HYAAAYGHROCLELLI RTNSGFEEDSGATYSDLILAVSEMP 5780 154 624 OPFFVTTCLFFGOPVRLYKSEPELTVAEVDESGEEKSEPV EISTSVVKGSHPPVGVVPPRAKSTPESSTIASYVTLRITKKOM DLRTERPRAVEQLCLASSTRPRHYTEECMERICAGCKGER KKQLMVIGASDQSPLGSFSNLRDNP RSIGGFMPREFRARSGGCLYBVFYTOFHOGERAYGGKGPGGAF PAPPVSGTCPPDLIYAPTEKAGGSQNMQPPPGERAYGGKGPGGAF PAPPVSGTCPPDLIYAPTEKAGGSQNMQPPPGERAYGGKGPGGAF PAPPVSGTCPPDLIYAPTEKAGGSQNMQPPPGERAYGKGPGGAF OARCAAGPTRVAVAAVARPPSCY-OPED, PGERPREGSQNAPPPLI VARSSTCGGC*TWDPALLVSF/PGDSTPELPAP\QOPTGGFBG CRGALPPQG*ROQPRGPRP, PTGASRSHPAKAKGCGGPFKIRW NIMD 5782 5176 1237 DRSMSSMADSSTDSTDTYEAYMUPPLPPEEPPTWPPLPPEE PPMTPPLPPEPPSEPPEGDALPTEGSALTAENTWITEVPSLSSESSY SQPEPPVSQSTISEPSAVAVEEREVUVERPVTCVAVEEAVATVETSTVL LESSIMSSHAMGSTDSTTDTYPEAYMUPPLPPEEPPTWPPLPPEEP PPMTPPLPPERPSSAVAVEERSAVTULESSTVLUTSSTVTUL ESSVUTYSEPVSASTATETDDBRASGHVASEVSTSLLVPAVTTSSTVL ESSUTTSVESAVVAEEREVUVERPVTCVAVETSSTVLT LESSIMSSHVMKGINLSSGONLAPEIGMGSIALBIGGEPALSSTVL ESSUTTSPTATSSAVATAELSTVTSSGONLAPEIGMGSIALBIGGEPALSTUL ENKLOPYSSEGHINLINGLAKMENSTVTSSTVTULTSSTVTUL ESSVUTYSEPVSVGOVSTVTVSEPVTVSGOVOUTPEHDMLISTOP ATGVTSKGIEFTTATSSLLVAKVOUTDLSLTTOPTHUBLISTOP LESSIMSSHVMKGINLSSGONLAPEIGMGSIALBIGGEPALISTOPPALB EHLKGDPYSSEGHINLINGLAKMENSTVTCAAGTSPVGE EKEKKDSTSTSSKSKSKSGSKGS\TESTERSSKTPGRRSKSKSKSK HIS UTTSSKSKS/RORRRSSKSRSKSRSKSKSKSKKSKSKSKSK HIS UTTSSKSKS/RORRRSSKSRSKSRSTPGRRSSTPFSRRSTPFRRSRS RTGSRSSTTPGRRSSTSTSRSSTPGRRSSTPFSRRSTPFRRSRS RTGSRSSTTPGRRSSTSTSRSSTPFSRRSTPFSRRSTPFRRSRS RTGSRSSTTPGRRSSTSTSRSSTPFSRRSTPFBRRSTPFRRSRS RTGSRSSTTPGRRSSTSTSRSSTPFRRSSTPFBRRSTPLRRRS RTGSRSSTTPGRRSSSRSVERSTSSSTPFRRSSTPFBRRSTPLRRRS RTGSRSSTPTAKRSSSSBORS/REGGLIGHTAANAAAAAAA PTPPKSOVTLTKRFFVSSGGGMTSFAAMKLIGGHLEPVGALMIGAAA LURAGGETDAAAQLIS IPGGPTGSTOVUTTORQLAANTGAAAA LURAGGETDAAAQLIS IPGGPTGSTOVUTTORQLAANTGAAAA R				NVNQPNNNGFTPLHFAAASTHGALCLELLVNNGADVNIQSKDGK
OXYSTYSLFSNEHULSAGFEIDTPDKFGRTCLHARAAGGOVEC KLLQSSGADPKKDKCGGTHHYARAANCHPICTETLYTTGANVE ETDDMGRTALHYAAASDMDRNKTIIGNAHDNEELERARELKEI EATLCLEFLICHDNAMPSIRKGGVYSHHAVGRQCLELLLI RTMSGFESDSGATXSPJHLAVSEMP OFFEVITCLEFLICHNOAMPSIRKGGVYSHHAVGRQCLELLLI RTMSGFESDSGATXSPJHLAVSEMP OFFEVITCLEFLICHNOAMPSIRKGVYSHHAVGRQCLELLLI RTMSGFESDSGATXSPJHLAVSEMP 5781 19 941 RGSLGGHPMRPVGVVPPRAKS PTPESSTIASYVTLRTKKMC DLRTERPREAVEQLCLAESTRPRMTVEECMERIRHOOACUREI KAGNAVIGABOOSPLOSPENLENDP PAPPVSGTCPDLIVAPTPEKAGGGSGNOMOPPGERAHROG OAPCRAGFTRKVAVAPRPSCP*GEV PGEBRURKLOAPKT VAPPVSGTCPDLIVAPTPEKAGGGSGNOMOPPGERAHROG OAPCRAGFTRKVAVAPRPSCP*GEV PGEBRURKLOAPKT VAPSATCGGC **TMPPALLVS*P*QGGDSTPELDAP \(\text{OQPTGPSR}\) VAPSATCGGC **TMPPALLVS*P*QGGDSTPELDAP \(\text{OQPTGPSR}\) CROALPPQG*RQPRGRP*PTGASSHPAKAKGCGPPKIRW* NIMD 5782 5782 5782 5786 1237 DRSMMSMAADSYTDSYTTTYEGASHPAKAGCGOPPKIRW* NIMD SRSMMSMAADSYTDSYTTYTEGASHPAKAGCGOPPKIRW* NIMD DRSMMSMAADSYTDSYTTYTEGASHPAKAGCGOPPKIRW* NIMD SRSMMSMAADSYTDSYTTYTEGASHPAKAGCGPPKIRW* NIMD DRSMMSMAADSYTDSYTTYTEGASHPAKAGCGPPKIRW* NIMD SRSMMSMAADSYTDSYTTYTYTYTYTAMPVPLPPPEEPPTMPPLPPE PPPTPPLPPPEPPEPPEPPEPPEPPEPPTSYTSSASPOTYTULESATYTVLE ESILEPPAMAAPESSANAVLESSAVTVLESSTYTVLESSTYTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTYTVLESSTYTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTYTVLESSTYTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTYTVLESSTYTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTYTVLESSTYTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTYTVLESSTYTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTYTVLISSTYTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTYTVLISSTYTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTYTVLISSTYTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTYTVLISSTYTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTYTVLISSTYTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTYTVLISSTYTVL ESILEPPAMAAPESSANAVLESSAVTVLISSTYTVLISSTYTVL ESILESSINSSHVRKGININHILAKEMPTNCAAGTSPALEP LIAMSSPALEPAMAAPESSANAVLESSAVTVLISSTYTVLISSTYTVL ESILEPPAMAAPESSANAVLESSAVAVRESSTYTTOTTOTTEMBLISTATGAS ELEKKROSSLESSAVAVRESPERGEPPASSAVERGTESSAVSKAKKRSPH SAGGERARKRSSVANAVRESPERGERGSAVERGSAVERGSAVERGS REKKREPSARBERTSRRSRSTSRSRSTSRSRSTERSRSTSTRSRSTYSRRS RTSBRSKTSSS	1			FLIINTI ITECADTA COLUMNOS INCOMENTATION OF THE STATE OF T
KLLQSSGADPHKENKCGRTFLHYRAANCHHCIETLYTTGANV ETDDMGRTALHYAAASDMENKT LIGMANDEN FLARELEERE PLEAFELEE EATLCLEFLLQNDANFS IRKGGYNS HYYAAAYGHRQCLELLIE EATLCLEFLLQNDANFS IRKGGYNS HYYAAAYGHRQCLELLIE RTMSGFEESISGATX SPLHLAUSEMP EIETSVYKGSHPPYGVYPFRAKS PTPESST LASYVTLETKKME DLERTERPESAVEQLCLAES TERRTWYEEGEMER IRRHQOACLREIF KKQLAWIGASDQSPLQS PSNLEDNP 941 RSIGGHEMB PPMRASGCELVS VYGFHQERAYGGRGFGGA PAPPYSGTCPPDLIYAPTPEKAEGGS(KNHQPPPGERAHROAC QAPCRAGPTEKVAVAPAPPS CP+ QGFE VGERPLORS PLOC VPHTISQDAKS AEDERDRENG KKQLAWIGAS PPLE VAPSTCGSC "TWDPALLUS" PYQODSTETER VQPPGLES CRQALPPQB "RQPRQR PKPPGA PKHPERHORS QAPPLE VAPSTCGSC "TWDPALLUS" PYQODSTETER QOPPGLES CRQALPPQB "RQPRQ PKP PGASRSHPAKAKGCQPPKIRW INIM 5782 5176 1237 DESMMSNAADSYTDSYTDTYTEAVNVPPLDPEEPTYMPLPPE PPEPSSITLIPVESAVVAERENVETWSTLEVSLESSESV SQFEPPVSQS I SEPSAVPTDYSVS ADDESULVE EAAVTVPEPP PPEPSSITLIPVESAVVAERENVETWSTLEVSLESSESTULL ESILEPPAMAAPESSANAVLESSAVTVLESSTVILLESSTTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTVILLESSTTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTVILLESSTTVL ESILEPPAMAAPESSANAVLESSAVTVLESSTVILLESSTTVL ESILEPPEKSPTTIPVESAVAERENVENERVEVERVENVELVERAVSVLQ EMINUSPEVSVOG SETTOSPALED ATQTSKGIEPTTASTLSLVAKYDVULSLITTQDTEHDMLISTSP SGGSEADIECHPAKDIHLDLESNINLVSSDTWELDSTREDHVKROBQA ELKKRDSSLESSENSKSGSKENSKSKENKINGENSE SGGSEADIECHPAKDIHLDLESNINLVSSDTWELDSTREDHVKROBQA LUREVSSPRTNNVLPSPRRGL (SEP VLLASSPGSRANISDINKSPV VSSMPLERASGO (SSECKSGY VSI FF VKVAUDTHEKSKKNKNDOG SEKEKKRDSSLESSENSKSGSRENKSKSKKKKKNSPKR SKSREKKKRSSSENNKTVTRARSSTPSRESSTTSRERSFRSKKKSKSKK HSS (TISSASS / SDERRGS / SEPSRESTESSRESSKKKRSKSKKK KSSEN BRASSSPRESSRESSKSKSKENKERSPT PRRS RSF SRESSRFT PERRRSR SVERRSPS SI PVRLERGRTPLRRFR RSF SRESSRFT PERRRSR SVERRSPS SI PVRLERGRTPLRRFR RSF SRESSRFT PERRRSR SVERRSPS SI PVRLERGRTPLRRFR RSF SRESSRFT PERRRSR SVERRSPS SI PVRLERGRTPLRRFR RSF SRESSRFT PERRRSR SVERRSPS SI PVRLERGRTPLRRFR RSF SRESSRFT PERRRSR SVERRSPS SI PVRLERGRTPLRRFR RSF SRESSRFT PERRRSR SVERRSPS SI PVRLERGRTPLRRFR RSF SRESSRFT PERRRSR SVERRSPS SI PVRLERGRTPLRRFR RSF SRESSRFT PERRRSR SVERRSPS SI PVRLERGRTPLRRFR RSF SRESSR				OKYSIVSLESNEUU SACEELDEDDVEGDEG
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S781 19 941 85161				RTNSGFEESDSGATKSPLHLAVSEMP
EISTSVKGSHPPVGVVPPRAKSTESSTIASVVILRITKKM DLATERPRSAVEQLCLASSTRPRNTVERRIRKHQACCHEI KKGLNVIGASDOSPIGSTSPNILENDP RGSLGGHPMRFPMRASGGCLPVSFVTGFHQERAYGGRGFGGAN PAPPVSGTCPPLLIVAPTPEKARGGSGKNHQPPPGERAHRDGE QAPCRAGFTKVAVAPRPPSCP-40PL\DEPERPLEGSPLIGG VOPHTISGDAKSADEDASPRILGKHQPPSGAVGSRILDALQGPX QHSIHTVTCKSPRQKEDBSPKLPGOPKGRGPGGALAGQBX QHSIHTVTCKSPRQKEDBSPKLPGOPKGRGPGGALAGQBX QHSIHTVTCKSPRQKEDBSPKLPGOPKGRGPGARAHRDGE CRGALPQG*RQPRQPPR/PTGASRSHPRAKGCGSPPKLRW NIND 5782 5176 1237 DRSMMSMAADSYTDSYTDTYTEAYMVPPLPFEEPPTMPPLPPE PPMTPPLPPEEPPEGPALPTGSSALTAENTWPTEVPSLPSEESY SQFEPPVSGSEISBPSAVPDTYSVSASDVLSEANTVEEP PPMSPPLPPEEPPGALPTTSVASADVLSEANTVEEPPTMSPLSPSESY VLASSPPVMSGETAETPGOMRASGHVASEVSTILVPAUTTPVLA ESILEPPAMAAPESSAVAVLESSAVTVLESSTVTULESSTVTUL ESSVUTVPEPPVVASADVATULESSTVTULESSTVTUL ESSVUTVPEPPVVASADVASEVSTULTSSTVTUL ESSVUTVPEPPVVASADVASEVSTULTSSTVTUL ESSVUTVPEPPVVASADSSAVVLESSAVTVLESSTVTULESSTVTUL ESSVUTVPEPPVVASADGSALGESSVTULESSTVTULESSTVTUL ESSVUTVPEPPVVASADGSALGESSAVVLESSTVTULESSTVTUL ESSVUTVPEPPVVASADGSALGESSVTULESSTVTULESSTVTUL ESSVUTVPEPPVVASADGSALGESSAVTULESSTVTULESSTVTUL ESSVUTVPEPPVVASADGSALGESSAVTULESSTVTULESSTVTUL ESSVUTVPEPPVVASADGSALGESSAVTULESSTVTULESSTVTUL ESSVUTVPEPPVVASADGSALGESSAVTULESSTVTULESSTVTUL ESSVUTVPEPPVVASADGSALGESSAVTULESSTVTULESSTVTUL ESSVUTVPEPPVASEDAGSALGESVARTSVCRIVENVCANGTSPVGE ILGERKLIPTSETKQRTULDTYPQUSADAGGETLSSTVTLESSTVTUL ESSLANDARVAGGERGVERPVACAGGENARGEDAGGENARGAGGALGE ATAC\TSKGGETSTVANVLDSSTARALGEDHALSSTVT ILGESIMSSIVMKGINLSSCHONLAFETGATGSTVCKRROKGKG EKEKKDSSLRSSKAKSKSEMSKSKIKSDEPVACAGGENARGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	5780	154	624	QFFRVITCLPFKGPDYRLYKSEPELTTVAEVDESNGERKSEPVS
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QAPCRAGPTRKVAVAPRPPSCP*GPE\PCEBPRRFLDRSPPLOR VQPHFISQDAKSABEDEAPSRHLDKHQPRSAQVGSRLDALQGPKT QHSIHTVTCKSPRQKEDRSPKPPQAPKHPERHRGRS\QAPPPLE VAPSRTCGGS-TWDPALLVSF/PGGISTEPAP\QOPTGGPSR CRQALPPQG*RQPPQRPR/PTGASRSHPAKAKGCQPPKIRNY NIND 5782 5176 1237 DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPTMPPLPPEE PPMTPPLPPEEPPBEPALPTEGSALTAEATWFTEPSLSEESEV SQPEPPVSQSEISBPSAVPTDYSVSASDPSVLVSEBAVTVPEPP PPMTPPLPPEEPPBEPALPTEGSALTAEATWFTEPSLSEESEV SQPEPPVSQSEISBPSAVPTDYSVSASDPSVLVSEBAVTVPEPP PPMESSITLTPVESAVVABEHEVBRYVTCHSETAYMTYPLA ESILEPPAMAAPISSANAVLESSAVTVLLESSTVTVL ESSVUNSETAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPISSANAVLESSAVTVLUSSTVTVLESTYVTVL PPSVVVSPPVVSADPDYVTIPVVVSALEPSVSVULEPAVSVLQ PSMIVSEPSVSVDSTTVTVSEPAVTVSEQTQVIPTEVALESTPM ILLESSIMSSHVMKGINLSSGQDNLAPFLOKEPALEPD ATG\TSKGLIPFTTASTLSJLVNAVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSTTMSPLEVKRD\DQ TLAALI\SLKSSEGGEKEVPPS*REHLPDSGFSANIEDINEAD LVPPVSSPRTMVLUSPSPRGL\LDSPGFGVULTSSPVV \SSMP\ERASGS\SGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKSKSRRSVSVKERKRSKKKN RSKSERKRKRSSSRDNRTVVRARSRTPSRRSRSHTPSRRRSR SGGSEADIEGPLPAKDIHLDLPSNINLVSSTTMSPLEVKRD\DQ TSKASTSSSRSKSKSRSSSKSKERKRSVSKEKKSVEKKRS HES\QTRSSSRSKSRSKSKSKERKTSSKSKK RSKSERKRKSSSRDNRTVVRARSRTPSRRSRSTPSRRRSR SGRRFSFSISPSRRSRSFSRRSTPSRRRSRS SGRRFSFSISPSRRSTPSRRRSPSRRSTPSRRSRS SGRRFSFSISPSRRSFSRSFSFRRSPSRRSPSRRS SGRRFSFSISPSRRSFSTSPRRRSPSRRSPSRRS SGRRFSFSISPSRRSPSTPSRRRSPSRRSPSRRSPSRRSPSRRS SGRRFSFSSSRRSPSVRRRSSSERKSPSVREWREGEN RDDDVIVMEPHVSDEBEEPPFYHHPFKLSEPVLENGEN KDDDNVSSNLPSEPPDISTAMSERALAQKRLSENFPLEMANA PTPPKSQVTLTKEFFVSSGCHRKKEADSVCGWPVEVENGEN KDDDNVSSNLPSEPPDISTAMSERALAQKRLSENFPLEMARA LNRAGERIDMAQLASIPGPFGSTGVVUTGPLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGGGLGKNKEGKREPILV DFKTDRKGLVAVGERQKRSGNFSAAMKDLSGKHPVSALMEICN KRRQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTTINIPASPFM QKLGFTGVNVVLMKRSPRGLSHSPWAVKLKBPLCDDHYSPVQ QKLGFTGVNVVLMKRSPRGLSHSPWAVKLKBPLCDDHYSPVQ QKLGFTGVNVVLMKRSPRGLSHSPWAVKLKBPLCDDHYSPVQ			3.2	PAPPVSGTCPPDLIVADTDEKAECCCOVATIONDECTES AVERGE
VQPHFTSQDAKSAEDEAPSKHLGKHQPRSQVGSLDALQQPXI CHSHTVTCKS PDGKEDRSPKPPQAPKHPEHBRQS QAPPPLE VAPSRTCGGC*TWDPALLVSP/PQGDSTEELPAP\QQPTGPPSR CRQALPPQG*RQPRQPR/PTGASRSHPAKAKGCQGPPKIRW NIND 5762 5176 1237 DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPBGPALPTEQSALTAEATHWFTEVPSLPSEESV SQPEPPPVSQSEISEBSAVPTUSYSASDPSULVEBAAVTVEPEP PPDESSITLTPVESAVVABEHEVVPBRPVTCMVSETPAMSAEPT VLASEPPVMSGTAETFDSMRASGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTUL EPSVVTVPEPPVAEDPJVTIPVPVVSALEPSVPVLEPAVSVIQ PSMIVSEPSVSVQESTVTVSEPAVTVSEQTVUPTEVALESTTM LLESSIMSSHYMKGINLSSGDQMLAPETGMGEIALHGEEPHAE EHLKGDFYESHGINIDLAINNHLIAKEMEINTVCAAGTSPVGE IGGEKLIPTSSTKGKRTVLDTYPQVVSALEDSVPVLEPAVSVIQ ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHHMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\S\LKESSGGKEVPPPSRADAGETLSSTGPFALED ATG\TSKGIEFTTASTLSLVNKYDVHLESTVTWLDTSPVGE LVRPVSSPRTWNVLPSPRAGI\EGP\LLASDFGFVONLYSSPVV \SSMP\ERASGS\SGGKEVPPPSRANIEDINEAD LVRPVSSPRTWNVLPSPRAGI\EGP\LLASDFGFVONLYSSPVV \SSMP\ERASGS\SGGKEVPPPSRANIEDINEAD LVRPVSSPRTWNVLPSPRAGI\EGP\LLASDFGFVONLYSSPV \SSMP\ERASGS\SGEKEVPPPSKKITSERSKRRSSKKSK HRS\GTRSSRSKRSKSKSKKKITSERSKRRSKRSSKRKSSKHKRSSKKRS RSKRRKSKSKSKSKSKSKRKSSSHKKITSERSKRRSKSKSKS RKSKRRKSSSRSKRSSSRRSKRSSSRKSKSSGRRSVSKEKRKRSPKH RS\GTRSSRSTFSRRSSRTFSRRSRTFSRRSRTFSRRSFTFSRRSR RTPSRSSRTFSRRRSRSVVRRRSFSISPVRRRSFTSRRSRTFSRRSRTFSRRSRTFSRRSRTFSRRSRTFSRRSRTFSRRSRTFSRRSRTFSRRSRTFSRRSRTFSRRSRSFTSRRSRSTFSRRSRTFSRRSRTFSRRSRTFSRRSRSFTFSRRSFTFSRRSRSFTFSRRSRSFTFSRRSRSFTFSRRSFTFSRRSRSFTFSRRSRSFTFSRRSFTFSRRSRSFTFSRRSFTFSRRSRSFTFSRRSRSFTFSRRSFTFSRRSRSFTFSRRSFTFSRRSRSFTFSRRSFTFSRRSFTFSRRSRSFTFSRRSRSFTFSRRSFTFSRRSFTFSRRSRSFTFSRRSFTFSRRSFTFSRRSRSFTFSRRSFTFSRRSFTFSRRSRSFTFSRRSFTFSRRSFTFSRRSFTFSRRSRSFTFSRRSFTFSRRSFTFSRRSFTFSRRSFTFSRRSFTFSRRSFTFSRRSFTFSRRSFTFSRRSFTFSRRSFTFSRRSFTFSRFTFSRSFTFSRRSFTFSRRSFTFSRRSFTFSRFTFSRTSFTFSRRSFTFSRFTFSRTSFTFSRRSFTFS				QAPCRAGPTRKVAVAPRPPSCP*GPE\PGERBPPDIDECPRICO
OHSINTYTCKSPRQMEDRSPKPPQAPKHPEHRGRQS\QAPPPLE VAPSTRCGGG*TMPDALLUS*P\QQDSTPELPAP\QQPTGPFS CRQALPPQG*RQPRPPTGASRSHPARAKGCQFPPKIRNY NIMD DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVLVSEAAVTVPEEP PPMTPPLPPEEPPEGPALPTEQSALTAENTWPTEVPSLPSEESV VLASEPPWASPTAETFDSMRASGHVASEVSTSLLVPAAVTTYPLA ESILEPPAMAAPESSAMAULESSAVTVLESSTVTVLE EPSVVTVPEPPVVAEPPVVAILPPAVSVLQ PSMIVSEPSVSVQESTVTVSSPAVTVSESTVTVLESTVTVL EPSVVTVPEPPVVAEPDYVTIPVEVVSALEESVPVLEPAVSVLQ PSMIVSEPSVSVQESTVTVSSPAVTVSSQTQVIPTEVAIRSTPM ILESSIMSSHWKKGINLSSGQDLAFBIGMGSIALHSGEEPHAE EHLKGDFYSSEGIIIDLNINHILIAKEMEHNTVCAAGTSPVGE IGEKLIPTSSTIKGRTVLDTYPGVSEAADGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVMKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLFAKDIHLDLPSNINLVSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*RHLPDSGFSANIFDINRAD LVRPVSSPRTMNVLPSSPAGL\EGP\LLASDFGPVQNLVSSPVV \SSMP\EBASGS\SSGEKGG\YEIFVKVKDTHEKSKKNNNDKG EKEKKDSSLRSSKSKSSKSSKRSKLTSESRSRARKRSKKSKS SGGRRSSSISPSRSKTSSRSKTSFSRSKSKSKKSKNNNDKG EKEKKDSSLRSSFKSKSSERSKTSFSRSKSFSRSKSKSKKSKSKSK SVGRRSFSISPSFRSRTSFSRSRSTFSRRSFTSRRSFTSRR SVGRRSFSISPSFRSRTSFSRRSFTSRRSFTSRRSFTSRR SVGRRSFSISPSFRSRTSFSRRSFTSRRSFTSRRSFTSRR SVGRRSFSISPSFRSRTSFSRRSFTSRRSFTSRRSFTSRRS SVGRRSFSISPSFRSRSFTSRRSFTSRRSFTSRRSFTSRR SVGRRSFSISPSFRSRSFTSRRSFTSRRSFTSRRSFTSRR SVGRRSFSISPSFRSRSFTSRRSFTSRRSFTSRRSFTSRR SVGRRSFSISPSFRSRSFTSRRSFTSRRSFTSRRSFTSRR SVGRRSFSISPSFRSRSFTSRRSFTSRRSFTSRRSFTSRR SVGRRSFSISPSRSFTSPRRSFTSRRSFTSRRSFTSRR SVGRRSFSISPVKLRRSFTILDLKAQLLEIAKANAAAMCAKA GVPLPPHLKRAPPPTIEEVAKKSGGATIELIEKKQIAQKS DDDVIVKKPHVSDEBEEEPPFYHPPKLSEPXPIFFNINIAAAK PTPPKSQVTLTKEFPVSSGQHRKKEADSVYGEWVPVEKNGEEN LNRAGERIDAWQQLNSIPGOFTGSTGVQVLTOGQLANTGAQMI KXDQPLRAPVTGGMGAVLMRKNGWRGEGGLGKNEKGEILD KRRWQPPEPLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DFKTDRKGLVAVGGRAQKKSGNFSAMKCLLSKKHPVSALMBICN KRRWQPPEPLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DGGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGNVYLMKSSPRGLESSPANDIGLSMPYGGRSGL				VQPHFTSQDAKSAEDEAPSRHLGKHOPRSAOVGSRLDALOGDKT
VARSR/GGG**TWDPALLVSP/PQGDSTPELPAP\QQPTGSPS CRQALPPQG*RQQPRQPRP/PTGASRSHPARAKGCQDPKIRNY NIMD DRSMMSMAADSYTDSYTDTYTEAYMVPFLPPEEPPTMPPLPPEEP PPMTPPLPPEEPPEGPALPTEQSALTAENTMPTEVPSLPSEESV SQPEPPVSQSEISEPSAVPTDYSVSASDPSVIVSEAAVTVPEPP PPBPESSITLTPVESAVVABEMEVVPERPYTCMVSETPAMSAEPT VLASEPPVMSETAETFDGMRASGHVASEVSTLUPAVTTPVLA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVAEPPVVAIPPVVTIPVPVVSALEPSVEVLEPAVSVLQ PPMMIVSEPSVSVQSESTVTVSEPAVTVSEOTQVJPTEVAIRSTPM LILESSIMSSHVMKGINLESGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESEHGINIDLININHHIJAKEMENTVCAAGTSPVGE LIGEEKILETSSTKORTVLDTYPGVSEADAGETISSTOPPALED ATG\TSKGIEFTTASTLSLVMKYDVLISLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDHILDLPSNILVSDTTMEPLPVKRD\DQ TILAALI\SLKESSGGEKEVPPPS*RELIPDSGFSANIEDINRAD LVRPVSSPRTNNVLPSPRAGL\EOP\LLASDFGFVONLYSSPVV \SSM^\ERASGS\SSGEKGG\YEIFVKVXDTHEKKKNENDKG EKEKKRDSSLRSRSKSSGEKGSVYEIFVKVXDTHEKKKNENDKG EKEKKRDSSLRSRSKSSGRRSVVSKEKRRSPKH RS\\GTRSRSKS/ADRRRSSSSSKSKGRSVVSKEKRRSPKH RSS\\GTRSRSKS/ADRRRSSSSSSKSKGRSVVSKEKRRSPKH RSS\GTRSRSKS/ADRRRSSSSSKSKGRSVVSKEKRRSPKH RSS\GTRSRSRSFSRRSRSFSRSRSFTPSRRSRTFSRRRRS SVGRRSFSISPSRRSTFSRRRSFTPSRRSRTTPSRRR RTPSRRSRTFSRRRRSSVVRRSFSISPVRLRSSTTPLRRFS SPURRRSSSSSBORSPKLTUDLDKAQLLEIAKAMAAMCAKA GVPLPPNLKPAPPPTIEKVAKKSGGATIEBLIEKCKQIAGSKE DDDVIVMKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNINIAAAK PTPPKSQVTLTKEFPVSSGSJGHKKEADSVYGEWPVEKNGEN LNRAQRRIDAWAQLNSIPGFPTGSTGVVLTQGQLANTGAQAWI KKDQFLRAPVTGGMGAVLMRKNGWREGBGLGKNKEGNKEPILV DFKTDRKGLVAVGGRAQKRSGNFSAMKDLSGKHPVSALMBICN KRRQPPEPILVHDSGPDHRKHFLFRVLINGSAYQPNCMFFINR YKRQPPEPILVHDSGPDHRKHFLFRVLINGSAYQPNCMFFINR PKGVLGFGRWYLMKSSPRGLESBKSGR				QHSIHTVTCKSPRQKEDRSPKPPOAPKHPERHGROS\OADDDID
CRQALPQG*RQQFRQPF/PTGASRSHPAKAKGCQGPKIRNY NIND 5782 5176 1237 DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEFPTMPPLPPEE PPMTPPLPPEEPPEGGALTAENTWPTEVPSLPSEESV SQPEPPVSQS: 15EPSAVPTDYSVASDPSVLVSEAAVTVPEPP PPMTPPLPPEEPPEGGALTAENTWPTEVPSLPSEESV SQPEPPVSQS: 15EPSAVPTDYSVASDPSVLVSEAAVTVPEPP PPESS: ITLTPVESAVABEHEVVPERPVTCMVSETPAMSAEPT VLASEPPWASTAETFDSMRASGHVASEVSTSLLVPAVTTYPULA ESILEPPAMAAPESSAMAVLESSAVTVLESSTVTVLE EPSVVTVPEPPVVAEPPVVTIPVPVVSALEESVEVLEPAVSVLQ PSMIVSEPSVSVQBSTVTVSEPAVTVSEQTQVIPTEVALESTPM LIESSIMSSHVMKGINLSSGDQNLAPEIGMQEIALHSGEEPHAE EHLKGDFYESHGINIOLNINNHLIAREMENTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGVSEADAGETLSTOPFALEPD ATG\TSKGIEPTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPARDIHIDLPSNINLVSSDTMEPLPVKRD\Q TLAALI\SLKESSGGEKSVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTNNVLPSPRAGL\EGP\LLASDFGPVQNIENSEVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKUTHEKSKKNKNRDKG EKEKKRDSSLRSRSKSSKSSEHKSRKLTSESRSRARKSSKKSK HSS\GTRSRSSLRSRSKSKSSEHKSRKLTSESRSRARKSSKKSK HSS\GTRSRSSLRSRSKSKSSEHKSRKLTSERSRSRTPSRRSRS SVGRRRSFSISPSRRSKTPSRRSRTPSRRSRTPSRRSRT RTPSRRSRTPSRRRSRSVVRRRSFSISPVRRRSRSTPSRRSRTPSRRS SVGRRRSFSISPSRRSKTPSRRSRTPSRRSRTPSRRSRTPSRRS SFIRRKRSSSEEMGSPKRLTDLDKAQLEIAKANAAMCKA GVPLPPHLKPAPPFTIEBKVAKKSGGATIBELTEKCKQIAQSKE DDDVIVNKPHVSDEEEEPPFYHHPFKLSEPKPIFFNLIAAAK FTPFKSQVTLTKEFPVSSGSQHRKKEADSVYGWPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLINSIPGOFTGSTWQVLTGEQLANTGAQAWI KKQOFLRAAPVTGGMGAVLMRKMGWREGBGIGKNKEGKHEPILV DFKTDRKGLVAVGERAQKRSGNFSAMKDLSGKHPVSALMEICN KKRWQPPEFLLVHDSGPDDIRKHFLFRVLINGSAYQPNCMFFLNR Y DFKTDRKGLVAVGERAQKRSGNFSAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDDIRKHFLFRVLINGSAYQPNCMFFLNR Y CKLMDEAKLLKSLHPNIVGYRAFTEANDGSLCLAMEYGGRESI KRLMDEAKLLKSLHPNIVGYRAFTEANDGSLCLAMEYGGRESI KRLMDEAKLLKSLHPNIVGYRAFTEANDGSLCLAMEYGGRESI KRLMDEAKLLKSLHPNIVGYRAFTEANDGSLCLAMEYGGRESI				VAPSRTCGGC*TWDPALLVSP/POGDSTPELPAP\OOPTGGBSB
DRSMMSMAADSYTDSYTDTYTEAYMVPPLPPEEPPTMPPLPPEE PPMTPPLPPEPPEGPALPTEGSALTAENTWPTEVPSLPSEESV SQPEPPVSQSE18EPSAVPTOYSVASDPSVLVSEAAVTVPPEN PEPESSITLTPVESAVVABEHEVVPBRPVTCMVSETPAMSAPET VLASEPPVMSETTAETTDSMRASGHVASEVSTSLLUPAVTTPVLA ESILEPPAMAAPESSAMAVLESSTVTVLESSTVTVLESSTVTVL EPSVVTVPEPPVVABEPJVT1PVVVSALEPSVPVLEPAVSVLQ PSMIVSEPSVSQBSTVTVSEPAVTVSEQTQVI PTEVALESTPM ILESSIMSSHVMKGINLSSGDQNLAPPIGMQBIALHSGEPPHAE EHLKGDFYRSEGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKLLPTSETKQRTVLDTYPGVSBADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTTS SGGSEADIEGPLPAKDIHLDLESNTNLVSSDTMEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPTWNVLPSPRAGL\EGP\LLASDFGFVQNLYSSVV \SSMP\ERASGS\SGEKGG\TEIFVKVXDTHEKSKKKNENKK EKKKKDSLRSRSKSKSSBHKSRKLTSESRSRAKRSSKSKS HSS\OTRSRSRS\SRSRTSRSRSRSRSRSRSKTSRSRSKHKRRSPKH RSKARERKKRSSSLDNRKTVRARSRTPSRRSRTFSRRSR SVGRRRSFSISFSRRSRTPSRRSRTPSRRSRTFSRRSRTPSRRS SVGRRRSFSISFSRRSRTPSRRSRTPSRRSRTFSRRSRTPSRRS RTPSRRSRTPSRRRSRSVRKRSSSBLOKKKKKARSPKH RSKARERKKRSSSEDRRSFKRLTDLDKAQLLEITAKANAAMCKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPPYHHPFKLSERVPITFFNLNIAAAK GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPPYHHPFKLSERVPITFFNLNIAAAK KDDDNVFSSNLPSEPVITSTAMSERALAQKRLSENAPDLEAMSM LNRAQERIDAWAQLNSIPGGPTGSTGVQVLTQEGLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWRGEGGIKNKEGMKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFIFFVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNYVIMKRSPRGLSHBPMAVKKUNPICNDHYRRSVYG KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMBFYGGRKSG				CRQALPPQG*RQQPRQRPR/PTGASRSHPAKAKGCQGPPKIRNY
PPMTPPLPPEEPPEGALTHENTWPTEVPSIPSEESV SQPEPPVSQSEISEPSAVABEHEVVPBEPPTMPPLPPSESSY SQPEPPVSQSEISEPSAVABEHEVVPBEPVTCMYSETPAMSAEPT VLASEPPVMSETAETDSMRAGHVASEVSTSLLVPAVTTPVLA ESILEPPAMAPESSAMAVLESSAVTVLESSTVTVLESSTVTVL ESSVVTVEPPPVABPDYVTIPVVYSALEPSVPVLEPAVSVLO, PSMIVSEPSVSVOSETVTVSEPAVTVSEQTQVIPTEVAIESTPM ILESSIMSSHVMKGINLSSGDQNLAPEIGMQBIALHSGEPHAE EHLKGDFYRSEHGINDLNINNHLIAKEMEHNTVCAAGTSPVGE GEEKLLPTSETKQRTVLOTPYGVSEADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLEPSINLVSSDTMEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAS LVRPVSSPRTNNVLPSPRAGL\EGP\LLASDEGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVXDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSEKSKKKKLTSESRSRKRSSSKSK HKS\QTRSRSRS\FDRRRSSSSRSKSRGRRSVSKEKKRKSPKH RSK\GTRSRSRS\FDRRRSSSTSRSKRSGRRSVSKEKKRKRSKK HKS\QTRSRSRS\FDRRRSSSTPSRRSTTSRRSRTFSRRSRTFSRRRS SVGRRSFSISPSRRSTTSRRSTTSRRSTTSRRSRTPSRRS TSPSRRSRTFSRRSTSRSVVRRSSSIGPVLRRSSTPFRRRS ENFRRSRSSERGRSVKRKKSSEKVRLRSSSIGTELTEKCKGIAGSKE DDDVIVNKPHVSDEEEEEPVHPPFKLSEPKPIFFNLNIAAAK GVPLPPPNLKPAPPPTIEKVAKKSGGATIELITEKCKGIAGSKE DDDVIVNKPHVSDEEEEEPVHPPFKLSEPKPIFFNLNIAAAA PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWPVEKNGEEN KDDDNVTSSNLPSEPVISTAMSERALAQKKLSENAFDLEMMSM LNRAQERIDAMAQLNSIPGGTGSTGVQVLTQEQLANTGAQAMI KKQQFLRAAPVTGGMGAVLMRKMGWRGGGGGKMKGGNKEEPILV DFKTDRKGLVAVGERGAGKSGNFSAAMKDLGKHPVSALMEICN KRRWQPPEFLLVHDSGDPHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM KRLMQPEFLIVHDSGDPHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM KRLMDEAKILKSLHHPNIVGYRAFTENNOSCICLAMBYGGRKGI	5782	5176	1277	
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EHLKGDFYFSEHGINIDLNINNHLIAKEMEHNTVCAAGTSPVGE IGEEKILPTSETKQRTVLDTYPGV3EADAGETLSSTGPFALEPD ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTQDTEHDMLISTSP SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKEVPPPS*REHLPDSGFSANIEDLNEAD LVRPVSSPTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKKKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS EKEKKRDSSLRSRSKRSKSSENKSRCHTSESRSRARKSSKSKS HRS\QTRSRSSF\RDRRRTSSRSKSKGRSVSKEKRKRSPKH RS\SQTRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSR SVGRRRSFSISPSRRSTPSRRSRTPSRRSRTPSRRSRTPSRRS RTPSRRSRTPSRRRSRSVVRRSFSISPVRLRESTPLRRFS RSPIRKKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGGFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y 5783 1693 698 DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSL				PSMIVSEPSVSVQESTVTVSEPAVTVSEQTQVIPTEVAIESTPM
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SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DQ TLAALI\SLKESSGGEKCVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASGS\SSGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSRS/RDRRRSSRSRSKSRGRRSVSKEKRKRSPKH RSKSRERKRKRSSSRDNRKTVRARSRTPSRRSRSHTPSRRSRS SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRRRRSSVVRRRSFSISPVRLRRSRTPSRRSR RTPSRRSRTPSRRRRRSSVVRRRSFSISPVRLRRSRTPLRRFFS RSPIRRRRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSGHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGGFTGSTGVQVLTQEQLANTGAQAWI KKQQFLRAAPVTGGMGAVLMRKMGWREGGGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVQYRAFTEANDGSLCLAMEYGGERGL		1		ATG\TSKGIEFTTASTLSLVNKYDVDLSLTTODTEHDMLTSTSD
TLAALT/SLKESSGGEKEVPPPS*REHLPDSGFSANIEDINEAD LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVQNLYSSPVV \SSMP\ERASG\SSGEKGG\YEIFVKVKDTHEKSKKKKNRDKG EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRAKRSSSKSK HRS\QTRSRSRS/RDRRRSSRSKSKGRRSVSKEKKRSPKH RSKSRERKRKSSSRDNRKTVRARSRTPSRRSRTPSRRSRSR SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPSGPTGSTGVQVLTQEQLANTGAQAWI KKQQFIRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVQYRAFTEANDGSLCLAMEYGGERGL				SGGSEADIEGPLPAKDIHLDLPSNINLVSSDTNEPLPVKRD\DO
\SSMP\ERASGS\SGEKGG\YEIFVKVKDTHEKSKKNKNRDKG EKEKKRDSLRSRSKRSKSEHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSRS/RDRRRSSRSRSKSRGRRSVSKEKRKRSPKH RSKGRERKRKSSSRDNRKTVRARSRTPSRRSRSHTPSRRSRS SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEEEEPPFYHHPFKLSEPKPIFFNLNIAAAX PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGGFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVQYRAFTEANDGSLCLAMEYGGERSL	ļ		,	TLAALI\SLKESSGGEKEVPPPS*REHLPDSGESANIEDINEAD
EKEKKRDSSLRSRSKRSKSSEHKSRKLTSESRSRARKRSSKSKS HRS\QTRSRSRS/RDRRRSSRSKSRGRRSVSKEKRKRSPKH RSSKSRERKRKSSSRDNRKTVRARSRTPSRRSRSTFSRRSR SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSR RTPSRRSRTPSRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSSPLPDISTAMSERALAQKRLSENAFDLEAMSM LNRAQBRIDAWAQLNSIPGGFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVQYRAFTEANDGSLCLAMEYGGERSL				LVRPVSSPRTWNVLPSPRAGL\EGP\LLASDFGPVONLYSSPVV
HRS\QTRSRRS/RDRRRSSRSKSRGRRSVSKEKRKRSPKH RSKSRERKKRSSRDNRKTVRARSRTPSRRSRSHTPSRRRSR SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRS RTPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSTPLRRFS RSPIRRKRSRSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSGHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGGFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVQYRAFTEANDGSLCLAMEYGGERGL				ASSIGN LENGTH L
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SVGRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSRTPSRRSRRSRSRSRS				RSKSRERKRKRSSSRDNRKTVRAPSPTDSDDSDSDSDSDSDS
RTPSRRSRTPSRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS RSPIRRKRSRSERGRSPKRLTDLDKAQLLEIAKANAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFPNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGERSL			ļ	SVGRRRSFSISPSRRSRTPSRRSRTPSRRSRTPSRRSPTDEDDO
RSPIRRKRSRSSERGRSPKRLTDLDKAQLLEIAKANAAAMCAKA GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFMLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGGFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGERSI.	1		1	RTPSRRSRTPSRRRRSRSVVRRRSFSISPVRLRRSRTPLRRRFS
GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKQIAQSKE DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSQHRKKEADSVYGEWUPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLINSIPGGFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGERGL				RSPIRRKRSRSSERGRSPKRLTDLDKAOLLEIAKANAAAMCAKA
DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK PTPPKSQVTLTKEFPVSSGSGHRKKEADSVYGEWVPVEKNGEEN KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQERIDAWAQLNSIPGGPTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSL]			GVPLPPNLKPAPPPTIEEKVAKKSGGATIEELTEKCKOIAOSKE
KDDDNVFSSNLPSEPVDISTAMSERALAQKRLSENAFDLEAMSM LNRAQBRIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLGSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGERSL			{	DDDVIVNKPHVSDEBEEEPPFYHHPFKLSEPKPIFFNLNIAAAK
LNRAQERIDAWAQLNSIPGQFTGSTGVQVLTQEQLANTGAQAWI KKDQFLRAAPVTGGMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y 5783 1693 698 DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSL				PTPPASQVTLTKEFPVSSGSQHRKKEADSVYGEWVPVEKNGEEN
KKDQFLRAAPVTGSMGAVLMRKMGWREGEGLGKNKEGNKEPILV DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSL				LNPAOEPIDAMAOLNEI DOOPPOORTONOMANA LNPAOEPIDAMAOLNEI DOOPPOORTONOMANA LNPAOEPIDAMAOLNEI DOOPPOORTONOMANA LNPAOEPIDAMAOLNEI DOOPPOORTONOMANA LNPAOEPIDAMAOLNEI DOOPPOORTONOMANA LNPAOEPIDAMAONA
DFKTDRKGLVAVGERAQKRSGNFSAAMKDLSGKHPVSALMEICN KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSL				KKDOFLRAAPVTGGMGAVI.MDKMGWDEGEGG.
KRRWQPPEFLLVHDSGPDHRKHFLFRVLINGSAYQPNCMFFLNR Y DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGERGI.				DFKTDRKGLVAVGERAOKRSGNFSAAMKDI.SCKUDUSAT MET CO.
5783 1693 698 DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSL				KRRWQPPEFLLVHDSGPDHRKHFLFRVI.INGSAYOPNOMEDI NE
QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSL				Y
QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYQ KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSI	5783	1693	698	DSGLRVAFTMEGISNFKTPSKLSEKKKSVLCSTPTINIPASPFM
KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEK9I			1	QKLGFGTGVNVYLMKRSPRGLSHSPWAVKKINPICNDHYRSVYO
NDLIEE/PI*SQ/PKILFOOP/LILKVALNMARGI.KVI.HOPKUT		İ	i .	KRLMDEAKILKSLHHPNIVGYRAFTEANDGSLCLAMEYGGEKSI.
				NDL1EE/PI*SQ/PKILFQQP/LILKVALNMARGLKYLHOEKKI

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i		to first	L=Leucine, M=Methionine, N=Asparagine,
l	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	to first		S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LHGDIKSSNVVIKGDFETIKICDVGVSLPLDENMTVTDPEACYI
i			GTEPWKPKEAVEENGVITDKADIFAFGLTLWEMMTLSIPHINLS
ĺ	1		NDDDDEDKTFDESDFDDEAYYAALGTRPPINMEBLDESYQKVIE
Į.	Į.		LFSVCTNEDPKDRPSAAHIVEALETDV
5784	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH
3/03	1 2003	1300	GILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH
ļ.	1		RMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL
į		1	QDNYNLGSFTFQATLLMDGRIIFGYKBIPVLVTQISSTNHPVKV
1			GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM
			TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW
\	1		VDSGCPBESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP
]			E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL
1			HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
		1	WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
5785	2669	1388	PRVRPRVRTDHNYYISRIYGPSDSASRDLWVNIDQMEKDKVKIH
1			GILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVVH
1			RMLTATOYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHL
			QDNYNLGSFTFQATLLMDGRIIFGYKEIPVLVTQISSTNHPVKV
			GLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKITNISAVEM
İ			TPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDW
	ì		VDSGCPEESKEKMCENTEPVET\FLEPPQP*ERQPPSSGS*LPP
			E/DAVTSQFPTSLPTEDDTKIALHLKDNGASTDDSAAEKKGGTL
]			HAGLIVGILILVLIVATAILVTVYMYHHPTSAASIFFIERRPSR
			WPAMKFRRGSGHPAYAEVEPVGEKEGFIVSEQC
5786	2532	1674	SYKLPAAERRASSCSQPPTPTRRRWPAPGRTSRGHRPQM*SGTP
1		1	APRPPARSTVSPASPLPKPRAGRCGSRPRSACSTFRPC*SLN*M
i			S*H*KRNLSQRSSSMSRRPLSCARPHR**RQGLTVAARLPTWAK
	1	1	SPPLACSFCQAAQKSQSLSSGRSTR*PERMSFRP\SPPGNPAIP
1	1		SLAPSSRP/PKGRPQCTWIPSRWPASPTAPPTTT*APTSSPGST
	1		GRSMMTCPTRWTATPWSARASSRPRNWPTP*WRPSGRLSTV*RA
1			TGGSTATAPPKRFPRNWNPMMAE
5787	+2	1460	MASAASVTSLADEVNCP\ICQGTLKEAGSLSNCG/HKNFCRACL
3/8/	1 *	1	T\RYCEIP\GPD\LEESP\TCP\LCKEPFRP\GSFRPNWQLANV
	1		VENIERLQLVSTLGLGEEDVCQEHGEKIYFFCEDDEMQLCVVCR
	1		EAGEHATHTMRFLEDAA\APYREQIHKCLKCLIKEREEIQEIQS
1		}	RENKRMOVLLTOVSTKROOVISEFAHLRKFLEEQQSILLAQLES
	j	1	ODGDILRORDEFDLLVAGEICRFSALIEELEEKNERPARELLTD
1			IRSTLIRCETRKCRKPVAVSPELGQRIRDFPQQALPLQREMKMF
		1	
1		1 .	LEKLCFELDYEPAHISLDPQTSHPKLLLSEDHQRAQFSYKWQNS
1]	PDNPQRFDRATCVLAHTGITGGRHTWVVSIDLAHGGSCTVGVVS
1		1	EDVQRKGELRLRPEEGVWAVRLAWGFVSALGSFP\TRLTLKEQP
			RQVRVSLDYEVGWVTFTNAVTREPIYTFTASFTRKVIPFFGLWG
		1	RGSSFSLSS
5788	2	6860	EHSVSGRSSAYGDATAEGHPAGPGSVSSSTGAISTTTGHQEGDG
			SEGEGEGETEGDVHTSNRLHMVRLMLLERLLQTLPQLRNVGGVR
			AIPYMQVILMLTTDLDGEDEKDKGALDNLLSQLIAELGMDKKDV
			SKKNERSALNEVHLVVMRLLSVFMSRTKSGSKSSICESSSLISS
1		1	ATAAALLSSGAVDYCLHVLKSLLEYWKSQQNDEEPVATSQLLKP
			HTTSSPPDMSPFFLRQYVKGHAADVFEAYTQLLTEMVLRLPYQI
			KKITDTNSRIPPPVFDHSWFYFLSEYLMIQQTPFVRRQVRKLLL
		1	FICGSKEKYRQLRDLHTLDS\HVRGIKKLLEEQGIFLRASVVTA
1			SPOSALQYDTLISLMEHLKACAEIAAQRTINWQKFCIKDDSVLY
	1		FLLQVSFLVDEGVSPVLLQLLSCALCGSKVLRALAASSGSSSAS
1	1		SSPAPVAASSGQATTQSKSSTKKSKKBEKEKEKDGETSGSQBDQ
			LCTALVNQLNKFADKETLIQFLRCFLLESNSSSVRWQAHCLTLH
1			IYRNSSKSQQELLLDLMWSIWPELPAYGRKAAQFVDLLGYFSLK
1			TPQTEKKLKEYSQKAVEILRTQNHILTNHPNSNIYNTLSGLVEF
1			DGYYLESDPCLVCNNPEVPFCYIKLSSIKVDTRYTTTQQVVKLI
			GSHTISKVTVKIGDLKRTKMVRTINLYYNNRTVQAIVELKNKPA
1		}	RWHKAKKVQLTPGQTEVKIDLPLPIVASNLMIEFADFYENYQAS
1			TETLOCPRCSASVPANPGVCGNCGENVYQCHKCRSINYDEKDPF
L			

Predicted Pred		Predicted	Predicted end	Amino acid segment containing signal peptide
Note	-			
corresponding to first amino acid amino acid residue of amino acid amino acid sequence corresponding to first amino acid amino acid amino acid amino acid amino acid amino acid sequence corresponding to first amino acid amino acid sequence corresponding to the corresponding	1	, , ,		
corresponding to first amino acid amino acid residue of amino acid amino acid sequence corresponding to first amino acid amino acid amino acid amino acid amino acid amino acid sequence corresponding to first amino acid amino acid sequence corresponding to the corresponding	NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence seque		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first smino acid residue of amino acid sequence ### Typtophan, Y=Tyrosine, X=Unknown, *=Stop Codon, Y=possible nucleotide deletion, V=possible nucleotide insertion) LUNAGE/EXPANDED, HULEOTIDE NUCLEOTIDE STASSWINTLL LUNKDRYMOLMGHRPOLENLICKUMEAAPERODOSSTAGGIS STASSWINTLICLAGE/EXPACE/COMPIBEREDRIKAVSNINTL LUNKDRYMOLMGHRPOLENLICKUMEAAPERODOSSTAGGIS STASSWINTLICLAGE/EXPACE/COMPIBEREDRIKAVSNINTL LUNKDRYMOLMGHRPOLENLICKUMEAAPERODOSSTAGGIS STASSWINTLICLAGE/EXPACE/COMPIBEREDRIKAVSNINTL LUNKDRYMOLMGHRPOLENLICKUMEAAPERODOSSTAGGIS STASSWINTLICLAGE/EXPACE/COMPIBEREDRIKAVSNINTL LUNKDRYMOLMGHRPOLENLICKUMEAAPERODOSSTAGGIS STASSWINTLICLAGE/EXPOCACHISTISTRYCYG CASAVTERCIT. AMREEVEGLMCLITENDEATQUMDLIGKUSTALKGHMANP DLASSIC/STMLLITOSISTRAGLIRELENTINGLIGHEN PERFECTIVERAGA AAMREEVEGLMCLITENDEATQUMDLIGKUSTALKGHMANP DLASSIC/STMLLITOSISTRAGLIRELENSITTYMEYON LUCKEKLVVQRYKLILORUMDLIASSWINTSLIALGULFENTYTYMEYON LUCKEKLVVQRYKLILORUMDLIASSYVEVSIS KHRYSRAUVOTIVALDED GARRIALMINTLISLALDIASSYVEVSIS KHRYSRAUVOTIVALDED GARRIALMINTLISLALDIASSYVEVSIS KHRYSRAUVOTIVALDED GARRIALMINTLISLALDIASSYVEVSIS KHRYSRAUVOTIVALDED GODILGGRMFGRPYSSNEGIGPIMDLIKKILCODOLUVALLED DASMELLUNKNILTSLALDIASSYVEVSIS KHRYSRAUVOTIVALDED GODILGGRMFGRPYSSNEGIGPIMDLIKKILCODOLUVALLED DASMELLUNKNILTSLALDIASSYVEVSIS KHRYSRAUVOTIVALDEN LURANGERICKUMANTISLALDIASSYVEVSIS KHRYSRAUVOTIVALDEN NUMGHINALDIASSYS KANTAGERSENTYSPEVIOLENIA RUMGHINALDIASSYS KORTAGENTSPEVIOLENIA RUMGHINALDIASSYS KORTAGENTSPEVIOLENIA RUMGHINALDIASSYS KORTAGENTSPEVIOLENIA RUMGHINALDIASSYS KORTAGENTSPEVIOLENIA RUMGHINALDIASSYS KORTAGENTA KANTAGENTA RETRABEKKAMMAMAMAGNALDITACHINITAGIA (HTTNERGOVOT/TETAILLEA DIBELLEREN/LURANGENSANCALBERPOUNTHIDA (HTTNERGOVOT/TETAILLEA DIBELLEREN/LURANGENSANCALBERPOUNTHIDA (HTTNERGOVOT/TETAILLEA DIBELLEREN/LURANGENSANCALBERPOUNTHIDA (HTTNERGOVOT/TETAILLEA DIBELLEREN/LURANGENSANCALBERPOUNTHIDA (HTTNERGOVOT/TETAILLEA DIBELLEREN/LURANGENSANCALBERPOUNTHIDA (HTTNERGOVOT/TETAILLEA DIBELLEREN/LURANGENSANCALBERPOUNTHIDA (HTTNERGOVOT/TETAILLEA DIBELLEREN/LURANGENSANCALBERPOUNTHIDA (HTTNERGO	1	corresponding	to first	•
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TLETDLOGOYALKSLITGILSSFYEVESIKRIFYSRILUTYLINGY LCCRKLVVGPIKLIDETLOGMLIEMLEDMTGSEYTKAPMAVCI ETAKRYNLDDYRTPYPIFERLCSIIYPEENEVTEFFVTLEKDPO QEDFILGGRMPGNPYSSNEPGIGTPIMEDIKNIKICDLOTVALLED DSGMELLVMKNIISDLDLVAEVYKKVWCTTREGEPPRIVYRMRG LLGDATEFFISILDSTTDEEEDEEEVYKMAGVMAQCGGLECHLM RLAGIRDFROGRHLITVLLKIFSYCVKVWGTVEMGQLVKLEMMTIN VMLGTINIALVAEGEKDSGGAAVAEQVLSIMEIT, OADFIVEE LSBDKGNLLILIGOKDGLVMALLDGINSTFYRSPYLOGLIKIP YLSFGEVERMGILVEFFKEYCNPDKYDEDHSGDDKYVLDGFCK LAAGIK\NNSGGRULKUL, LINGSTIONALD\YMKKHIP\SAA RIWADI\WKSFCLRPALPFILRLLRGLAIQHPGTQVLIGTDSI PNIHKLEOVS\SDBGIGTIAA\ENL\LESERHEDVNKILDA\GREEN ENRAEKKRAMAMAQKALGTLA\UNTUTC\HLA\UNSLAFRHEDVNKILDA\GREEN ENRAEKKRAMAMAGKALGTLA\UNTUTC\HLA\UNSLAFRHEDVNKILDA\GREENSAA LQNANTKCNGLLPVWGPHVPESAPATCLARINTYLOGGUE ENRYERTSRATSTYSHRHIVHYDC\HLA\UNSLAFRGEEMSSAA LQNANTKCNGLLPVWGPHVPESAPATCLARINTYLOGGTGGEE TYQINHIDIKLLFLRFAREOSFSADTGGGENIHLIPYITH GLYVINTTRATSREEKNLQGPLEOPREKWVESAPEVDGPYFTV LAAHILPEGOWATRIVE ILRILLUTSGAARDGATRILTDKAV KDYSAYRSSLLFWALVDLIYNMFKKVPTSNTEGGNSCSLAEYIR HNDMIYERAADKALKTRQEEFMPVETFSEFLDVAGLLSEITDPS FIKKLLKNSV TEKEKEKKEKKFKSKTEEILAEEESTVPFKAGVYKKKAEPSEVDNN SPRSKKAKK, KEEPSGNDISPKTKSLIRKKKEPIEKSVVSSKTKK VTNNEEPSEEELIAPAFDKKKEKEMNETERSPKLLKNGPHE EPDCHPSEAASEESNBEIEGGEIEVECKEG\APSNPPISEETIIL LKGGUTELPFIQAKTFHIVYSGKDLIAQARTGGKFTEKGPH EPDCHPSEAASEESNBEIEGGEIEVECKEG\APSNPPISEETIIL LKGGUTELPFIQAKTFHIVYSGKDLIAQARTGGKFTEKGPH EPDCHPSEAASEESNBEIEGGEIEVECKEG\APSNPPISEETIIL KKHIVLDEUVINVSGKGDCRTIFFCETKERSPKLKKREPIERSPLLNGPHE EPDCHPSEAASEESNBEIEGGEIEVECKEG\APSNPPISEETIILL KKGGUTELPFIQAKTGHTYSGKDLIAQARTGGKTEGKTFSFAIPL LKGGGUTELPFIQAKTGHTYSGKDLIAQARTGGKTEGKTFSFAIPL LKGGGYTELPFIQAKTGHTYSGKDLIAQARTGGKTGKTFSFAIPL IRLKGGGTELPFIQAGGTTIFFCETKGFKGFTKGKTFFAIPL VEGASGFFRAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG			l	
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ETAKRYNLDDYRTPYFIFERLOSITYPERNEYTFFYTLENDPO QEDFLOGENPONPYSSNERGIGPLMRDIKNKICQDCDLVALLED DSOMELLVINKIISLDLPVAEVYKKVWCTTREGEPHRIVYMRG LIGDATEFFISLDSTTDEEBDEEDYKHAGVMAQCGGLECMLM RLAGIRDFXGCRHLLTVLLKIFSYCVKVWGQUVKLEMMTIN RLAGIRDFXGCGHLLTVLLKIFSYCVKVWGQUVKLEMMTIN VMLGTINLALVAEQESKDSGGAAVARQVLSIMEIT, JAAPHVEE LSBOKGNLLLTGOKDQLWMLLDQINSTFYRNPSYLQGLLKIL YLSFGGVEKMQILUBEFKPYCNPDXVDEDHSGDDXVFL\DCPCK LSAGKKNLLLTGOKDQLWMLLDQINSTFYRNPSYLQGLKILFY YLSFGGVEKMQILUBEFKPYCNPDXVDEDHSGDDXVFL\DCPCK LAAGIK\NNSNGHQL\KDL\LIQKGITQNALD\YMKKHIF/SAA RIMDADI\WKSFCLRFALPFILLERGLAIGHRGTQVLIGTDSI FNLHKLEOVS\SDEGIGTIA\ENI\LESKRHPDVMKIDA\AR RETRABKKRAMAMQKALGTLA\TWHYDC\LLAALSLARGREEMSSAA LQNANTKCNGLLPVWGPHVPESAPATCLARINTYLQECTGQREP TYGINIHDIKLLEPLRFAREOSFSADTGGGGRESN HILPYIIHT GLYVLINTTRATSREENLQGFLBOYRGKWYSAFEVDGFYYFTV LAHHILPPEGWRATRVEILRRLLVTSQARAVAPGGATLITNKAV KDYSAYRSSLEFMALDULIYMMFKVPTSNTEGGNSCSLAEYIR HNDMPIYBAADKALKTFQEEFMPVETFSEFLDVAGLLSEITDPE SFLKDLLNSVP 1 2407 LPHAVBERTGRFGQPALKMFGKLRSDAGLESDTAMKKGETLRKQ VTSASTASLHFALVDLIYMMFKKVPTSNTEGGNSCSLAEYIR HNDMPIYBAADKALKTFQEEFMPVETFSEFLDVAGLLSEITDPE SFLKDLLNSVP 5789 1 2407 LPHAVBERTGRFGQPALKMFGKLRSDAGLESDTAMKKGETLRKQ TEEKEKKEKKENSDKYTEEIABEEBTVPFRAKQYKKKEABFSEVDMN SPRSKKAKK,KKEPSQNDISFYKTSLIKKNSPFPISESTHIL LKGRGVTFLFFIQAKTFHVYSGKDLIAQARTGTGKTFSFAIPL IEKLAG\SLODRERGRAPQVIVLAAFTRELANQVSKDFSDITKKL LKGRGVTFJFPIQAKTFHVYSGKDLIAQARTGTGKTFSFAIPL IEKLAG\SLODRERGRAPQVIVLAAFTRELANQVSKDFSDITKKL SVACFYGGTFYGGQFERMKSBOLFIVENGKFRINFORITLES ATCFHMVFNVAKKYMSTSTREVOULIGKKTOKTATTVEHLAIKCH WTGRAAVIGOVIRVYSGHQGRTIIFCETKKEAGBLSGNSAIKOD AQSIHGDIPQKGRETILKGPRNGSPGVVATNAVARGLDIPPTS ATCFHMVFNAKKYMSTSTREVOULIGKTOKTATTVEHLAIKCH WTGRAAVIGOVIRVYSGHQGRTIIFCETKKEAGBLSGNSAIKOD AQSIHGDIPQKGGRTIIFCETKKEAGBLSGNSAIKOD LVTGSSFFKAFGG REGSRGFRGQRONRTFRGQREGSGRFRGGRGGONKSNRSONK GGRASIFSKAFGG REGSRGFRGQRONRTFRGQREGSGGRONSNRSONK GGRASIFSKAFGG REGSRGFRGQRONRTFRGQREGSGGRONSNRSONK GGRASIFSKAFGG SAGELIEBERGEBESBEBGBSGBGEBG DAEEBEEEKERSHKWSTGBYIAVGDFTAQQVGDLTFKKGEI LUVIEKKPIOWMIALDAKTSCARTYDFTSPTSBEEBSTEDSBCBSGGBEB DAEEBEEEKERSHWSTGBYIAVG	1	[LCLRKLVVQRTKLIDETQDMLLEMLEDMTTGTESETKAFMAVCI
QEDFLGGRMGENPYSSNREGIGPLMINNKICQDCDLVALLED DSGMELLVMINIISIDLDPASVYKKWCTTREGPWRITYREG LLGDATEFIESLDSTTDEEDEEEVYKMAGVMAQCGGLECMLN RLAGIRDFKQGRHLLTVLLKLFSYCVKVKVNRGQLKLEMTIK VMLGTHINLAUNAGGE KIDEGAAVARQUYSIMEI \QAEPHYEE LSEDKGNLLLTGDKDQLVMLLDQINSTFVRSNPSVLQGLKIIF YLSFGBVEKMGILVERFKYCNPKYKDEDDKVYFL\DCFL LSEDKGNLLLTGDKDQLVMLLDQINSTFVRSNPSVLQGLKIIF YLSFGBVEKMGILVERFKYCNPKYKDEDDKVYFL\DCFL LAGIR\NNSNGHQL\KDL\LLGSITONALD\YMKKHIP\SAA RIMDADI\WKSFCLRPALPFYLDRLEGGLONGVYFL\DCFL LAGIR\NNSNGHQL\KDL\LLGSITONALD\YMKKHIP\SAA RIMDADI\WKSFCLRPALPFILRLEGGLONGTYTTKRVVLGGW ENKPRETSRATSTVSHFRIVHYDC\JHLA\AVSLARGREEMSAA LQMANTKCNGLIPWGPHYPSAPARICLAUTYTTKRVVLGGW ENKPRETSRATSTVSHFRIVHYDC\JHLA\AVSLARGREEMSAA LQMANTKCNGLIPWGPHYPSAPARICLAHTYLGGTGGEE TYQIN.HDIKLLFLRPAMEQSFSADTGGGGRESNIHLPYIIHT GLYVINTTRATSREENLOGGPLEOPEKKWYSAFEVDGFYYFTY LALHILPPEQWRATRVEILRRLLVTSQARAVAPGGATRLTDKAV KDYSAYRSSLLFFRALVDLIYMMFKKYPTSNTEGGWSCSLASYIR HNDMPIYRADKALKTYGEGOPALKMPGKLRSDAGLESDTAMKKGETLDRX KDYSAYRSSLLFFRALVDLIYMMFKKYPTSNTEGGWSCSLASYIR HNDMPIYRADKALKTYGEGOPALKMPGKLRSDAGLESDTAMKKGETLDRX SFLKDLLMSUP 5789 1 2407 LEPHAVBKTRIGFGOPALKMPGKLRSDAGLESDTAMKKGETLDRX VTYNEEPSEED IDAFKRKNKKKEMMGETTERSFYLLNGGSFSEDWDM SPKSKAKAK,KEEPSONDISPKTKSLRKKKKEPILKRYPEFELWVSSKTKX VTYNEEPSEED IDAFKRKNKKKEMMGETTERSFYLLNGGFPH EPPCMPSEAASEESNBEIBGGIFVEGKG\AFSNFFISEETIKL LKGRGVTIFLFIQAKTFHYYSGKDLIAQARTGTGKTFSFAIL IEKLHG\SLODRKRGRAPQVUVLAPTRELANQVSKDFSDITKKI SVACFYGGTYPGGOFERNRYNINILDILUTGPRIKDHIONGKLDLT KLMHVVLDEVDQHLDMGPADQVEETLSVAYKKGSEDNDOTLLFS ATCPHWFYNVAKKYMKSTYEQVDLIGKKTQATAITVEHLAIKCH WTQRAAVIGDVIRVTSGGGRTIFCETKKEAQBLSGNSAIKQD LVYGSSPRIVAVKYNSTEGGRGRGGGNKSNKSQNK QKRSIFKRAGGU VECKAGIKFRIGVPSATEIIKASSKDAIRLLDSVPTAISHFK QSAELIEKGAAVEALAALAHAHISGATSVCICTCYGKREYQLUQ VECKAGIKFKRIGVPSATEIIKASKDAIRLJDSVPTAISHFK QSAELIEKGAAVEALAALAHAHISGATSVCICTCYGKREYQLUQ VECKAGIKFKRIGVPSATEIIKASKDAIRLJDSVPTAISHFK QSAELIEKGAAVEALAALAHAHISGATSVOTCCTYGKREYGLUG QRGSSENGKSKSFRGGRGGNONKSNRSQNK GKRSFSKAFGG GGRSGFKARFGG GGRSGFRAFGG GGRSGFRAFGG GGRSGFRAFGG GGRSGFRAFGGBGBEBBGDBSGGEBB DAEEEEEKEBEEKEBEBSBCBSGBEBB GG	1			
DSGMELLVANKI ISLDLPVAGVYKKVMCTITNGGEPMRI VYRMRG LIGDATERFIESLDSTTDEEDEEDEVYKKORQVAGCGLECMLN RLAGIRDFKQGRHLLTVLIKLFSICVKVKVNRQQLVKLENNTLN RLAGIRDFKQGRHLLTVLIKLFSICVKVKVNRQQLVKLENNTLN VMLGTLNLALVARGESKDSGGAAVAEQVLSIMSI IQAEPMVEP LSEDKONLLTCDRDQLVMLLDQINSTVVSNPSVLQGLLSIIP YLSFGEVERMQILVERFKPYCHFDKYDEDHSGDKVFL\DCFCK KAAGIK\NNSNGHQL\DLADL\JUKKETPJSANPSVLQGLLSIIP YLSFGEVERMQILVERFKPYCHFDKYDEDHSGDKVFL\DCFCK KAAGIK\NNSNGHQL\DLADL\JUKKETPJSANPSVLQGLLSIIP YLSFGEVERMQILVERFKPYCHFDKYDEDHSGDKVFL\DCFCK RIMADOI\WKSFCLRPALPFILRLLRGLAIQHPGTQVLIGTDSI PNLHKLEQVS\SDEGIGTLA\BNL\LBSILRHPDVNKIDA\JUKTALEA RETRAKKRMAMARGKALGITG\MTTUREGQVVD\TTATALLEA DWEELLEEP\GLITCICREGYKFQFTKVLGIYTYFKRVVLGGWW ENKPRETSRATSTVSHFNIVHDC\HLA\AVSLARGREEMSAA LQNANTKCNGLLPWGPHVPESAPATCLARHNTYLQECTGQREP TYQLNIHDIKLLFLPRAMEQSFSADTGGGRESNIHLIFYIIHT GLYVLNTTRATSREERINLQGFLEOPKEKWVESAFEVOGPYYFTV LALHILPPEQWRATRVEILRRLLVTSQARAVARGGATRLITDKAV KDYSAYRSSLLFWALUDLIYNNFKKVFISNTEGGNSCLLAEYIR HNDMPIYRAADKALKTFQEEFMPVETFSEFLDVAGLLSEITDPE SFLKDLLNSVP 1 2407 LPHAVEKTGRFQQPALKMFGKLRSDAGLESDTAMKKGETLRKQ TEBKEKKSKFKSDKTEEIAEEETVFFKAKQVKKKASESSVDMN SPHSKRAKK\SPESPONJSIS PKTKSLKKEPIEKVVSKSTKK VTNNEFPSEEIIDAPKPKMKKKKEPIMGETTEKSFYLKNGFPHP EPDCNPSSEAASESNSHSEINGIPUGAJSNSHPFISETTIKL LKGRGVTFLFFIQAKTFHLVYSGKDLLAOARTOTKKTFSPAIDL IEKLHG\ELQDEKGRGRAPQVLVLAPTRELANQVSKDFSDTITKKL SVACFYGGTFYGGGFERMENGIDTILVGTPGRIKDHIQNGKLDLT KLMHVVLDEVDQMLDMGFADQVEEILSVAYKKDSDMPQTLLFS ATCFHWYNVAKKYMRSTYEGVDLIGKKTNGTATIVVEHLAIKCH WTGRAAVIGDVIRVYSGHGGRTIIFCETKKEAGELSONSAIKOD AQSIMGDIPQKORBITIKGFRNGSFGULVATNVAARGLDIPBVD LVYGSSPKVOSYIHRSGRTGRAGRTGVCICFYQHKEEVQLVQ VZCKAGIFFRRIGVPSATTIIKASSKDAIRLLDSVPPTAISHEK GSAEKLIEEKGAVEALAAALAHISGATCHATVVAARGLDIPBVD LVYGSSPKVOSYIHRSGRTGRGGGRGGNKSNRSONK GGRRFSKARGQ PUVTASVYTEIOEWHISSRWOLSVATRODYSLINGNVCFVTM ILQCSIEMPNISVAWKELKEGLGEEIDSKVKGMVPLKGKLGVCF DVYTASVYTEIOEWHISSRWOLSVATRODYSLINGREEBITLLD KLTGLQCGLAVTISRRITITEVQAPTEEBEESESSBSDSGGEBB DAEEEEEKEENESHKWSTGBYIAVQDPTAQQVGDLTFKKGEI LLVIEKKPOWMTAKDAKKNSGBYPATVLEPYSEEBEGGGSSES GSEEDVEAVVDETAGAGEVK\QRTPTHANAVACKSEITLLDS	1	1		
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SVACFYGGTPYGGQFERMRNGIDILVGTPGRIKDHIQNGKLDLT KLMHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS ATCPHWVFNVAKKYMKSTYBQVDLIGKKTQKTAITVEHLAIKCH WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPPVD LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVPLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRFFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ 5790 3786 1585 ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEESESEDSEDSGGEEE DAEEEEEKEENESHKWSTGEBYIAVGDFTAQQVGDLTFKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSEE GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN				LKGRGVTFLFPIQAKTFHHVYSGKDLIAQARTGTGKTFSFAIPL
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KLNHVVLDEVDQMLDMGFADQVEEILSVAYKKDSEDNPQTLLFS ATCPHWVFNVAKKYMKSTYEQVDLIGKKTQKTAITVEHLAIKCH WTQRAAVIGDVIRVYSGHQGRTIIFCETKKEAQELSQNSAIKQD AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDIPEVD LVIQSSPPKDVESYIHRSGFRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVFLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGNKSNRSQNK GQKRSFSKAFGQ 5790 3786 1585 ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEESSEDSBGGEEB DAEEEEEEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSEE GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN	1			
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LVIQSSPPKDVESYIHRSGRTGRAGRTGVCICFYQHKEEYQLVQ VEQKAGIKFKRIGVPSATEIIKASSKDAIRLLDSVPPTAISHFK QSAEKLIEEKGAVEALAAALAHISGATSVDQRSLINSNVGFVTM ILQCSIEMPNISYAWKELKEQLGEEIDSKVKGMVPLKGKLGVCF DVPTASVTEIQEKWHDSRRWQLSVATEQPELEGPREGYGGFRGQ REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGGNKSNRSQNK GQKRSFSKAFGQ 5790 3786 1585 ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHIY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEESESEDSEDSGGEEE DAEEEEEEKEENESHKWSTGEEYIAVGDPTAQQVGDLTFKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEGQESSEE GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN	1		,	AQSLHGDIPQKQREITLKGFRNGSFGVLVATNVAARGLDTPRVD
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REGSRGFRGQRDGNRRFRGQREGSRGPRGQRSGGNKSNRSQNK GQKRSFSKAFGQ 5790 3786 1585 ARRQRDPLQALRRRNQELKQQVDSLLSESQLKEALEPNKRQHTY QRCIQLKQAIDENKNALQKLSKADESAPVANYNQRKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEESESEDSEDSGGEEE DAEEEEEEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEBGQESSEE GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN	1			
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QRCIQLKQAIDENKNALQKLSKADESAPVANYNORKEEEHTLLD KLTQQLQGLAVTISRENITEVGAPTEEEESESEDSEDSGGEEB DAEEEEEEKEENESHKWSTGEEYIAVGDFTAQQVGDLTFKKGEI LLVIEKKPDGWWIAKDAKGNEGLVPRTYLEPYSEEEEBGQESSEE GSEEDVEAVDETADGAEVK\QRTDPHWSAVQKAISEAGIFCLVN				GQKRSFSKAFGQ
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I INVSFCIBIVERION REFERENCE SERVICES ELGENAMINA Ó SEGRIPLOS EL				
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	, , _ ,		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	1	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ľ	k	sequence	Codon, /=possible nucleotide deletion,
<u></u>	sequence		\=possible nucleotide insertion)
			PVLQQINTVDVLTTMGAIPAGFRPSTLSQLLEEGNQFRANYFLQ
1			PELMPSQLAFROLMWDATEGTIRSRPSRISLILTLWSCKMIPLP
1			GMSIQVLSRHVRLCLFDGNKVLSNIHTVRATWQPKKPKTWTFSP
			QVTRILPCLLDGDCFIRSNSASPDLGILFELGISYIRNSTGERG
1	1	ļ	ELSCGWVFLKLFDASGVPIPAKTYELFLNGGTPYEKGIEVDPSI
1			SRRAHGSVFYQIMTMRRQPQLLVKLRSLNRRSRNVLSLLPETLI
			GNMCSIHLLIFYRQILGDVLLKDRMSLQSTDLISHPMLATFPML
			LEQPDVMDALRSSWAGQES\TLKRSEKR\PKEFLKVPRFLLVYH
			\GCVLPLL/HTPTRLPPFRWAEEETETARWKVITDFLKQNQENQ
5791	 	1626	GALQALLSPDGVHBPFDLSEQTYDFLGEMRKNAV
2/91	3	1636	LRVAEFAGTSR/IGAGLIQPLHRAPARDHGLLRGGAAPALSVSH
1	1		GN/GKQL/AMSSQGSDDEQIKRENIRSLTMSGHVGFESLPDQLV
			NRSIQQGFCFNILCVGETGIGKSTLIDTLFNTNFEDYESSHFCP
		1 .	NVKLKAQTYELQESNVQLKLTIVNTVGFGDQINKEESYQPIVDY
ļ			IDAQFEAYLQEELKIKRSLFTYHDSRIHVCLYFISPTGHSLKTL
ł			DLLTMKNLDSKVYIIPVIAKADTVSKTELQKFKIKLMSELVSNG
			VQIYQFPTDDDTIAKVNAAMNGQLPFAVVGSMDEVKVGNKMVKA
		i	RQYPWGVVQVENENHCDFVKLREMLICTNMEDLREQTHTRHYEL
ĺ			YRRCKLEEMGFTDVGPENKPVSVQETYEAKRHEFHGERQRKEEB
			MKQMFVQRVKEKEAILKEAERELQAKFEHLKRLHQEERMKLEEK
1			RRLLEEEIIAFSKKKATSEIFHSQSFLATGSNLRKDKDRKNSQF
			FVKQKVPEHRRSSSQANFIKKKLEVCFDFAVICFITSIFGEQPQ
5792	2263	653	LLIFMEKYFQVQGQYISQSE
3/32	2263	653	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY
			LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER
			TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT
-			YMVPKPEEINLLTGESDTQQIEADKKPTSALDEPVSHWRPRLAL
1			NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDQLSN
ł			RVKDLMVINRSTTELPLTVSYDKVSLGRLRFWIHMQDAVYSLQQ
			FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND
}			ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEQTSLLVLVP
į	1		AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY
			DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV
1			YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF
1			IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD
5793	2263	653	
3/33	2203	033	AAAAPSPAWWCGVFVVYVVHTCWVMYGIVYTRPCSGDASCIQPY
			LARRPKLQL\RHSFTTTRSHLGAENNIDLVLNVEDFDVESKFER
		1	TVNVSVPKKTRNNGTLYAYIFLHHAGVLPWHDGKQVHLVSPLTT YMVPKPEEINLLTGESDTOOIEADKKPTSALDEPVSHWRPRLAL
			NVMADNFVFDGSSLPADVHRYMKMIQLGKTVHYLPILFIDOLSN
			DIRECT ACTIVE COMPANY OF CHARLES AND DESCRIPTION OF CHARLES
		1	FGFSEKDADEVKGIFVDTNLYFLALTFFVAAFHLLFDFLAFKND
}			ISFWKKKKSMIGMSTKAVLWRCFSTVVIFLFLLDEOTSLLVLVP
l .			1
1	1	1	AGVGAAIELWKVKKALKMTIFWRGLMPEFQFGTYSESERKTEEY
		1	DTQAMKYLSYLLYPLCVGGAVYSLLNIKYKSWYSWLINSFVNGV
			YAFGFLFMLPQLFVNYKLKSVAHLPWKAFTYKAFNTFIDDVFAF
			IITMPTSHRLACFRDDVVFLVYLYQRWLYPVDKRRVNEFGESYE EKATRAPHTD
5794	1	5016	
3/34	1 *	2010	MGPRLSVWLLLLPAALLLHEEHSRAAAKGGCAGSGCGKCDCHGV
ļ			KGQKGERGLPGLQGVIGFPGMQGPEGPQGPPGQKGDTGEPGLPG
			TKGTRGPPGASGYPGNPGLPGLPGQDGPPGPPGIPGCNGTKGER
		1	GPLGPPGLPGFAGNPGPPGLPGMKGDPGEILGHVPGMLLKGERG
		l	FPGIPGTPGPPGLPGLQGPVGPPGFTGPPGPPGPPGPPGEKGQM
			GLSFQGPKGDKGDQGVSGPPGVPGQAQVQEKGDFATKGEKGQKG
			EPGFQGMPGVGEKGEPGKPGPRGKPGKDGDKGEKGSPGFPGEPG
			YPGLIGRQGP\QGEKGEAGPPGPPGIVIGTGPLGEKGERGYPGT
			PGPRGEPGPKGFPGLPGQPGPPGLPVPGQAGAPGFPGERGEKGD
1		1	RGFPGTSLPGPSGRDGLPGPPGSPGPPGQPGYTNGIVECQPGPP
			GDQGPPGIPGQPGFIGEIGEKGQKGESCLICDIDGYRGPPGPQG PPGEIGFPGQPGAKGDRGLPGRDGVAGVPGPQGTPGLIGQPGAK
			· Person reservationed Relational Disputs available Principle (2010/2018)

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
			GEPGEFYFDLRLKGDKGDPGFPGQPGMPGRAGSPGRDGHPGLPG
			PKGSPGSVGLKGERGPPGGVGFPGSRGDTGPPGPGYGPAGPIG
j			DKGQAGFPGGPGSPGLPGPKGEPGKIVPLPGPPGABGLPGSPGF
			PGPQGDRGPPGTPGR\PGL\PGEKGAVG\QPGIGFPGPPGPKGV
1			DGLPGDMGPPGTPGRPGFNGLPGNPGVQGQKGEPGVGLPGLKGL
			PGLPGIPGTPGEKGSIGVPGVPGEHGAIGPPGLQGIRGEPGPPG
1			LPGSVGSPGVPGIGPPGARGPPGGQGPPGLSGPPGIKGEKGFPG
İ			FPGLDMPGPKGDKGAQGLPGITGQSGLPGLPGQQGAPGIPGFPG
1			SKGEMGVMGTPGQPGSPGPWGAPGLPGEKGD\HGFPGSSGPRGD
1			PGLKGDKGDVGLPGKPGSMDKVYMGSMKGQKGDQGEKGQIGPIG
			EKGSRGDPGTPGVPGKDGQAGQPGQPGPKGDPGISGTPGAPGLP
			GPKGSVGGMGLPGTPGEKGVPGIPGPQGSPGLPGDKGAKGEKGO
			AGPPGIGIPGLRGEKGDQGIAGFPGSPGEKGEKGSIGIPGMPGS
			PGLKGSPGSVGYPGSPGLPGEKGDKGLPGLDGIPGVKGEAGLPG
			TPGPTGPAGQKGEPGSDGIPGSAGEKGEPGLPGRGFPGFPGAKG
			DKGSKGEVGFPGLAGSPGIPGSKGEQGFMGPPGPOGOPGLPGSP
	1		GHATEGPKGDRGPQGQPGLPGLPGPGPPGLPGIDGVKGDKGNP
			GWPGAPGVPGPKGDPGFQGMPGIGGSPGITGSKGDMGPPGVPGF
	1		QGPKGLPGLQGIKGDQGDQGVPGAKGLPGPPGPPGPYDIIKGEP
			GLPGPEGPPGLKGLQGLPGPKGQQGVTGLVGIPGPPGIPGFDGA
			PGQKGEMGPAGPTGPRGFPGPPGPDGLPGSMGPPGTPSVDHGFL
İ			VTRHSQTIDDPQCPSGTKILYHGYSLLYVQGNERAHGQDLGTAG
			SCLRKFSTMPFLFCNINNVCNFASRNDYSYWLSTPEPMPMSMAP
			ITGENIRPFISRCAVCEAPAMVMAVHSQTIQIPPCPSGWSSLWI
			GYSFVMHTSAGAEGSGQALASPGSCLEEFRSAPFIECHGRGTCN
			YYANAYSFWLATIERSEMFKKPTPSTLKAGELRTHVSRCQVCMR
5795	1192	61	
		01	STRSPTVEYISAHPHILFMLLKGYEAPQIALRCGIMLRECIRHE
			PLAKIILFSNQFRDFFKYVELSTFDIASDAFATFKDLLTRHKVL
			VADFLEQNYDTIFEDYEKLLQSENYVTKRQSLKLLGELILDRHN FAIMTKYISKPENLKLMMNLLRDKSPNIQFEAFHVFKVFVASPH
			KTQPIVEILLKNQPKLIEFLSSFQKERTDDEQFADEKNYLIKQI
1	1		RDLKKTAP*RALRDSKR
5796	2	1078	GRVGWELWCMYISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKF
1			FGEIGLLDPGMDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIE
ŀ			RKKKPYNSNIGFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENP
			GIDIGDVSERRALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGE
			LRNNKAKDVCLDQGPLENHTAILYPCHGWGPQLARYTKEGFLHL
	1		GALGTTTLLPDTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQ
			NGAIMNKGTGRCLEVENRGLAGIDLILRSCTGORWTIKNSIK*R
			EGAGALEPGPQDMAAPPNIWTSCPGGETARGRQVLDGPPRASPG
			QHRDPG
5797	2	891	PRVRQKTLVDVTLENSNIKDQIRNLQQTYEASMDKLREKQRQLE
	1		VAQVENQLLKMKVESSQEANAEVMREMTKKLYSOYEEKLOEEOR
			KHSAEKEALLEETNSFLKAIEBANKKMQAAEISLEEKDORIGEL
		ĺ	DRLIERMEKERHQLQLQLLEHBTEMSGELTDSDKERYOOLEEAS
		Ì	ASLRERIRHLNDMVHCQQKKVKQMVEEIESLKKKLOOKOLLILO
		İ	LLEKISFLEGENNELQSRLDYLTETQAKTEVETREIGVGCDLLP
			SQTGRTREIVMPSRNYTPYTRVLELTMKKTLT
5798	644	115	KILGSRWKSMSNQEKQPYYEEQARLSKIHLEKYPNYKYKPRPKR
		İ	TCIVDGKKLRIGEYKQLMRSRRQEMRQFFTVGOOPOIPITTGTG
			VVYPGAITMATTTPSPQMTSDCSSTSASPEPSLPVIOSTYGMKT
5799	2655		DGGSLAGNEMINGEDEMEMYDDYEDDPKSDYSSENEAPEAVSAN
5/99	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELOORAVEYL
			TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
			DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
		,	PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP
		[EADBLLNKFVCKNNGVLFENQLLQIGVKSEFRONLGRMYLFYGN
	1	1	KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVOQVL
i I	1	1	NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFOPTEM
L			AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA
			· · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
1 -	1		
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	
1			P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ĭ	amino acid	sequence	Codon, /=possible nucleotide deletion,
		bequence	1
	sequence		\=possible nucleotide insertion)
	ļ		LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
l	1	[RTSKEPVSRHLCELLAQQF
5800	2679	1435	LLSTYIKFINLFPETKATIQGVLRAGSQLRNADVELQORAVEYL
3000	2075	1 1133	
İ		l	TLSSVASTDVLATVLEEMPPFPERESSILAKLKRKKGPGAGSAL
			DDGRRDPSSNDINGGMEPTPSTVSTPSPSADLLGLRAAPPPAAP
		1	PASAGAGNLLVDVFDGPAAQPSLGPTPEEAFLSPGPEDIGPPIP
		1	EADELLNKFVCKNNGVLFENQLLQIGVKSEFRONLGRMYLFYGN
ł	ł	1	
		Ì	KTSVQFQNFSPTVVHPGDLQTQLAVQTKRVAAQVDGGAQVQQVL
		•	NIECLRDFLTPPLLSVRFRYGGAPQALTLKLPVTINKFFQPTEM
			AAQDFFQRWKQLSLPQQEAQKIFKANHPMDAEVTKAKLLGFGSA
1.			
ľ	1		LLDNVDPNPENFVGAGIIQTKALQVGCLLRLEPNAQAQMYRLTL
			RTSKEPVSRHLCELLAQQF
5801	3	1413	FPRLYHLIPDGEITSIKINRVDPSESLSIRLVGGSETPLVHIII
			QHIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRLLROP
1			CQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEE
1	1		
Į.			QLGIKLVRKVDEPGVFIFNVLDGGVAYRHGQLEENDRVLAINGH
İ			DLRYGSPESAAHLIQASERRVHLVVSRQVRQRSPDIFQEAGWNS
1			NGSWSPGPGERSNTPKPLHPTITCHEKVVNIQKDPGESLGMTVA
		İ	GGASHREWDLPIYVISVEPGGVISRDGRIKTGDILLNVDGVELT
l		i	
1	•	{	EVSRSEAVALLKRTSSSIVLKALEVKEYEPQEDCSSPAALDSNH
	1	(NMAPPSDWSPSWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIVG
1	(i	GYEEYNGNKPFFIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSG
	1	1	MIHACLARLLKELKGRITLTIVSWPGTFL
5000		l	1
5802	3	290	CFSLYQIMERIMDLPTLLRHAFREMFSVGGLFWMFRIRIILCLM
1	1	1	GAFFYLISPLDFVPEALFGILGFLDDFFVIFLLLIYISIMYREV
			ITQRLTR
5803	2234	1299	EAQFGTTAEIYAYREEQDFGIEIVKVKAIGRORFKVLELRTOSD
3003	2234	12,55	
			GIQQAKVQILPECVLPSTMSAVQLESLNKCQIFPSKPVSREDQC
	ı	ļ .	SYKWWQKYQKRKFHCANLTSWPRWLYSLYDAETLMDRIKKQLRE
		ļ	WDENLKDDSLPSNPIDFSYRVAACLPIDDVLRIQLLKIGSAIQR
	i		LRCELDIMNKCTSLCCKQCQETEITTKNEIFSLSLCGPMAAYVN
			PHGYVHETLTVYKACNLNLIGRPSTEHSWFPGYAWTVAOCKICA
ļ			,
1			SHIGWKFTATKKDMSPQKFWGLTRSALLPTIPDTEDEISPDKVI
I			rcr .
5804	2	1707	EMEKQRQEEQRKRTEEERKRRIEQDMLEKRKIQRELAKRAEQIE
1	_		DINNTGTESASEEGDDSLLITVVPVKSYKTSGKMKKNFEDLEKE
1	ļ		1
1			RBEKERIKYEEDKRIRYEEQRPSLKEAKCLSLVMDDEIBSEAKK
1			ESLSPGKLKLTFEELERQRQENRKKQAEEEARKRLEEEKRAFEE
1			ARROMVNEDEENODTAKIFKGYRPGKLKLSFEEMERORREDEKR
ł			KAEEEARRRIEEEKKAFAEARRNMVVDDDSPEMYKTISQEFLTP
1			
1			GKLEINFEELLKQKMEEEKRRTEEERKHKLEMEKQEFEQLRQEM
	1	1	GEEEEENETFGLSREYEELIKLKRSGSIQAKNLKSKFEKIGQLS
1)	EKEIQKKIEEERARRRAIDLEIKEREAENFHEEDDVDVRPARKS
1			EAPFTHKVNMKARFEQMAKAREEEEQRRIEEQKLLRMQFEQREI
1			DAALQKKREEEEEEGSIMNGSTAEDEEQTRSGAPWFKKPLKNT
1	1		
1			SVVDSEPVRFTVKVTGEPKPEITWWFEGEILQDGEDYQYIERGE
i	1		TYCLYLPETFPEDGGEYMCKAVNNKGSAASTCILTIESKN
5805	3	776	YISDTLGQVYKSKIRWWIEENGGNGNISVDDLIALLDLAEHASS
1	1		AFKESQQQSEDREYEVKERLYPKSKRRYDTYNIAGYQGEIEVGL
1			
1		1	YTIQILQLIPFFDNKNELSKRYMVNFVSGSSDIPGDPNNEYKLA
1	,	1	LKNYIPYLTKLKFSLKKSFDFFDEYFVLLKPRNNIKQNEEAKTR
1			RKVAGYFKKYVDIFCLLEESONNTGLGSKFSBPLOVERCRRNLV
1	1	[
	 		ALKADKFSGLLEYLIKSQEDAISTMKCIVNEYTFLLK
5806	1257	877	AVFTFHNHGRTANLYSLHSWLGITTVFLFACORFLGFAVFLLPW
1			ASMWLRSLLKPIHVFFGAAILSLSIASVISGINEKLFFSLKNTT
			RPYHSLPSEAVFANSTGMLVVAFGLLVLYILLASSWKRP
F000	 	1200	
5807	2267	1302	RFSKKTFRRPMAVDIQPACLGLYCGKTLLFKNGSTEIYGECGVC
1	1	Ì	PRGQRTNAQKYCQPCTESPELYDWLYLGFMAMLPLVLHWFFIEW
I			YSGKKSSSALFQHITALFECSMAAIITLLVSDPVGVLYIRSCRV
1			LMLSDWYTMLYNPSPDYVTTVHCTHEAVYPLYTIVFIYYAFCLV
	L	L	- HEDDRITTHEREDIALIANCEMENALERITAALITAKCHA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
_		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
	 		LMMLLRPLLVKKIACGLGKSDRFKSIYAALYFFPILTVLQAVGG
	ł		GLLYYAFPYIILVLSLVTLAVYMSASBIENCYDLLVRKKRLIVL
ì			FSHWLLHAYGIISISRVDKLEQDLPLLALVPTPALFYLFTAKFT
			EPSRILSEGANGH
	ļ		1
5808	2	433	SLPDSGVVEYLSNGGVADNHKDFGELRYNECLMNFSCNGKNGSS
1			EGRITHGFQLKSAYENNLMPYTNYTFDFKGVIDYIFYSKTHMNV
	1	ļ	LGVLGPLDPQWLVENNITGCPHPHIPSDHFSLLTQLELHPPLLP
			LVNGVHLPNRR
5809	464	2422	ILVPGFQGILHPGVYCALQSQHQAQELVADIDECEVSGLCRHGG
1			RCVNTHGSFECYCMDGYLPRNGPEPFHPTTDATSCTEIDCGTPP
		1	EVPDGYIIGNYTSSLGSQVRYACREGFFSVPEDTVSSCTGLGTW
		1	ESPKLHCQEINCGNPPEMRHAILVGNHSSRLGGVARYVCQEGFE
t		1	SPGGKITSVCTEKGTWRESTLTCTEILTKINDVSLFNDTCVRWQ
İ		1	<u>-</u>
		1	INSRRINPKISYVISIKGQRLDPMESVREETVNLTTDSRTPEVC
		1	LALYPGTNYTVNISTAPPRRSMPAVIGFQTAEVDLLEDDGSFNI
	ŀ		SIFNETCLKLNRRSRKVGSEHMYQFTVLGQRWYLANFSHATSFN
l			FTTREQVPVVCLDLYPTTDYTVNVTLLRSPKRHSVQITIATPPA
		1	VKQTISNISGFNETCLRWRSIKTADMEEMYLFHIWGQRWYQKEF
1			AQEMTFNISSSSRDPEVCLDLRPGTNYNVSLRALSSELPVVISL
		1	TTQITEPPLPEVEFFTVHRGPLPRLRLRKAKEKNGPISSYQVLV
· ·			LPLALQSTFSCDSEGASSFFSNASDADGYVAAELLAKDVPDDAM
		Į	EIPIGDRLYYGEYYNAPLKRGSDYCIILRITSEWNKVRRHSCAV
ļ		J	WAQVKDSSLMLLQMAGVGLGSLAVVIILTFLSFSAV
	<u> </u>	1.643	
5810	3	1641	KVFGTHKDHEVSTLDTAISAVKVQLAEFLENLQEKSLRIEAFVS
		1	BIESFFNTIEENCSKNEKRLEEQNEEMMKKVLAQYDEKAQSFEE
	i		VKKKKMEFLHEQMVHFLQSMDTAKDTLETIVREAEELDEAVFLT
			SFEEINERLLSAMESTASLEKMPAAFSLFEHYDDSSARSDQMLK
			QVAVPQPPRLEPQEPNSATSTTIAVYWSMNKEDVIDSFQVYCME
1		1	BPQDDQEVNELVEEYRLTVKESYCIFEDLEPDRCYQVWVMAVNF
	ì		TGCSLPSERAIFRTAPSTPVIRAEDCTVCWNTATIRWRPTTPEA
i			TETYTLEYCRQHSPEGEGLRSFSGIKGLQLKVNLQPNDNYFFYV
1]	}	RAINAFGTSEQSEAALISTRGTRFLLLRETAHPALHISSSGTVI
1	1		SFGERRRLTEIPSVLGEELPSCGQHYWETTVTDCPAYRLGICSS
ł		1	-
			SAVQAGALGQGETSWYMHCSEPQRYTFFYSGIVSDVHVTERPAR
ł			VGILLDYNNQRLIFINAESEQLLFIIRHRFNEGVHPAPALEKPG
L		L	KCTLHLGIEPPDSVRHK
5811	1918	851	AAALADPLPEDKWSAEKRRPLKSSLGYEITFSLLNPDPKSHDVY
1			WDIEGAVRRYVQPFLNALGAAGNFSVDSQILYYAMLGVNPRFDS
I			ASSSYYLDMHSLPHVINPVESRLGSSAASLYPVLNFLLYVPELA
1	Í		HSPLYIODKDGAPVATNAFHSPRWGGIMVYNVDSKTYNASVLPV
1			RVEVDMVRVMEVFLAOLRLLFGIAOPOLPPKCLLSGPTSEGLMT
I	1		WELDRLLWARSVENLATATTTLTSLAQLLGKISNIVIKDDVASE
	1		VYKAVAAVQKSAEELASGHLASAFVASQEAVTSSELAFFDPSLL
1	•		
1			HLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSWRKPE
L			KTD
5812	5204	2744	GGRQRCQRGRSCGAREBEVEPGTARPPPAASAMDASLEKIADPT
1	1		LAEMGKNLKEAVKMLEDSQRRTEEENGKKLISGDIPGPLQGSGQ
1	1		DMVSILQLVQNLMHGDEDEEPQSPRIQNIGEQGHMALLGHSLGA
			YISTLDKEKLRKLTTRILSDTTLWLCRIFRYENGCAYFHBEERE
			GLAKICRLAIHSRYEDFVVDGFNVLYNKKPVIYLSAAARPGLGO
1	1		YLCNQLGLPFPCLCRVPCNTVFGSQHQMDVAFLEKLIKDDIERG
	1		
1	1		RLPLLLVANAGTAAVGHTDKIGRLKELCEQYGIWLHVEGVNLAT
			LALGYVSSSVLAAAKCDSMTMTPGPWLGLPAVPAVTLYKHDDPA
			LTLVAGLTSNKPTDKLRALPLWLSLQYLGLDGFVERIKHACQLS
Ţ			QRLQESLKKVNYIKILVEDELSSPVVVFRFFQELPGSDPVFKAV
			PVPNMTPSGVGRERHSCDALNRWLGEQLKQLVPASGLTVMDLEA
1			EGTCLRFSPLMTAAVLGTRGEDVDQLVACIESKLPVLCCTLQLR
1			EEFKOEVEATAGLLYVDDPNWSGIGVVRYEHANDDKSSLKSYPQ
	1		GENIHAGLLKKLNELESDLTFKIGPEYKSMKSCLYVGMASDNVH
			1
			AAELVETIAATAREIEDNSRLLENMTEVVRKGIQEAQVELQKAS
L		<u> </u>	EERLLEEGVLRQIPVVGSVLNWFSPVQALQKGRTFNLTAGSLES

SEQ	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
10.		location	Glutamic Acid, F=Phenvlalanine G-Glycine
	location	corresponding	H=H1St1dine, I=Isoleucine, K=Iysine
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	Waltrantophan V. Transier v. T.
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	Bequence	sequence	Codon, /=possible nucleotide deletion,
	Dequence		\=possible nucleotide insertion)
1		ļ.	TEPIYVYKAQGAGVTLPPTPSGSRTKQRLPGQKPFKRSLRGSDA
i i			LSETSSVSHIEDLEKVERLSSGPEQITLEASSTEGHPGAPSPQH
	<u></u>	İ	TDQTEAFQKGVPHPEDDHSQVEGPESLR
5813	2936	699	HRDGVSGSLERPLTDRSRTGAFAQQRGKMATAGGGSGADPGSRG
	1		LLRLLSFCVLLAGLCRGNSVERKIYIPLNKTAPCVRLLNATHQI
1	1	[GCOSSISCOMOUTHURING
	1		GCQSSISGDTGVIHVVEKEEDLQWVLTDGPNPPYMVLLESKHFT
	1		RDLMEKLKGRTSRIAGLAVSLTKPSPASGFSPSVQCPNDGFGVY
- 1	l .		SNSYGPEFAHCREIQWNSLGNGLAYEDFSFPIFLLEDENETKVI
	İ		KQCYQDHNLSQNGSAPTFPLCAMOLFSHMAWLSFSTAT\ CMPPS
			SIQSTESINPKIVCDPLSDYNVWSMLKPINTTGTLKPDDPLAGA
i	1		ATRLDSRSFFWNV\APGAESAVASFVTQLAAAEALQKAPDVTTL
j	J I		PRNVMFVFFQGETFDYIGSSRMVYDMEKGKFPVQLENVDSFVEL
			GQVALRTSLELWMHTDPVSQKNESVRNQVEDLLATLEKSGAGVP
	i		AVII PROVISOR PROST OF THE STANDARD LATER SCACE
			AVILRRPNQSQPLPPSSLQRFLRARNISGVVLADHSGAFHNKYY
			QSIYDTAENINVSYPEWLEPLKE/ETWNFG*QDTAKALADVATV
			LGRALYELAGGTNFSDTVQADPQTVTRLLYG\FLIKANNSWFQS
ľ			ILQGRDLRSYLG*RGLFQH\YLAV\SSPTNTIYV/VLOVALANT
			TGTVVNLTREQCQDPSKVPSENKDLYEYSWVOGPLHSNETDPLD
	İ		RCVRSTARLARALSPAFELSQWSSTEYSTWTESRWKDIRARIFL
l i			IASKELELITLTVGFGILIFSLIVTYCINAKADVLFIAPREPGA
L	1		VSY
5814	8500	432	ALKCRPRRVLAILVGPVQPDRMAEEGAVAVCVRVRPLNSREESL
1 !			GETACUVWKTUNDUTVDUDGGKGTUDDUV
			GETAQVYWKTHNNVIYPVDGSKSFNFDRVLHGNETPKNVYEA\I
1 1			AAPIIDSAIQGYNGTIFA\YGQT\ASGKTYTMMGSEDHLGVIPQ
	i i		GQFHGHFSQKI*EVFLDREFLLRVSYMEIYNETITDLLCGTQKM
i			KPLIIREDVNRNVYVADLTEEVVYTSEMALKWITKGEKSRHYGE
			TKMNQRSSRSHTIFRMILESREKGEPSNCEGSVKVSHINIJVDLA
1 1			GSERAAQTGAAGVRLKEGCNINRSLFILGQVIKKLSDGQVGGFI
1 1	' .]		NYRDSKLTRILQNSLGGNPKTRIICTITPVSFDETLTALQFAST
1 1			AKYMKNTPYVNEVSTDEALLKRYRKEIMDLKKQLEEVSLETRAQ
i			AMEKDQLAQLLEEKDLLQKVQNEKIENLTRMLVTSSSLTLQQEL
1	ţ		KAYEVEDIETICI GYTYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYYY
1	1		KAKRKRRVTWCLGKINKMKNSNYADQFNIPTNITTKTHKLSINL
i			LREIDESVCSESDVFSNTLDTLSEIEWNPATKLLNQENIESELN
i :			SLRADYDNLVLDYEQLRTEKEEMELKLKEKNDLDEFEALERKTK
1	ļ		KDQEMQLIHEISNLKNLVKHREVYNQDLENELSSKVELLREKED
1			QIKKLQEYIDSQKLENIKMDLSYSLESIEDPKQMKQTLFDAETV
1		j	ALDAKRESAFLRSENLELKEKMKELATTYKOMENDIOLYOSOLE
			AKKKMQVDLEKELQSAFNEITKLTSLIDGKVPKDLLCNLFLFGV
			ITDLQKELNKEVEENEALREEVILLSELKSLPSEVERLRKEIQD
			KSEELHIITSEKDKLFSEVVHKESRVQGLLEEIGKTKDDLATTQ
]			SNYKSTDQEFQNFKTLHMDFEQKYKMVLEENERMNQEIVNLSKE
į l	.		AQKFDSSLGALKTELSYKTQELQEKTREVQERLNEMEQLKEQLE
1		1	NRDSPLQTVEREKTLITEKLQQTLEEVKTLTQEKDDLKQLQESL
	ł		QIERDQLKSDIHDTVNMNIDTQEQLRNALESLKQHQETINTLKS
1	i		VICEEUCDNI INTERNACIONALES LICHQUETINTLES
1 1	1		KISEEVSRNLHMEENTGETKDEFQQKMVGIDKKQDLEAKNTQTL
	l l	1	TADVKDNEIIEQQRKIFSLIQEKNELQQMLESVIAEKEQLKTDL
1	İ		KENIEMTIENQEELRLLGDELKKQQEIVAQEKNHAIKKEGELSR
1	į.	}	TCDRLAEVEEKLKEKSQQLOEKOOOLLNVOEEMSEMOKKINEIE
1 1			NLKNELKNKELTLEHMETERLELAOKLNENYEEVKSITKERKUT.
			KELQKSFETERDHLRGYIREIEATGLQTKEELKIAHIHLKEHQE
1 1			TIDELRRSVSEKTAQIINTQDLEKSHTKLQEEIPVLHEEQELLP
[I	NVKKVSETQETMNELELLTEQSTTKDSTTLARIEMERLRLNEKF
1 1		1	QESQEEIKSLTKERDNLKTIKEALEVKHDQLKEHIRETLAKIQE
			SOSKOROSI NWKEKDNETTATIOETT VANDAUKEHIKETLAKIQE
1 1			SQSKQEQSLNMKEKDNETTKIVSEMEQFKPKDSALLRIEIEMLG
			LSKRLQESHDEMKSVAKEKDDLQRLQEVLQSESDQLKENIKEIV
			AKHLETEEELKVAHCCLKEQEBTINELRVNLSEKETEISTIOKO
		ľ	LEAINDKLQNKIQEIYEKEEQLNIKOISEVOEKVNELKOFKFHD
			KAKDSALQSIESKMLELTNRLQESOEEIOIMIKEKEEMKRVOFA
			LQIERDQLKENTKEIVAKMKESQEKEYQFLKMTAVNETQEKMCE
			IEHLKEQFETQKLNLENIETENIRLTQILHENLEEMRSVTKERD
		İ	DLRSVEETLKVERDQLKENLRETITRDLRKQEELKIVHMHLKEH
		———— <u> </u>	STWOATE THE ATTACHMENT THE THE THE THE THE THE THE THE THE TH

CEO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	204	\=possible nucleotide insertion)
	504.0		QETIDKLRGIVSEKTNEISNMQKDLEHSNDALKAQDLKIQEELR
			IAHMHLKEQOETIDKLRGIVSEKTDKLSNMQKDLENSNAKLQEK
			IQELKANEHQLITLKKDVNETQKKVSEMEQLKKQIKDQSLTLSK
			LEIENLNLAQKLHENLEEMKSVMKERDNLRRVEETLKLERDQLK
			ESLOETKARDLEIQQELKTARMLSKEHKETVDKLREKISEKTIQ
			ISDIQKDLDKSKDBLQKKIQBLQKKELQLLRVKEDVNMSHKKIN
			EMEOLKKOFEPNYLCKCEMDNFQLTKKLHESLEEIRIVAKERDE
			LRRIKESLKMERDQFIATLREMIARDRQNHQVKPEKRLLSDGQQ
			HLMESLREKCSRIKELLKRYSEMDDHYECLNRLSLDLEKEIEFH
			RIMKKLKYVLSYVTKIKEEQHECINKFEMDFIDEVEKQKELLIK
			IOHLOODCDVPSRELRDLKLNONMDLHIEEILKDFSESEFPSIK
			TEFQQVLSNRKEMTQFLEEWLNTRFDIEKLKNGIQKENDRICQV
		i	NNFFNNRIIAIMNESTEFEERSATISKEWEQDLKSLKEKNEKLF
			KNYOTLKTSLASGAOVNPTTODNKNPHVTSRATQLTTEKIRELE
1		1	NSLHEAKESAMHKESKIIKMOKELEVTNDIIAKLQAKVHESNKC
		1	LEKTKETIOVLODKVALGAKPYKEEIEDLKMKLGKIDLEKMKNA
			KEFEKEISATKATVEYQKEVIRLLRENLRRSQQAQDTSVISEHT
			DPOPSNKPLTCGGGSGIVONTKALILKSEHIRLEKEISKLKOON
1			EQLIKQKNELLSNNQHLSNEVKTWKERTLKREAHKQVTCENSPK
			SPKVTGTASKKKQITPSQCKERNLQDPVPKESPKSCFFDSRSKS
			LPSPHPVRYFDNSSLGLCPEVQNAGAESVDSQP\GPWARLFQGK
İ			DVP\ECKTQ
5815	23	1460	SELVMWTVONRESLGLLSFPVMITMVCCAHSTNEPSNMSYVKET
5015			VDRLLKGYDIRLRPDFGGPPVDVGMRIDVASIDMVSEVNMDYTL
1			TMYFQQSWKDKRLSYSGIPLNLTLDNRVADQLWVPDTYFLNDKK
ì			SFVHGVTVKNRMIRLHPDGTVLYGLRITTTAACMMDLRRYPLDE
			QNCTLEIESYGYTTDDIEFYWNGGEGAVTGVNKIELPQFSIVDY
			KMVSKKVEFTTGAYPRLSLSFRLKRNIGYFILQTYMPSTLITIL
			SWVSFWINYDASAARVALGITTVLTMTTISTHLRETLPKIPYVK
			AIDIYLMGCFVFVFLALLEYAFVNYIFFGKGPQKKGASKQDQSA
			NEKNKLEMNKVQVDAHGNILLSTLEIRNETSGSEVLTSVSDPKA
			TMYSYDSASIQYRKPLSSRE\A*GRAPDRHGVPSKGRIRRRAS\
1			QLKVKIPDLTDVNSIDKWSRMFFPITFSLFNVVYWLYYVH
5816	861	191	TSSRSRAAAQEGDAETPGSVERRGRRAGAEDGMSQAPGAQPSPP
1		1	TVYHERORLELCAVHALNNVLQQQLFSQEAADBICKRLAPDSRL
			NPHRSLLGTGNYDVNVIMAALQGLGLAAVWWDRRRPLSQLALPQ
			VLGLILNLPSPVSLGLLSLPLRRRHLRWPCARL/VTVSYYNLDS
			K\LRAPEGPGGLRTE*GPFLAAALAQGLCEVLLVVTKEVEEKG
			SWLRTD
5817	851	118	RLFRGPGANRGRSCRGCSGGREPSGGALPKRHCPC*PPSPPAAD
			VMSNTTVPNAPQANSDSMVGYVLGPFFLITLVGVVVAVVMYVQK
1			KKRVDRLRHHLLPMYSYDPAEELHEAEQELLSDMGDPKVV\QAG
1			RVATSTSGCHCWMSRRDLTPLPHPSEPGVLDCLGPCHLLPLLSP
1			GSPCWVLGLHFSLHPPSAASASHALTITSLPPGLLPFVGVELTA
			HPQALMGRGFPSGMAAAGRHLCFL
5818	3	3918	QALRDKLWIFLVQSFYAVRHTESWKLMSTDDQQKIQAAAFDKGD
			DRRLGKKPIFSSSQQRKQVSDSGDIKIKSWRGNNKKECWSYLST
1			NKKMKSDGLGASGHSSSTNRNSINKTLKQDDVKEKDGTKIASKI
-			TKELKTGGKNVSGKPKTVTKSKTENGDKARLENMSPRQVVERSA
1			TAAAAATGQKNLLNGKGVRNQEGQISGARPKVLTGNLNVQAKAK
			PLKKATGKDSPCLSIAGPSSRSTDSSMEFSISTECLDEPKENGS
			TEEEKPSGHKLSFCDSPGQMMKNSVDSVKNSTVAIKSRPVSRVT
			NGTSNKKSIHEQDTNVNNSVLKKVSGKGCSEPVPQAILKKRGTS
	1		NGCTAAQQRTKSTPSNLTKTQGSQGESPNSVKSSVSSRQSDENV
1			AKLDHNTTTEKQAPKRKMVKQVHTALPKVNAKIVAMPKNLNQSK
			KGETLNNKDSKQKMPPGQVISKTQPSSQRPLKHETSTVQKSMFH
			DVRDNNNKDSVSEQKPHKPLINLASEISDAEALQSSCRP\DPQK
			PLNDQEKEKLALECQNISKLDKSLKHELESKQICLDKSETKFPN
			HKETDDCDAANICCHSVGSDNVNSKFYSTTALKYMVSNPNENSL
1	1		NSNPVCDLDSTSAGQIHLISDRENQVGRKDTNKQSSIKCVEDVS
1			LCNPERTNGTLNSAQEDKKSKVPVEGLTIPSKLSDESAMDEDKH
	į.	1	

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NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
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· ·	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ı	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			ATADSDVSSKCFSGQLSEKNSPKNMETSESPESHETPETPFVGH
			WNLSTGVLHQRESPESDTGSATTSSDDIKPRSEDYDAGGSQDDD
			GSNDRGISKCGTMLCHDFLGRSSSDTSTPEELKIYDSNLRIEVK
]		MKKQSSNDLFQVNSTSDDEIPRKRPEIWSRSAIVHSRERENIPR
	i		GSVQFAQEIDQVSSSADETEDERSEAENVAENFSISNPAPQQFQ
1			GIINLAFEDATENECREFSANKKFKRSVLLSVDECEELGSDEGE
			VHTPFQASVDSFSPSDVFDGISHEHHGRTCYSRFSRESEDNILE
1			CKQNKGNSVCKNESTVLDLSSIDSSRKNKQSVSATEKKNTIDVL
1			SSRSRQLLREDKKVNNGSNVENDIQQRSKFLDSDVKSQERPCHL
}			DLHQREPNSDIPKNSSTKSLDSFRSQVLPQEGPVKESHSTTTEK
}			ANIALSAGDIDDCDTLAQTRMYDHRPSKTLSPIYEMDVIEAFEQ
İ	Į		KVESETHVTDMDF*DDQHFAKQDWTLLKQLLSEQDSNLDVTNSV PEDLSLAQYLINQTLLLARDSSKPQGITHIDTLNRWSELTSPLD
			SSASITMASFSSEDCSPQGEWTILELETQH
5819	1	5557	AAAGLLGALHLVMTLVVAAARAEKEAFVQSESIIEVLRFDDGGL
	ļ	_	LQTETTLGLSSYQQKSISLYRGNCRPIRFEPPMLDFHEQPVGMP
ł			KMEKVYLHNPSSE*TITLVSIFATTSHFHASFFQNRKILPGGNT
			SFDVS/VFLARVVGNVENTLFINTSNHGVFTY\QVFGVGVPNPY
			RLRPFLGARVTVNSSFSPIINIHNPHSEPLQVVEMYSSGGDLHL
1			ELPTGQQGGTRKLWEIPPYETKGVMRASFSSREADNHTAFIRIK
			TNASDSTEFIILPVEVEVTTAPGIYSSTEMLDFGTLRTQDLPKV
			LNLHLLNSGTKDVPITSVRPTPQ\NDAITVHFKPITLKAS\ESK
j			YTKVASISFDASKAKKPSQFSGKITVKAKEKSYSKLEIPYQAEV
1			LDGYLGFDHAATLFHIRDSPADPVERPIYLTNTFSFAILIHDVL
			LPEEAKTMFKVHNFSKPVLILPNESGYIFTLLFMPSTSSMHIDN NILLITNASKFHLPVRVYTGFLDYFVLPPKIEERFIDFGVLSAT
		•	EASNILFAIINSNPIELAIKSWHIIGDG\LSIELVAVDRGNRTT
			IISSLPECEKSSSSDQSSVTLASGYF\AVFRVKLTAKKL\EGIH
1			DGAIQITTDYEILTIPVK\AVIAVGSLTCSPKHVVLPPSFPGKI
			VHQSLNIMNSFSQKVKIQQIRSLSEDVRFYYKRLRGNKEDLEPG
1		·	KKSKIANIYFDPGLQCGDHCYVGLPFLSKSEPKVQPGVAMQEDM
			WDADWDLHQSLFKGWTGIKENSGHRLSAIFEVNTDLQKNIISKI
			TAELSWPSILSSPRHLKFPLTNTNCSS\EEEITLENP/SQDVPV
			YVQFIPLALYSNPSVFVDKLVSRFNLSKVAKIDLRTLEFQVFRN
			SAHPLQSSTGFMEG\LSPHLILNLILKPGEKKSVKVK\FTPVHN
			RTVSSLIIVRNNLTVMDAVMVQGQGTTENLRVAGKLPGPGSSLR FKITEALLKDCTDSLKLREPNFTLKRTFKVENTGQLQIHIETIE
			ISGYSCEGYGFKVVNCQEFTLSANASRDIIILFTPDFTASRVIR
			ELKFITTSGSEFVFILNASLPYHMLATCAEALPRPNWELALYII
			ISGIMSALFLLVIGTA\YLEAQGIWEP\FRRRLS\FEASNPPFD
		!	VGRPFDLRRIVGISSEGNLNTLSCDPGHSRGFCGAGGSSSRPSA
			GSHKQ*GPSGHPHSSHSNRNSADVDDVRAYNSGRTSSMTSAOAA
			SSQPANKTRPLVLDSNTGAQGHSAGRKSKGAKQSQHGSQHHAHS
			PLEQHPQPPLPPPVPQPQEPQPERLSPAPLAHPSHPERASSARH
			SSEDSDITSLIBAMDKDFDHHDSPALEVFTEQPPSPLPKSKGKG
			KPLQRKVKPPKKQEEKEKKGKGKPQEDELKDSLADDDSSSTTTE
			TSNPDTEPLLKEDTEKQKGKQAMPEKHESEMSQVKQKSKKLLNI KKEIPTDVKPSSLELPYTPPLESKQRRNLPSKIPLPTAMTSGSK
			SRNAQKTKGTSKLVDNRPPALAKFLPNSQELGNTSSSEGEKDSP
			PPEWDSVPVHKPGSSTDSLYKLSLQTLNADIFLKQRQTSPTPAS
			PSPPAAPCPFVARGSYSSIVNSSSSSDPKIKQPNGSKHKLTKAA
			SLPGKNGNPTFAAVTAGYDKSPGGNGFAKVSSNKTGFSSSLGIS
			HAPVDSDGSDSSGLWSPVSNPSSPDFTPLNSFSAFGNSFNLTGE
			VFSKLGLSRSCNQASQRSWNBFNSGPSYLWESPATDPSPSWPAS
			SGSPTHTATSVLGNTSGLWSTTPFSSSIWSSNLSSALPFTTPAN
			TLASIGLMGTENSPAPHAPSTSSPADDLGQTYNPWRIWSPTIGR
5820	210	1082	RSSDPWSNSHFPHEN
5620	310	1270	RVSLSGPVSLGVLLCARSSTMGKRDNRVAYMNPIAMARSRGPIQ
			SSGPTIQ\VI*IDQGLPGKK*KSN*KRKRK/DSKALAEFEEKMN
1 1		ļ	ENWKKELEKHREKLLSGSESSSKKRQRKKKEKKKSW*\DSSSS\ SSSSDSSSSSSSDSEDEDKKQGKRRKKKNRSHKSSESSMSETES
L			A T T T T T T T T T T T T T T T T T T T

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
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NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
-			DSKDSLKKKKKSKDGTEKEKDIKGLSKKRKMYSEDKPLSSESLS
			ESEYIEEVRAKKKKSSEEREKATEKTKKKKKKKKKKKKKKKKKAA
ł			SSSPDSP*H*EKSGFPYKESAMSEEISTVKTTTYLLKCMNFLVF GIIPGLFSSHSDATV
5000	170	915	KWRNQSWRWPKPGTNWMLSCSVCWRRVTWTGSVWMRKLGKHPQT
5821	179	313	PT/IKDCSIAATGKRPSARFPHQRRKKRREMDDGLAEGGPQRSN
1			TYVIKLFDRSVDLAOFSENTPLYPICRAWMRNSPSVRERECSPS
ŀ			SPLPPLPEDEEG\SEVTNSKSR*CVQACPPTHTPGGQPKNACR\
			SRIPSPLAALRMOGTP*RWSPFEPEPSPSTLIYRNMQRWKRIRQ
}			RWKEASHRNOLRYSESMKILREMYERO
5822	464	4379	OTLKEMPIVMARDLEETASSSEDBEVISQEDHPCIMWTGGCRRI
3022	""	75.15	PVLVFHADAILTKDNNIRVIGERYHLSYKIVRTDSRLVRSILTA
			HGFHEVHPSSTDYNLMWTGSHLKPFLLRTLSEAQKVNHFPRSYE
Į.			LTRKDRLYKNIIRMQHTHGFKAFHILPQTFLLPAEYAEFCNSYS
			KDRGPWIVKPVASSRGRG\VYLINNPNQISLBENILVSRYINNP
			LLIDDFKFDVRLYVLVTSYDPLVIYLYEEGLARFATVRYDQGAK
			NIRNQFMHLTNYSVNKKSGDYVSCDDPEVEDYGNKWSMSAMLRY
		İ	LKQEGRDTTALMAHVEDLIIKTIISAELAIATACKTFVPHRSSC
			FELYGFDVLIDSTLKPWLLEVNLSPSLACDAPLDLKIKASMISD
			MFTVVGFVCQDPAQRASTRPIYPTFESSRRNPFQKPQRCRPLSA
			SDABMKNLVGSAREKGPGKLGGSVLGLSMEEIKVLRRVKEENDR
			RGGFIRIFPTSETWEIYGSYLEHKTSMNYMLATRLFQDRMTADG
			APELKI*SLNSKAKLHAALYERKLLSLEVRKRRRRSSRLRAMRP
			KYPVITQPAEMNVKTETESEEEEEVALDNEDEEQEASQEESAGF
		1	LRENQAKYTPSLTALVENTPKENSMKVREWNNKGGHCCKLETQE LEPKFNLMQILQDNGNLSKMQARIAFSAYLQHVQI\RLMKDSGG
			QTFSASWAAKEDEQMELVVRFLKRASNNLQHSLRMVLPSRRLAL
			LERTRILAHQLGDFIIVYNKETEQMAEKKSKKKVEEEEEDGVNM
			ENFOEFIROASEAELEEVLTFYTOKNKSASVFLGTHSKISKNNN
			NYSDSGAKGDHPETIMEEVKIKPPKQQQTTEIHSDKLSRFTTSA
			EKEAKLVYSNSSSGPTATLQKIPNTHLSSVTTSDLSPGPCHHSS
1		1	LSQIPSAIPSMPHQPTILLNTVSASASPCLHPGAQNIPSPTGLP
			RCRSGSHTIGPFSSFOSAAHIYSOKLSRPSSAKAGSCYLNKHHS
			GIAKTOKEGEDASLYSKRYNOSMVTAELQRLAEKQAARQYSPSS
			HINLLTQQVTNLNLATGIINRSSASAPPTLRPIISPSGPTWSTQ
ì			SDPQAPENHSSSPGSRSLQTGGFAWEGEVENNVYSQATGVVPQH
			KYHPTAGSYQLQFALQQLEQQKLQSRQLLDQSRARHQAIFGSQT
			LPNSNLWTMNNGAGCRISSATASGQKPTTLPQKVVPPPSSCASL
			VPKPPPNHEQVLRRATSQKASKGSSAEGQLNGLQSSLNPAAFVP
L _			ITSSTDPAHTKIMNHKHTEKQPVHHSWVHD
5823	42	2293	LLTALSMEGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF
1			DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP
1			TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP
1	1		EDPRSQGVERFIQESKF\KINLFEKEKEMKKSPTSLKRETYYLS
			DSPLLGPPVGEPRLLASSPALPSSGAQARLTRAPGPPHSAHALP RESCTAHAASOAATORKPGTKLLLPRAASVRGRGIPGAAEKPKK
1			RESCTAHAASQAATQRKPGTKLLLPRAASVRGRGTPGAAEKPKK EIPASPSRTKIPAEKESHRDVLPDKPAPGAVNVPAAGSHLGOGK
			RAIPVP\NKLGLKKTLLKAPGSYSN\LQRKSSSGA\VWSGASSA
			CTPQPVAKAKSSEFASIPAN*LPGLCPNISKS\GRMGPAMLRPA
			L\PAGPVG\ASSWQAKRVDVSELAAEQLTAPP\SASPTQPQTPE
			GGG\QWLNSSCAWSESSQLNKTRSIRRRDSCLNSKTKVMPTPTN
			QFKIPKFSIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTPVR
			RSSGPAPQSLLSAWRVSALPTPASRRCSGLPPMTPKTMPRAVGS
			PL\CVPARRRSSEPRKNSAMRTEPTRESNRKTDSR\LVDVSPDR
1			GSPPSRVPQALNFSPEESDSTFSKSTATEVAREEAKPGGDAAPS
			EALLVDIKLEPLAVTPDAASQPLIDLPLIDFCDTPEAHVAVGSE
			SRPLIDLMTNTPDMNKNVAKPSPVVGQLIDLSSPLIQLSPEADK
			ENVDSPLLKF
5824	42	2293	LLTALSMEGGGRDEPSACRAGDVNMDDPKKEDILLLADEKFDF
			DLSLSSSSANEDDEVFFGPFGHKERCIAASLELNNPVPEQPPLP
1	1		TSESPFAWSPLAGEKFVEVYKEAHLLALHIESSSRNQAAQAAKP

NO: nucleotide location corresponding to first amino acid residue of amino acid amino acid sequence	SEQ	Predicted	Dunglated and	
NO: nucleotide clocation corresponding to first amino acid residue of amino acid sequence seq			Predicted end	Amino acid segment containing signal peptide
corresponding to first amino acid amino acid residue of residue of amino acid sequence sequen			1	Clutaria Arid E-Phanelalaria G Gl.
to first amino acid residue of amino acid sequence sequ	1	1		Giddanic Acid, Farhenyldianine, Gaglycine,
to first amino acid residue of sanino acid sequence seque	1			L-Laucine M-Methionine N-Assessmen
amino acid residue of anino acid sequence sequen				P-Proline O-Glutamine B-Arginine
residue of amino acid sequence Codon, /=possible nucleotide deletion,				
amino acid sequence Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) EDPRSGGVERPIGESKY_KIMIFEREKEHKKEPTELKRETYYL DSPLLGPPVGEPRILASSPALPSGAQARLTRAGPPHSAHAL RESCTHANASQATQRKOTKLLLPRAYCRGGI PGAAEKEW EIPASPSRTKIPAEKESHRDVLPDKPAPGAWNVPAAGSHLGGG RAIPVP\KKLGLKKTLLKAPGGYSN\LQKKSSGAG\WSGASS CTTQPVANKASSEFASIPAN*LPGLCPNISKS\GRMGPAMLRP L\PAGFVG\ASSMQAKRUVSELAAEQLTAPP\SASTYQATY GGG\OMNASCAMSESSQLDLKTRSIRFOLISKS\GRMGPAMLRP L\PAGFVG\ASSMQAKRUVSELAAEQLTAPP\SASTYQATY GGG\OMNASCAMSESSQLDLKTRSIRFRATGER\AYDVSPD GSPPRVPQALNFSPESSSTFISKSTATEVARERKEGRAPGADAP PL\CVPARRRSSPERRINSAMRTEPTERSCLIMEKTWHPTPY GSFLVFKFIGDS\PDSSTPKLSRAQRPQSCTSVGRVTVHSTFV RSSGRAPGSLLSARRVSALPTTASRCSLLPPMTFKTMPRAWG FL\CVPARRRSSPERRINSAMRTEPTERSCLIMEKTGDRA\PVDVSPD GSPPSRVPQALNFSPESSSTFISKSTATEVARERKEGGAPAP EALLVOILLEPLAVTTPDAMKNVAKPSPVGQLIDLSSPLIQLSPEAD ENVORSPLLKE SRPLIDLMTNTPDMNKNVAKPSPVGQLIDLSSPLIQLSPEAD ENVORSPLLKF SAAPPAPPPBVTATARPCLCSVGRRGGGKMAAGALERSFVV SAAPPAPPPBVTATARPCLCSVGRRGGGKMAAGALERSFVV SAAPPAPPPBVTATARPCLCSVGRRGGGKMAAGALERSFVV SGAEKERFRFFRFFTVSGTGTANAVAGVXSESAGGFTYVES SCAEKERFRFFFTVSGTGTANAVAGVXSESAGGFTYVES SCAEKERFRFFFTGSTGTLANHVAGGWAAAALERSFVV SGROSFTDIGKVDFTTDFORNVILLLLDRFSTRASELNW VLPGGVVVSTGNRVILLMLINGTVVRLLLLPRSTMTSELLW SGRALFALPCASGGIFVLKLPFYDIPGMVSVVELKQSSVMGRLL GMMPTAIRGDQSPSDRFJSLAWHCVEMDFIFTSGTCTLID AATSTDIMALWHDAERQYVVKSILRTAGTGHKLRLAYSPTMGLY YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLY YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLY YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLY YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLY YKEQMCLMVADMLEYVPVKKDLRLTAGTGHKLRLAYSPTMGLY YKEQMCLMVADMLEYPPVKKDLRLTAGTGHKLRLAYSPTMGLY YKEQMCLMVADMLEYPPVKKDLRLTAGTGHKLRAYSPTMGLY YKEQMCLMVADMLEYPPVKKDLRLTAGTGHKLLAYSPTMGLY YKEQMCLAYAGATLARTOTHALLOCHLLARSPTMING SGRALFALPCAGAGATLARTOTHALLOCHLLARSPTMUNG SGRALFALPCAGAGATLARTOTHALLOCHLLARSPTMALGCLATCHYDFOLTHAL DISMSTEMENTATIONAGGGGGEFFENLOGGFTCHC GROCYVOLOPYIOLLHPROCYNVSCERMLGGCATLTCHTGGGKAA ECFCQAASSGVEFEIDLSTIRSGGSUTTARGLEKGUNTHANDYTELLYAPHITRHNYKAA TOMPSYGMERSL POTOPSGAQLDLLGGUTGETGTEML VGPUSGAVGS	1			
L=possible nuclectide insertion	1	í		
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GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVTGEGQKAI ECFCQAASBVGKEFFLDRLIRSEDGEIVSTPRLQYYDKVLRLLI VIGLPELVIQLATSAITEASDDW\KSQATL\RTCIFKHHL\DLF \hnsqaygsl*pQIPDSSRQLDCLRQLVVVLCERSQLQDLVEF YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAC TVWFBYGMRLGREVRTLRGLEKQGNCYLAALNCLRLTRPEYANI VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE	j			LQHLSVLELTDSGALMANRFVSSPQTIVELFFQEVARKHIISHL
ECFCQAASEVGKEEFLDRLIRSEDGEIVSTPRLQYYDKVLRLLI VIGLPELVIQLATSAITEASDDM\KSQATL\RTCIFKHHL\DLF \hnsqaygsl*pqipdssrqldclrqlvvvlcersqlqdlvers YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAC TVMFEYGMRLGREVRTLRGLEKQGNCYLAALNCLRLTRPEYANI VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE				
VIGLPELVIQLATSAITEASDDW\KSQATL\RTCIFKHHL\DLC \hnsqaygsl*pqipdssrqldclrqlvvvlcersqlqdlvefs YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAG TVMFBYGMRLGREVRTLRGLEKQGNCYLAALNCLRLIRPEYAWJ VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE	•			GNCQYVQLQDYIQLLHPWCQVNVGSCRFMLGRCYLVTGEGQKAL
\\HNSQAYGSL*PQIPDSSRQLDCLRQLVVVLCERSQLQDLVEFS \text{YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAG} \text{TVMFEYGMRLGREVRTLRGLEKQGNCYLAALNCLRLIRPEYAWJ} \text{VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE}				
YVNLHNEVVGIIESRARAVDLMTHNYYELLYAFHIYRHNYRKAG TVMFBYGMRLGREVRTLRGLEKQGNCYLAALNCLRLIRPEYAWJ VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE]			
TVMFBYGMRLGREVRTLRGLEKQGNCYLAALNCLRLIRPEYANJ VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE				
VQPVSGAVYDRPGASPKRNHDGECTAAPTNRQIEILELEDLEKE				
				TVMFKYGMRLGREVRTLRGLEKQGNCYLAALNCLRLIRPEYAWI
CSLARIRLTLAQHDPSAVAVAGSSSAEEMVTLLVQAGLFDTAIS				
				LCQTFKLPLTPVFEGLAFKCIKLQFGGEAAQARAWAWLAANQLS
				SVITTKESSATDEAWRLLSTYLERYKVONNLYHHCVINKLLSHG
VPLPNWLINSYKKVDAAELLRLYLNYDLLDLTPYQVIRICGC	E035			
	3026	ا ع	871	KSQLLRDHSAPPPKPCTSVGAMGC*PRQ/SPKEQQRQLKKQKNR
				AAAQRSRQKHTDKADALHQQHESLEKDNLALRKEIQSLQAELAW
				WSRTLHVHERLCPMDCASCSAPGLLGCWDQAEGLLGPGPQGQHG
	1			CREQLELFQTPGSCYPAQPLSPGPQPHDSPSLLQCPLPSLSLGP
				AVVAEPPVQLSPSPLLFASHTGSSLQGSSSKLSALQPSLTAQTA
				PPOPLELEHPTRGKLGSSPDNPSSALGLARLQSREHKPALSAAT
WQGLVVDPSPHPLLAFPLLSSAQVHF	E 0 3 -7	101	0000	L
	5827	194	2287	GMGSENSALKSYTLREPPFTLPSGLAVYPAVLQDGKFASVFVYK
	1 1	1		RENEDKVNKAAKVP**HLKTLRHPCLLRFLSCTVEADGIHLVTE
	j			RVQPLEVALETLSSAEVCAGIYDILLALIFLHDRGHLTHNNVCL
	ļ			SSVFVSEDGHWKLGGMETVCKVSQATPEFLRSIQSIRDPASIPP
			i	EEMSPEFTTLPECHGHARDAFSFGTLVESLLTILNEQVSADVLS
] [SFQQTLHSTLLNPIPKWRPALCTLLSHDFFRNDFLEVVNFLKSL
TLKSEEEKTEFFKFLLDRVSCLSEELIASRLVPLLLNQLVFAEP	L			TLKSEEEKTEFFKFLLDRVSCLSEELIASRLVPLLLNQLVFAEP

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
10.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
			Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
L	sequence		VAV\KSFLPYLLGPKKDHAQGETPCLLSPALFQSRVIPVLLQLF
Į.			
!			EVHEEHVRMVLLSHIEAYVGALSLREQLKKV\IL\PQVLLG\LR
			D\TSDSIVAITLHSLAVLVSLLGPEVVVGGERTKIFKRTAP\SF
i			TK\NTDLSLEGDPFSQPIKFPINGLSDVKNTSEDSENFPSSSKK
			SEEWPDWSGPE\EPENQTVNI\QIWP\REP\CDDVKSQCTTLDV
			EESSWDDCEPSSLDTKVNPGGGITATKPVTSGEQKPIPALLSLT
<u> </u>			EESMPWKSSLPQKISLVQRGDDADQIEPPKVSSQERPLKVPSEL
			GLGEEFTIQVKKKPVKDPEMDWFADMIPEIKPSAAFLILPELRT
	1		EMVPKKDDVSPVMQFSSKFAAAEITEGEAEGWEEEGELNWEDNN
Ì		1	W
5828	2	257	AREGGSLGAVAACGELSYSCDFCPARPHTSWLTRFVKMEFQAVV
1	1		MAVGGGSRMTDLTSSIPKPLLPVGNKPLIWYPLNLLERVGFEEV
	}	1	IVVTTRDVQKALCABFKMKMKPDIVCIPDDADMGTADSLRYIYP
			KLKTDVLVLSCDLITDVALHBVVDLFRAYDASLAMLMRKGQDSI
1	1	1	BPVPGQKGKKKAVEQRDFIGVDSTGKRLLFMANEADLDEELVIK
	1	1	GSILQKHPRIRFHTGLVDAHLYCLKKYIVDFLMENG\SITSIRS
			BL\IPYLV/RGKQFSSASSQQGTRKEKEGGSKGKRGLKSFRISY
ļ.			SFY*KEANYTGTGAPY\D\ACWI
5829	260	1259	PDGRLIVSCSEDKTIKIWDTTNKQCVNNFSDSVGFANFVDFNPS
3023	200	1	GTCIASAGSDQTVKVWDVRVNKLLQHYQVHSGGVNCISFHPSGN
Į			YLITASSDGTLKILDLLKGRLIYTLQGHTGPVFTVSFSKGGELF
İ			ASGGADTOVLLWRTNFDELHCKGLTKRNLKRLHFDSPPHLLDIY
			PRTPHPHEBKVETVEDFFLHLLRLIQSLR*SICRSLLPLLWISF
1			LLILPQQQKPVVGLCQTRVKRPVDIS*TLP*CHQNVCQQPRKRK
			QKT*VTSPVKVK/VSIPLAVTDALEHIMEQLNVLTQTVSILEQR
			LTLTEDKLKDCLENQQKLFSAVQQKS
F000	1406	3139	GGKMAAPEERDLTOEOTEKLLOFQDLTGIESMDQCRHTLEQHNW
5830	4496	3139	NIEAAVODRLNEOEGVPSVFNPPPSRPLQVNTADHRIYSYVVSR
}			POPRGLLGWGYYLIMLPFRFTYYTILDIFRFALRFIRPDPRSRV
			TDPVGDIVSFMHSFEEKYGRAHPVFYQGTYSQALNDAKRELRFL
1		,	
			LVYLHGDDHQDSDEFCRNTLCAPEVISLINTRMLFWACSTNKPE GYRVSQALRENTYPFLAMIMLKDRRE*PV\VGRLEGLI\QPDDL
			INQLTFIMDANQTYLVSERLEREERNQTQVLRQQQDEAYLASLR ADQEKERKKREERERKRRKKEEVQQQKLAEERRRQNLQEEKERK
1			
ļ			LECLPPEPSPDDPESVKIIFKLPNDSRVERRFHFSQSLTVIHDF
1	-		LFSLKESP\EKFQIEA\NFPRR\VLPCIPSEE\WPNPPTLQE\A
			GLSHTEVLFVQDLTDE
5831	71	2897	FCSKDKCCLYLPDSINRSKSCTAKPGAHSQDRHAVMDSERQVKD
			TDDIESPKRSIRDSGYIDCWDSERSDSLSPPRHGRDDSFDSLDS
		1	FGSRSRQTPSPDVVLRGSSDGRGSDSESDLPHRKLPDVKKDDMS
[ARRTSHGEPKSAVPFNQYLPNKSNQTAYVPAPLRKKKAEREEYR
1	1		KSWSTATSPAGLGKKALQDYGPRT\PVS\DDAESTSMFDMRCEE
1			EAAVQPHSRARQEQLQLINNQLREEDDKWQDDLARWKSRKRSVS
	1	1	QDLIKKEEERKKMEKLLAGEDGTSERRKSIKTYREIVQEKERRE
	1	1	RELHEAYKNARSQEEAEGILQQYIERFTISEAVLERLEMPKILE
		1	RSHSTEPNLSSFLNDPNPMKYLRQQSLPPPKFTATVETTIARAS
			VLDTSMSAGSGSPSKTVTPKAVPMLTPKPYSQPKNSQDVLKTFK
			VDGKVSVNGETVHREEEKERECPTVAPAHSLTKSQMFEGVARVH
		1	GSPLELKQDNGSIEINIKKPNSVPQELAATTEKTEPNSQEDKND
		1	GGKSRKGNIELASSEPQHFTTTVTRCSPTVAFVEFPSSPQLKND
			VSEEKDQKKPENEMSGKVELVLSQKVVKPKSPEPEATLTFPFLD
			KMPEANQLHLPNLNSQVDSPSSEKSPVTTPFKFWAWDPEEERRR
			QEKWQQEQERLLQERYQ\KEQDK\LKEE\WEKAQKEVEEEBRRY
1			YEEEP*II\EDPVVPFTVSSSSADQLSTSSSMTEGSGTMNKIDL
1			GNCODEKODRRWKKSFQGDDSDLLLKTRESDRLEEKGSLTBGAL
1			AHSGNPVSKGVHEDHQLDTEAGAPHCGTNPQLAQDPSQNQQTSN
			PTHSSBDVKPKTLPLDKSINHQIESPSERRKSISGKKLCSSCGL
			PLGKGAAMIIETLNLYFHIQCFRCG\ICKGQLGDAVSGTDVRIR
			NGLLNCNDCYMRSRSAGQPTTL
5832	2454	829	PGRRFRHGSCAFQKQCIMLHICQYFLQGECKFGTSCKRSHDFSN
1 3032	2.2.7		SENLEKLEKLGMSSDLVSRLPTIYRNAHDIKNKSSAPSRVPPLF
	1	1	OBMODEVED TO A DESTREAM TO THE A SERVICE OF A SERVICE O

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion) VPQGTSERKDSSGSVSPNTLSQEEGDQICLYHIRKSCSFQDKCH
1			
ì	1		RVHFHLPYRWQFLDRGKWEDLDNMELIEEAYCNPKIERILCSES ASTFHSHCLNFNAMTYGATQARRLSTASSVTKPPHFILTTDWIW
1			YWSDEFGSWQEYGRQGTVHPVTTVSSSDVEKAYLAY/WYTGV*R
1	ì		PGSHLEVPGRKAQLRVRFQSLRSEKPGLWHN*KGLPQTQIR\AP
			QDVTTMQTCNTKFPGPKSIPDYWDSSALPDPGFQKITLSSSSEE
			YQKVWNLFNRTLPFYFVQKIERVQNLALWEVYQWQKGQMQKQNG
			GKAVDERQLFHGTSAIFVDAICQQNFDWRVCGVHGTSYGKGSYF
			ARDAAYSHHYSKSDTQTHTMFLARVLVGEFVRGNASFVRPPAKE
			GWSNAFYDSCVNSVSDPSIFVIFEKHQVYPEYVIQYTTSSKPSV
5000			TPSILLALGSLFSSRQ
5833	170	3289	SILCLLSPCVVQFGKPVVSILSSRSRHSPCTKKGWEGMRKHLHT
			RQGHK*VHVEISKALWVYRDDYFIRHSISVSAVIVRAWITHKYR
			GRDWNVKWEENLLHAVAKNYTLLQTIPPFERPFKDHQVCLEWNM
	‡		GYIWNLRANRIPQCPLENDVVALLGFPYASSGENTGIVKKFPRF
			RNRELEATRRQRMDYPVFTVSLWLYLLHYCKANLCGILYFVDSN EMYGTPSVFLTEEGYLHIQMHLVKGEDLAVKTKFIIPLKEWFRL
			DISFNGGQIVVTTSIGQDLKSYHNQTISFREDFHYNDTAGYFII
			GGSRYVAGIEGFFGPLKYYRLRSLHPAQIFNPLLEKQLAEQIKL
			YYERCAEVQEIVSVYASAAKHGGERQEACHLHNSYLDLQRRYGR
			PSMCRAFPWEKELKDKHPSLFQALLEMDLLTVPRNQNESVSEIG
-			GKIFEKAVKRLSSIDGLHQISSIVPFLTDSSCCGYHKASYYLAV
			FYETGLNVPRDQLQGMLYSLVGGQGSERLSSMNLGYKHYQGIDN
			YPLDWELSYAYYSNIATKTPLDQHTLQGDQAYVETIRLKDDEIL
			KVQTKEDGDVFMWLKHEATRGNAAAQQRLAQMLFWGQQGVAKNP
İ			EAAIEWYAKGALETEDPALIYDYAIVLFKGQGVKKNRRLALELM
			KKAASKGLHQAVNGLGWYYHKFKKNYA\KAAKYWLKA\EE\MGN
			PDASYNLGVLHLDGIFPGVPGRNQTLAGEYFHKAAQGGHMEGTL WCSLYYITGNLETFPRDPEKAVVWAKHVAEKNGYLGHVIRKGLN
			AYLEGSWHEALLYYVLAAETGIEVSQTNLAHICEERPDLARRYL
			GVNCVWRYYNFSVFQIDAPSFAYLKMGDLYYYGHQNQSQDLELS
Ì			VQMYAQAALDGDSQGFFNLALLIBEGTIIPHHILDFLEIDSTLH
	[SNNISILQELYERCWSHSNEESFSPCSLAWLYLHLRLLWGAILH
			SALIYFLGTFLLSILIAWTVQYFQSVSASDPPPRPSQASPDTAT
			STASPAVTPAADASDQDQPTVTNNPEPRG
5834	17	4020	RFRRGGGRVFPGAFPASPSDSLGQGNSQGPPRTPKPPRT/QECG
			SAAPGPIPGQSSS*VPLRLEQIQQKADCPLSLELALKPRMAAQV
			TLEDALSNVDLLEELPLPDQQPCIEPPPSSLLYQPNFNTNFEDR
			NAFVTGIARYIEQATVHSSMNEMLEEGQEYAVMLYTWRSCSRAI PQVKCNEQPNRVEIYEKTVEVLEPEVTKLMNFMYFQRNAIERFC
			GEVRRLCHAERRKDFVSEAYLITLGKFINMFAVLDELKNMKCSV
			KNDHSAYKRAAQFLRKMADPQSIQESQNLSMFLANHNKITQSLQ
			QQLEVISGYEELLADIVNLCVDYYENRMYLTPSEKHMLLKVMGF
			GLYLMDGSVSNIYKLDAKKRINLSKIDKYFKQLQVVPLFGDMQI
			ELARYIKTSAHYEENKSRWTCTSSGSSPQYNICEQMIQIREDHM
			RFISELARYSNSEVVTGSGRQEAQKTDAEYRKLFDLALQGLQLL
			SQWSAHVMEVYSWKLVHPTDKYSNKDCPDSAEEYERATRYNYTS
			EEKFALVEVIAMIKGLQVLMGRMESVFNHAIRHTVYAALQDFSQ
			VTLMEPLRQAIKKKKNVIQSVLQAIRKTVCDWETGHEPFNDPAL
		1	RGEKDPKSG*DIKVPRRAVGPSSTQLYMVRTMLESLIADKSGSK
			KTLRSSLEGPTILDIEKFHRESFFYTHLINFSETLQQCCDLSQL WFREFFLELTMGRRIQFPIEMSMPWILTDHILETKEASMMEYVL
		ļ	YSLDLYNDSAHYALTRFNKQFLYDEIEAEVNLCFDQFVYKLADQ
			IFAYYKVMAGSLLLDKRLRSECKNQGATIHLPPSNRYETLLKQR
1		1	HVQLLGRSIDLNRLITQRVSAAMYKSLELAIGRFESEDLTSIVE
			LDGLLEINRMTHKLLSRYLTLDGFDAMFREANHNVSAPYGRITL
		ļ	HVFWELNYDFLPNYCYNGSTNRFVRTVLPPSQEFQRDKQPNAQP
			QYLHGSKALNLAYSSIYGSYRNFVGPPHFQVICRLLGYQGIAVV
			MEELLKVVKSLLQGTILQYVKTLMEVMPKICRLPRHEYGSPGIL
			EFFHHQLKDIVEYAELKTVCFQNLREVGNAILFCLLIEQSLSLE
L			EVCDLLHAAPFQNILPRVHVKEGERLDAKMKRLESKYAPLHLVP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence	boquomee	\=possible nucleotide insertion)
 			LIERLGTPQQIAIAREGDLLTKERLCCGLSMFEVILTRIRSFLD
1			DPIWRGPLPSNGVMHVDECVEFHRLWSAMQFVYCIPVGTHEFTV
1		ì	EQCFGDGLHWAGCMIIVLLGQQRRFAVLDFCYHLLKVQKHDGKD
			EIIKNVPLKKMVERIRKFQILNDEIITILDKYLKSGDGEGTPVE
			HVRCFQPPIHQSLASS
5835	4209	1904	SGNIRMAQGSHQIDFQVLHDLRQKFPEVPEVVVSRCMLQNNNNL
3033	4203	1504	DACCAVLSQESTRYLYGEGDLNFSDDSGISGLRNHMTSLNLDLQ
1			SQNIYHHGREGSRMNGSRTLTHSISDGQLQGQSNSELFQQEPQ
			TAPAQVPQGFNVFGMSSSSGASNSAPHLGFHLGSKGTSSLSOOT
			PRFNPIMVTLAPNIQTGRNTPTSLHIHGVPPPVLNSPQGNSIYI
	1		RPYITTPGGTTRQTQQHSGWVSQFNPMNPQQVYQPSQPGPWTTC
			PASNPLSHTSSQQPNQQGHQTSHVYMPISSPTTSQPPTIHSSGS
			SOSSAHSOYNIONISTGPRKNQIEIKLEPPORNNSSKLRSSGPR
1			TSSTSSSVNSQTLNRNQPTVYIAASPPNTDELMSRSQPKVYISA
			NAATGDEQVMRNQPTLFISTNSGASAASRNMSGQVSMGPAFIHH
			HPPKSRAIGNNSATSPRVVVTQPNT\EYTFKITVSPNKPPAVSP GVVSPTFELTNLLNHPDHYVETENIHHLTDPTLAHVDRISETRK
		j	
			LSMGSDDAAYTQDI*RISNSWLGMVAHACNSSALGGQDGRII*A QEFETSWGNIWRLRLYRRF*NYAGMVAHTCSPSYSVD*ALLVHQ
			KARMERLQRELBIQKKKLDKLKSEVNEMENNLTRRLKRSNSIS
1			QIPSLEEMQQLRSCNRQLQIDIDCLTKEIDLFQARGPHFNPSAI
			HNFYDNIGFVGPVPPKPKDQRSIIKTPKTQDTEDDEGAQWNCTA
5836	361	2202	CTFLNHPALIRCEQCEMPRHF
3836	367	2303	FHITMCGICCSVNFSAEHFSQDLKEDLLYNLKQRGPNSSKQLLK
1			SDVNYQCLFSAHVLHLRGVLTTQPVEDERGNVFLWNGEIFSGIK
1			VEAEENDTQILFNYLSSCKNESEILSLFSEVQGPWSFIYYQASS
			HYLWFGRDFFGRRSLLWHFSNLGKSFCLSSVGTQTSGLANQWQE
1			VPAS\DFSELILSLLSFPDALFYNCILGNIFLGRILLKKMLIA*
1			VKFQQTYQHLYQR*QMKPNCILKNLLFL*I*CCHKLHWRLIAVI
			FPMCHLQERYFKSFLLMYT* KEVIQQFIDVLSVAVKKRVLCLPR
]			DENLTANEVLKTCDRKANVAILFSGGIDSMVIATLADRHIPLDE
İ			PIDLLNVAFIAEEKTMPTTFNREGNKQKNKCEIPSEEFSKDVAA
1			AAADSPNKHVSVPDRITGRAGLKELQAVSPSRIWNFVEINVSME
			ELQKLRRTRICHLIRPLDTVLDDSIGCAVWFASRGIGWLVAQEG
1			VKSYQSNAKVVLTGIGADEQLAGYSRHRVRFQSHGLEGLNKEIM
[MELGRISSRNLGRDDRVIGDHGKEARFPFLDENVVSFLNSLPIW
			EKANLTLPRGIGEKLLLRLAAVELGLTASALLPKRAMQFGSRIA
F	1000	 	KMEKINEKASDKCGRLQIMSLENLSIBKETKL
5837	4792	903	NGNAVAQAPVTNCCYLATGSKDQTIRIWSCSRGRGVMILKLPFL
			KRRGGGIDPTVKERLWLTLHWPSNQPTQLVSSCFGGELLQWDLT
			QSWRRKYTLFSASSEGQNHSRIVFNLCPLQTEDDKQLLLSTSMD
1			RDVKCWDIATLECSWTLPSLGGFAYSLAFSSVDIGSLAIGVGDG
1	1		MIRVWNTLSIKNNYDVKNFWQGVKSKVTALCWHPTKEGCLAFGT
1			DDGKVGLYDTYSNKPPQISSTYHKKTVYTLAWGPPVPPMSLGGE
i			GDRPSLALYSCGGEGIVLQHNPWKLSGEAFDINKLIRDTNSIKY
			KLPVHTBISWKADGKIMALGNEDGSIEIFQ\IPNLKLICTIQQH
1		1	HKLVNTISWHHE\HGSPAQKLSYL\MPSGSQQCSPFTCHNLKNC
1		1	P*KAAPESPSDPLQSPYRTPPQGHTAQDYPVWAWEPHIH*WEGL
}			VFCFPIDGYSPGCWD\AFPGKEAPVAIFRG\HQGRLLCVAWSPL
1			DPDCIYSG\ADDFCVHKWLTSMQDHSRPPQGKKSIELEKKRLSQ
			PKAKPKKKKKPTLRTPVKLESIDGNEEESMKENSGPVENGVSDQ
			EGEEQAREPELPCGLAPAVSREPVICTPVSSGFEKSKVTINNKV
			ILLKKEPPKEKPETLIKKRKARSLLPLSTSLDHRSKEELHQDCL
			VLATAKHSRELNEDVSADVEERFHLGLFTDRATLYRMIDIEGKG
1		1	HLENGHPELFHQLMLWKGDLKGVLQTAAERGELTDNLVAMAPAA
			GYHVWLWAVEAFAKQLCFQDQYVKAASHLLSIHKVYBAVELLKS
			NHFYREAIAIAKARLRPEDPVLKDLYLSWGTVLERDGHYAVAAK
1			CYLGATCAYDAAKVLAKKGDAASLRTAAELAAIVGEDELSASLA
1			LRCAQELLLANNWVGAQEALQLHESLQGQRLVFCLLELLSRHLE
1			EKQLSEGKSSSSYHTWNTGTEGPFVERVTAVWKSIFSLDTPEQY
l			QEAFQKLQNIKYPSATNNTPAKQLLLHICHDLTLAVLSQQMASW
			

	T 20 - 21 - 20 - 2	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted		,
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i		,	
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	004	\=possible nucleotide insertion)
	sequence		
1			DEAVQALLRAVVRSYDSGSFTIMQEVYSAFLPDGCDHLRDKLGD
			HQSPATPAFKSLEAFFLYGRLYEFWWSLSRPCPNSSVWVRAGHR
	ļ		TLSVEPSQQLDTASTEETDPETSQPEPNRPSELDLRLTEEGERM
		1	LSTFKELFSEKHASLONSORTVAEVQETLAEMIRQHQKSQLCKS
1			TANGPDKNBPEVEAEOPLCSSOSOCKEEKNEPLSLPELTKRLTE
i			ANORMAKFPESIKAWPFPDVLECCLVLLLIRSHFPGCLAQEMQQ
	1		-
1	}		QAQELLQKYGNTKTYRRHCQTFCM
5838	110	98	KTMPHLLVTFRDVAIDFSQEEWECLDPAQRDLYRDVMLENYSNL
	i	}	ISLDLESSCVTKKLSPEKEIYEMES\PSGRIWGNVSTITFQYNG
			LGDNMECKGNLEGOVSKSEGLYMCVKITCEEKATESHSTSSTFH
	1		· .
1			RII/HYQGKIVKCKECRQGFSYLSCLIQHEENHNI*KCSEVNKH
1			RNTFSKKPSYI*HQ\KFRLGEKPYECMECGKAFGRTSDLIQHQK
		1	IHTNEKPYQCNACGKAFIRGSQLTEHQRVHTGEKPYDCKKCGKA
		1	FSYCSQYTLHQRIHSGEKPYECKDCGKAFILGSQLTYHQRIHSG
1			EKPYECKECGKAFILGSHLTYHQRVHTGEKPYICKECGKAFLCA
			SOLNEHORIHTGEKPYECKECGKTFFRGSOLTYHLRVHSGERPY
1	1	ł	KCKECGKAFISNSNLIOHORIHTGEKPYKCKECGKAFICGKOLS
		1	
Į.			EHQRIHTGEKPFECKECGKAFIRVAYLTQHEKIHGEKHYECKEC
ł	}	1	GKTFVRATQLTYHQRIHTGEKPYKCKECDKAF/HLWLTILSEHQ
			RIHRGEKPYECKQCGR/LFIRGSHL/NEHLRTHTGEKPYECKEC
			GRAFSRGSEHTLHORIHTGEKPYTCVQCGKDFRCPSQLTQHTRL
		1	HN*EYSSHKICMHSIALASLDFAHLQEKNPEN
5839	 	2425	GRPFPRPPRALPRLPLRGRRODGRWTVDFEECLKD\SPRFRAAL
5033	1 -	1 2323	
İ	1	l	EEVEGDVAELELKL\DKLVKLCIA\MIDTGKAFCVANKQFMNGI
1]-	ì	RD\LAQNS\NNDA\VVETKFAPSFLDSLQEMINFHTIL/L*PNS
			EIN*GHSFQNFVKEDLRKFKDAKKQFENSQ*KRKKIALVKNAPV
			PSRPASLEL*KPPNILTATRKCFRHIALDYVLQINVLQSKRRSE
			ILKSMLSFMYAHLAFFHQGYDLFSELGPYMKDLGAQLDRLVGDA
			AKEKREMEQKHSTIQQKDFSRDDSKLKYNVDAANGIVMEGYLFK
		i	RASNAFKTWNRRWFSIQNNQVVYQKKFKDNPTVVVEDLRLCTVK
		1	· · · · · · · · · · · · · · · · · · ·
		1	HCEDIERRFCFEVVSPTKSCMLQADSEKLRQAWIKAVQTSI\AT
			AYREKDDESEKLDKKSSPSTGSLDSGNESKEKLLKGESALQRVQ
	ĺ	l .	CIPGNASCCDCGLADPRWASINLGITLCIECSGIHRSLGVHFSK
1		1	VRSLTLDTWEPELLKLMCELGNDVINRVYEANVEKMGIKKPQPG
1	}		QRQEKEAYIRAKYVERKFVDKIFL*SLSPP\EQQKK\FVSKSSE
1	ļ		EKRLSISKFGP\GDQVRASAQSSVRSNDSGIQQSSDDGRESLPS
		1	TVSANSLYEPEGERODSSMFLDSKHLNPGLQLYRASYEKNLPKM
	,		
1			AEALAHGADVNWANSEENKATPLIQAVLGGSLVTCEFLLQNGAN
1			VNQRDVQGRGPLHHATVLGHTGQVCLFLKRGANQHATDEBGKDP
1		1	LSIAVEAANADIVTLLRLARMNEEMRESEGLYGQPGDETYQDIF
			RDFSQMASNNPEKLNRFQQDSQKF
5840	698	3610	KHLHLPROHLTTLWOISSPRWRSPORAFMSALSKTOTOSAPALO
			GLSSLLQSVTGNPVPASEAASQSTSASPANTTVYTIKGRNLPSS
1			AOPFIPKSFNYSPNSSTSEVSSTSASKASIGOSPGLPSTAFKLP
	1	1	
			SNTKGFTATHNTSPAAPPTEVTICQSSEVSKPKL\ESESTSPSL
1			\EMKIHNFLKGNPGFSVA*NLKHPNPAGSLGSSAPSESHPSDFQ
1			RGPTSTSIDNIDGTPVRDERSGTPTQDEMMDKPTSSSVDTMSLL
			SKIISPGSSTPSSTRSPPPGRDESYPRELSNSVSTYRPFGLGSE
1			SPYKQPSDGMERPSSLMDSSQEKFYPDTSFQEDEDYRDFEYSGP
J			PPSAMMNLOKKPAKSILKSSKLSDTTEYOPILSSYSHRAOEFGV
1		1	KSAFPPSVRALLDSSENCDRLSSSPGLFGAFSVRGNEPGSDRSP
	1		SPSKNDSFFTPDSNHNSLSOSTTGHLSLPOKOYPDSPHPVPHRS
	I		1
1	1		LFSPONTLAAPTGHPPTSGVEKVLASTISTTSTIEFKNMLKNAS
	1		RKPSDDKHFGQAPSKGTPSDGVSLSNLTQPSLTATDQQQQEEHY
1			RIETRVSSSCLDLPDSTEEKGAPIETLGYHSASNRRMSGEPIQT
			VESIRVPGKGNRGHGREASRVGWFDLSTSGSSFDNGPSSASELA
1			SLGGGGSGGLTGFKTAPYKERAPQFQESVGSFRSNSFNSTFEHH
	1)
	1		LPPSPLEHGTPFQREPVGPSSAPPVPPKDHGGIFSRDAPTHLPS
			VDLSNPFTKEAALAHAAPPPPPGEHSGIPFPTPPPPPPGEHSS
			SGGSGVPFSTPPPPPPPPVDHSGVVPFPAPPLAEHGVAGAVAVFP
			KDHSSLLQGTLAEHFGVLPGPRDHGGPTQRDLNGPGLSRVRESL
	-1		

	15. 1	12.31.	
SEQ	Predicted beginning	Predicted end	Amino acid segment containing signal peptide
•		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
		 	TLPSHSLEHLGPPHGGGGGGGSNSSSGPPLGPSHRDTISRSGII
1			LECOPODE DEPORT CONDUCTION CONTROL CON
1	1		LRSPRPDFRPREPFLSRDPFHSLKRPRPPFFARGPPFFAPKRPFF PPRY
5841	1000		
2041	1908	762	GLRLFLVLTVWPMMKPSWLSRTEPSKRLLCRTLWCQSGWSSRSY
	1		TRSMLKMTTSINRRSRTSTKSTRTSARPGLTATVSIGLSDSPTW
1			RHCWMTARSCSGEKGGHWAPRQVGVYLLPGRVGCVSSRVSPSFP
1			GDGLDSGLARRGSAVSALASGLVEEPMLGPPFHPTPRFKAVSAK
I			SKEDLVSQGFTEFTIEDFHNTFMDLIEQVEKQTSVADLLASFND
	1		QSTSDYLVVYLRLLTSGYLQRESKFFEHFIEGGRTVKEFCQ\QE
1	ĺ		\VEPMCKESDHIHIIALAQGLQRVHPGWBYMGPRPRAATTNPHI
1	1		ED+CLDCDVVVLLVDDC/UDDILVVVCCCCCCCV
			FP*GLPSPKVYLLYRPG\HYDILYKIGLGSSPLGCPGCPLLARA
5842	302		LGHCYRGFSVVVKWSYFTPFFLSHDPPPMFY
3642	307	1918	QEPTADFKLRSTCGCGREMTCPDKPGQLINWFICSLCVPRVRKL
		1	WSSRRPRTRRNLLLGTACAIYLGFLVSQVGRASLQHGQAAEKGP
		1	HRSRDTAEPSFPEIPLDGTLAPPESQGNGSTLQPNVVYITLRSK
			RSKPANIRGTVKPKRRKKHAVASAAPGQEALVGPSLQPOEA\EG
			KLML*HLGTLREQTWLRLESDPGGWCGVRE/WRAGGPDFLOPSS
	1	i	RESNIRIYSESAPSWLSKDDIRRMRLLADSAVAGLRPVSSRSGA
1	1	j	RLLVLEGGAPGAVLRCGPSPCGLLKQPLDMSEVFAFHLDRILGL
			NRTLPSVSRKAEFIQDGRPCPIILWDASLSSASNDTHSSVKLTW
	1		GTYQQLLKQKCWQNGRVPKPESGCTEIHHHEWSKMALFDFLLQI
			YNRLDTNCCGFRPRKEDACVQNGLRPKCDDQGSAALAHIIQRKH
			DPRHLVFIDNKGFFDRSEDNLNFKLLEGIKEFPASAVYVLKSQH
			DPRADVFIDNAGFFDRSEDNENFALLEGIARFPASAVYVLKSQH
			LRQKLLQSLFLDKGYWESQGGRQGIEKLIDVIEHRAKILITYIN
5843	F20		AHGVKVLPMNE
5843	500	1453	GTARLVTCWVLHGQ*VKKPAWEPGVVWL*Q*RCRPKGWGLGAGM
			RGSRMSQPPQCLRRAQSSCCHFMVKLLDDGTFMIPGEKVAHTSL
[DALVTFHQQKPIEPRRELLTQPCRQKDPANVDYEDLFLYSNAVA
i			EEAACPVSAPEEASPKPVLCHQSKERKPSAEM/RQNNHQGSHFL
	1		LPPKIPSWRDPPETLEEPQNAPRERPEGPAAAKKPPRHCELVVT
1			LGCPEIHGDLRPWDRKRQPRSLRGSHLGGQRLHGSLCGHISQKP
į	1		LTAPGTKRQKGPHQEGREVGQLH*GDPRGQELAPNGSESPILPG
İ	}		VQARAPGLGRA
5844	202	2471	FDSAVLSSINVMAVLPGPLQLLGVLLTISLSSIRLIQAGAYYGI
		61,1	VEL PROTEROMEROL CONTRACTOR CONTR
	1		KPLPPQIPPQMPPQIPQYQPLGQQVPHMPLAKDGLAMGKEMPHL
	1		QYGKEYPHLPQYMKEIQPAPRMGKEAVPKKGKEIPLASLRGEQG
	1		PRGEPGPRGPPGPPGLPGHGIPGIKGKPGPQGYPGVGKPGMPGM
			PGKPGAMGMPGAKGEIGQKGEIGPMGIP*PQGPPGPHGLPGIGK
) ;		PGGPGLPGQPGPKGDRGPKGLPGPQGLRGPKGDKGFGMPGAPGV
			KGPPGMHGPPGPVGLPGVGKPGVTGFPGP\OGPLGK\PGAPGEP
			GPQGPIGVPGVQGPPGIPGIGKPGQDG\IPGQPGFPGGKGEQGL
	[PGLPGPPGLPGIGKPGFPGPKGDRGMGGVPGALGPRGEKGPIGA
			PGIGGPPGEPGLPGIPGPMGPPGAIGFPGPKGEGGIVGPQGPPG
			PKGEPGLQGFPGKPGFLGEVGPPGMRGFPGPIGPKGEHGQKGVP
	·		GLPGVPGLLGPKGEPGIPGDQGLQGPPGIPGIGGPSGPIGPPGI
	[PGDKGEDGI.DGDDGEDGTGVDGVXGTVGDDGVDGYSGVIGPPGI
			PGPKGEPGLPGPPGFPGIGKPGVAGLHGPPGKPGALGPQGQPGL
	.		PGPPGPPGPPGPPAVMPPTPPPPQGEYLPDMGLGIDGVKPPHAYG
			AKKGKNGGPAYEMPAFTAELTAPFPPVGAPVKFNKLLYNGRONY
			NPQTGIFTCEVPGVYYFAYHVHCKGGNVWVALFKNNEPVMYTYD
			EYKKGFLDQASGSAVLLLRPGDRVFLQMPSEQAAGLYAGQYVHS
			SFSGYLLYPM
5845	215	2061	HASNKSASLQDKMANPKEKTAMCLVNELARFNRVQPQYKLLNER
			GPAHSKMFSVQLSLGEQTWESEGSSIKKAQQAVGNKALTESTLP
			KPI*KPPKSNVNNNPGCITPTVELNGLAMKRG\KPAIHRPLDPK
	}		PFPNNRANYNFQVMYNQRYHCPIPKIFYVQLTVGNNBFFGEGKT
			BOY DEMY WAS TO STORED THE STORE STO
			RQAARHNAAMKALQALQNEPIPERSPONGESGKDMDDDKDANKS
			EISLVFEIALKRNMPVSFEVIKESGPPHMKSFVTRVSVGEFSAE
ļ			GEGNSKKLSKKRAATTVLQELKKLPPLPVVEKPK\HFFKKRPKT
			IVKAGPEYGQGMNPISRLAQIQQAKKEKEPDYVLLSERGMPRRR
			EFVMQVKVGNEVATGTGPNKKIAKKNAAEAMLLQLGYKASTNLQ
			DQLEKTGENKGWSGPKPGFPEPTNNTPKGILHLSPDVYQEMEAS

SEO	Predicted	Predicted end	
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
1	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
•	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
1	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	sequence	bequence	Codon, /=possible nucleotide deletion,
		 	\=possible nucleotide insertion)
1			RHKVISGTTLGYLSPKDMNQPSSSFFSISPTSNSSATIARELLM
1			NGTSSTAEAIGLKGSSPTPPCSPVQPSKQLEYLARIQGFQVHYC DRQSGKECVTCLTLAPVQMTFHAIGSSIEASHDQV+YATAILLC
	1		YGPARKWKAIKMEAMCAHAALLSLIHYLLAPSARLEKSKLFALG
			N.
5846	1126	456	FSKLIMKTFIIGISGVTNSGKTTLAKNLQKHLPNCSVISQDDFF
ı		1	KPESEIETDKNGFLQYDVLEALNMEKMMSAISCWMESARHSVVS
			TDQESAEEIPILIIEGFLLFNYKPLDTIWNRSYFLTIPYEECKR
1			RRSTRVYQPPDSPGYFDGHVWPMYLKYRQEMQDITWEVVYLDGT
1			KSEEDLFLQVYEDLIQELAKQKCLQVTA*RRNTTNPS/CK*IRK
			LOGVI
5847	2769	505	APEMEDLSSPDSTLLQGGHNLLSSASFQESVTFKDVIVDFTQEE
1			WKQLDPGQRDLFRDVTLENYTHLVSIGLQVSKPDVISQLEQGTE
			PWIMEPSIPVGTCADWETRLENSVSAPEPDISEEELSPEVIVEK
			HKRDDSWSSNLLESWEYEGSLERQQANQQTLPKEIKVTEKTIPS
			WEKGPVNNEFGKSVNVSSNLVTQEPSPEETSTKRSIKQNSNPVK
			KEKSCKCNECGKAFSYCSALIRHORTHTGEKPYKCN*/CVEKAF
1			SRSENLINHORIHTGDKPYKCDQCGKGFIEGPSLTQHQRIHTGE
1			KPYKCDECGKAFSQRTHLVOHORIHTGEKPYTCNECGKAFSORG
İ			HFMEHQKIHTGEKPFKCDECDKTFTRSTHLTOHOKIHTGEKTYK
			CNECGKAFNGPSTFIRHHMIHTGEKPYECNECGKAFSOHSNLTO
1			HQKTHTGEKPYDCAECGKSFSYWSSLAOHLKIHTGEKPYKCNEC
			GKAFSYCSSLTQHRRIHTREKPFECSECGKAFSYLSNINOHOKT
ļ			HTQEKAYECKECGKAFIRSSSLAKHERIHTGEKPYOCHECGKTE
	1		SYGSSLIQHRKIHTGERPYKCNECGRAFNONIHLTOHKRIHTGA
			KPYECAECGKAFRHCSSLAQHQKTHTEEKPYOCNKCEKTEGOGG
ĺ	i		HLTQHQRIHTGEKPYKCNECDKAFSRSTHLTOHORIHTGEKPYK
			CNECGK\TFSQSTYLIQHQRIHSGEKPFGCNDCGKSFRYRSALN
5848	22		KHQRLHPGI
3045	22	2961	AAPRRLLRGGDGDRTPRFPLPALLRPGPPAEAAPERRKMPAVSK
1			GDGMRGLAVFISDIRNCKSKEAEIKRINKELANIRSKFKGDKAL
			DGYSKKKYVCKLLFIFLLGHDIDFGHMEAVNLLSSNRYTEKQIG
1 1			YLFISVLVNSNSELIRLINNAIKNDLASRNPTFMGLALHCIASV
[GSREMAEAFAGEIPKVLVAGDTMDSVKQSAALCLLRLYRTSPDL
			VPMGDWTSRVVHLLNDQHLGVVTAATSLITTLAQKNPEEFKTSV
]			SLAVSRLS\RIVTSASTDLQDYTY*FCPGFLGLSVKLLRLLQCY
			PPPDPAVRGRLTECLETILNKAQEPPKSKKVQHSNAKNAVLFEA
i			ISLIIHHDSEPNLLVRACNQLGQFLQHRETNLRYLALESMCTLA
	[i	SSEFSHEAVKTHIETVINALKTERDVSVRQRAVDLLYAMCDRSN
			APQIVAEMLSYLETADYSIREEIVLKVAILAEKYAVDYTW\YVD
			TILNLIRIAGDYVSEEVWYRVIQIVINRDDVQGYAAKTVFEALQ
		Ì	APACHENLVKVGGYILGEFGNLIAGDPRSSPLIQFHLLHSKFHL
	ł		CSVPTRALLLSTYIKFVNLFPEVKPTIQDVLRSDSQLRNADVEL QQRAVEYLRLSTVASTDILATVLEEMPPFPERESSILAKLKKKK
			GPSTVTDLEDTKRDRSVDVNGGPEPAPASTSAVSTPSPSADLLG
			LGAAPPAPAGPPPSSGGSGLLVDVFSDSASVVAPLAPGSEDNPA
! !			RFVCKNNGVLFENQLLQIGLKSEFRQNLGRMFIFYGNKTSTQFL
	Ì		NFTPTLICSDDLQPNLNLQTKPVDPTVEGGAQVQQVVNIECVSD
		1	FTEAPVLNIQFRYGGTFQNVSVQLPITLNKFFQPTEMASQDFFQ
İ			RWKQLSNPQQEVQNIFKAKHPMDTEVTKAKIIGFGSALLEEVDP
			NPANFVGAGIIHTKTTQIGCLLRLEPNLQAQMYRLTLRTSKEAV
			SQRLCELLSAQF
5849	3545	1895	KRREIKETVFHHVAQAGLELLSSSNPPSSASRSAGITGMRHQVQ
		İ	P*DPCMSLSPPCFTBEDRFSLEALQTIHKQMDDDKDGGIEVEES
1			DEFIREDMKYKDATNKHSHLHREDKHITIEDLWKRWKTSEVHNW
			TLEDTLQWLIEFVELPQYEKNFRDNNVKGTTLPRIAVHEPSFMI
	ļ		SQLKISDRSHRQKLQLKALDVVLFGPLTRPPHNWMKDFILTVSI
	l		VIGVGGCWFAYTQNKTSKEHVAKMMKDLESLQTAEQSLMDLQER
- 1			
			LEKAQEENRNVAVEKONL*RKMMDEINVAKREACDI.DET DECAR
		. 1	LEKAQEENRNVAVEKQNL*RKMMDEINYAKEEACRLREIREGAE
			LEKAQEENRNVAVEKQNL*RKMMDEINYAKEEACRLRELREGAE CELSRRQYAEQELEQVRMALKKAEKEFELRSSWSVPDALQKWLQ LTHEVEVQYYNIKRQNAEMQLAIAKDEAEKIKKKRSTVFGTLHV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	I-louging M Mathieria, K-Lysine,
	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
1	(residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			AHSSSLDEVDHKILEAKKALSELTTCLRERLFRWQQIEKICGFQ
			IAHNSGLPSLTSSLYSDHSWVVMPRVSIPPYPIAGGVDDLDEDT
	i		PPIVSQFPGTMAKPPGSLARSSSLCRSRRSIVPSSPQPQRAQLA
į			PHAPHPSHPRHPHHPQHTPHSLPSPDPDILSVSSCPALYRNEEE
1			EEAIYFSAEKQWEVPDTASECDSLNSSIGRKQSPP/SKPRDIPN
			LIC /DEDVOEMBODED TO COCKE
5850	3	1005	IIS/DERYQEMRCP*RIPSGGIL
3030	3	1895	KAVLNFSASGSVISLTGSNPMHDASMWHLKKNGIIVYLDVPLLN
			LICRLKLMKTDRIVGQNSGTSMKDLLKFRRQYYKKWYDARVFCE
1	Į.		SGASPEEVADKVLNAIKRYQDVDSETFISTRHVWPEDCEQKVSA
			EFFIEAVIEGLASDGGLFVPAKEFPKLSCGEWKSLVGATYVERA
1			QILLERCIHPADIPAARLGEMIETAYGENFACSKIAPVRHLSGN
			QFILELFHGPTGSFKDLSLQLMPHIFAQCIPPSCNYMILVATSG
	1		DTGSAVLNGFSRLNKNDKQRIAVVAFFPENGVSDFQKAQIIGSQ
			RENGWAVGVESDFDFCQTAIKRIFNDSDFTGFLTVEYGTILSSA
			NSINWGRLLPQVVYHASAYLDLVSQGFISFGSPVDVCIPTGNFG
ł			MILLANIVARMMCIDIEREI GAGNONERUMDDIERMGA INTER-
1			NILAAVYAKMMGIPIRKFICASNQNHVWTDFIKTG\HYDLRGKE
			N*AQTFFTVQ*IFLPNLSNLERHLHLMANKDGQLMTELFNRLES
1			QHHFQIEKALVEKLQQDFVADWCSEGECLAAINSTYNTSGYILD
			PHTAVAKVVADRVQDKTCPVIISSTAHYSKPAPAIMQALKIKEI
i	1	1	NETSSSQLYLLGSYNALPPLHEALLERTKQQEKMEYQVCAADMN
			VLKSHVEQLVQNQFI
5851	3120	1802	RCYLQFLALLLTSTSARAAAAIAAAEEPAGSPSVMTRAGDHNRQ
			RGCCGSLADYLTSAKFLLYLGHSLSTWGDRMWHFAVSVFLVELY
			GNSLLLTAVYGLVVAGSVLVLGAIIGDWVDKNARLKVAQTSLVV
			QNVSVILCGIILMMVFLHKHELLTMYHGWVLTSCYILIITIANI
		į.	ANLASTATAITIQRDWIVVVAGEDRSKLANMNATIRRIDQLTNI
1			LADMANGO INTERCODUZA AGRICA CONTRACTOR DE LA DIMANGO INTERCADA LA CONTRACTOR DE LA CONTRACT
	}		LAPMAVGQIMTFGSPVIGCGFISGWNLVSMCVEYVLLWKVYQKT
	1	}	PALAVKAGLKEEETELKQLNLHKDTEPKPLEGTHLMGVKDSNIH
J]		ELEHEQEPTCASQMAEPFRTFRDGWVSYYNQPVF/LGWHGSCFP
			LYDCPGL*LHHHRVRLHSGTEWFHPQYFDGSISYNWNNGNCSFY
			LATSKMWFGSDRSDLRIGTAFLFDLVCDLCIHAWKPPGLVRFSF
5852	1	422	KTTFPSSLCPLRQLPEVRGYSGQPLTDPLISLCRSHKCRGKGWG
	1		SSSYPSLPALLRARSAPGHCTHRSCGPEWRIDSISRLEMQGARR
	}		SGWAQAQPTILLLVPRLRKSLPSIWG/SLMGPFITSGPG/WFRQ
			YYFFISGRH*VLFTESDFYYVAMDFGGHGLSSHYSPGVPYYLQT
]	FVSBIRRVVAGKKQSVYFRRCGGCSRAPPLITGGGVGSRKQRWP
1	1		ESGAWALAPGLPAIHGRSWES
5853	223	1246	
) ,,,,,	""	1346	RLLGLSRVKGLHGPAASAWISDPETRGDPGGPWGMWRGSDLRPR
İ			PVSLTGLTLVCK*AAQGPQV\HSVKLCFGLGG\PCLL\FPIFRP
	1	1	LLLHPRRPRLHPGTRGVAVEPHALRVVHVAHGEEAGIRAAGPGH
	•		GGVEIPQG/VGSLGARRGLRPSRPSSRHRNRVPAPPPGRPLATP
	1		HRRRFPPDPALTCPGLGQDQGPREQQKQGSGRHDTILGDWGESE
			SRWVRGNFRTGTAATLIGFSRNPTLNGSENWGSLVSIQEEGPDT
			GWEREKRNPAEMGNPQRWASPIHTPPLGPEILRAMPEALRAMPE
			ALGLRPDPATSVPSALS/QTF/PESWPRSCLRNQGETLGMGPVP
			LSSLCITESPSQNWTPCLLLLTCPRGLF
5854	86	938	
5554		230	KGRNTAPEKKGAALNNRENASS*NGY/SRWKQDIRRIENHIIQE
			LKHLCAMIKRVLLERLENTRKLRELTEGRTLDWPQNRITEVSAK
			RQIVTEYREKGKRN*EEKKRDLEGRSRRYNLCIIGIPETEDRAS
			GAETIKULLE/ENFPELKNELULQMEKAHRIPLKFNEKKAASRH
1			IRVTFL/KFQRRNILQASSQRKQVTYKGAKVRLTSDFSPAILNA
			RROW/N/PISRVLRENNFEPRIIYSAKLSFLYKGNWKTFLDIQG
1			LGKYINQELSLKILLKDLLQLTENLN
5855	536	2391	LRSYGCKAPSRISHLHK\FLFLLLPSLLMGYSESPPPITDSWAP
1			FISLTHHVLSQSQSPLSSNCWICLSTHTQ*FTALPADLLTWTQS
I			A TODIANA DOGO CONTROL OF THE PADLLTWICS
1			NVSLHISYLAIPFLADSFLKPV/L*PGNSAKHLSFKLSSLSMVS
I .			GRAVALLHLIASGLTSIQTNTASSKPPIWGY\LSTQTSFISPPP
I			LCLSRTYPNPAHATMVGQVPQSLCGLIFTL/RTPCRPSILHPNY
1			KIISTSAWQKVLCPSGSPTIHTSLHLTTGSSFLSFHPIPGFPAA
L			NSALYVSSLKGPPGKNVTIPSPVTGT*QPPHRGSN/RLTVDKDN
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1		5	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		1	_ · · · · · · · · · · · · · · · · · · ·
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	sequence		1.:- *
1			FFLSPKPNSLHQLPSQ\TPYQALTGAALAGSYPIWENENTLSWL
İ	i .		PTFTYNFCLSTPSLFFLCDTN*YLCLPANWSGTCTLVFQAPTIN
1	ļ.		ILPPNQTILISVEASISSSPIRNKWALHLITLLTGLGITAALGT
	Į.	1	GIAGITTSITSYQTLFTTLSNTVEDMHTSITSLQRQLDFLVGVI
	i		
			LQNWRVLDLLTTEKGGTCIYLQEECCFCVNESGIVHIAVRRLHD
		1	RAAEL*HQVADSWWQGSSLLRWIPWVAPFLGPLIFLFLLLMIGP
1	1	ļ	CIFNLVSRFISQRLNCFIQASMQKHIDNIFHLCHV*YQSLRGNH
			SEAPEPRP
5856	173	1137	PWLHGLGLSAVFLFYL*/YVTFHLYGGIILLLLIFISIAGILYK
}		1	FQDVLLYFPEQPSSSRLYVPMPTGIPHENIFIRTKDGIRLNLIL
i			IRYTGDNSPYSPTIIYFHGNAGNIGHRLPNALLMLVNLKVNLLL
i			VDYRGYGKSEGEASEEGLYLDSEAVLDYVMTSPDLDKTKIYLSG
1		1	
1			RSLG\GAAAIHLASDNSHRISAIMVENTFLSIPHMASTLFSFFP
1			MRYLPLWCYKNKFLSYRKISQCRMPSLFISGLSDQLIPPVMMKQ
1		1	LYELSPSRTKRLAIFPDGTHNDTWQCQGYFTALEQFIKEVVKSH
1			SPEEMAKTSSNVTII
5857	1502	563	
505/	1597	263	KLIGKVLVLSVVADAMAAFAVEPQGPALGSEPMMLGSPTSPKPG
1	1	ľ	VNAQFLPGFLMGDLPAPVTPQPRSISGPSVGVMEMRSPLLAGGS
		i	PPQPVVPAHKDKSGAPPVRSIYDDISSPGLGSTPLTSRRQPNIS
			VMQSPLVGVTSTPGTGQSMFSPASIGQPRKTTLSPAQLDPFYTQ
	į		GDSLTSEDH\LDDSWGDCIWGFLKASA\SYILL\QFAQYGGIS*
ļ	i		
			NMWMSNTGNWMHIRYQSKLQARKALSKDGRIFGESIMIGVKPCI
	1	1	DKSVMESSDRCALSSPSLAFTPPIKTLGTPTQPGSTPRISTMRP
1		1	LATAYKASTSDYQVISDRQTPKKDESLVSKAMEYMFGW
5858	355	1419	PPHQPAAASTSXHQQQQPPPPPQDSSKPVVAQGPGPAPGVGSAP
3030) 333	1415	
	1	1	PASSSAPPATPPTSGAPPGSGPGPTPTPPPAVTSAPPGAPPPTP
ļ		1	PSSGVPTTPPQAGGPPPPPAAVPGPGPGPKQGPGPGGPKGGKMP
		l .	GGPKPGGGPGLSTPGGHPKPPHRGGGEPRGGRQHHPPYHQQHHQ
	1	1	GPPPGGPGGRSEEKISGPRRGFKANLSLLRRPGEKTYTQRCRFC
1	ł		LLGIYLLISRRMNSRRLFAKIWENQEKFLSTKAKDSEFIKLESR
Ì			
ľ			ALA*NCPKPELG*YTP*GGRQLPSSLFPTHACLPLSCSVIFSPF
	l	1	MFPQ*NCWGRKPFRPNLGPHLKGAVCNRWDDPWEGPTGKGHCLN
	1	1	FAS
5859	307	1503	GGSSARPRASSRRMLSRKKTKNEVSKPAEVQGKYVKKETSPLLR
3033	1	1303	
	1	1	NLMPSFIRHGPTIPRRTDICLPDSSPNAFSTSGDGVVSRNQSFL
	1		RTPIORTPHEIMRRESNRLSAPSYLARSLADVPREYGSSQSFVT
			EVSFAVENGDSGSRYYYSDNFFDGQRKRPLGDRAHEDYRYYEYN
1	1		HDLFQRMPQNQGRHASGIGRVAATSLGNLTNHGSEDLPLPPGWS
	1		VDWTMRGRKYYIDHNTNTTHWSHPLEREGLPPGWERVESSEFGT
ì	ł		YYVDHTNKKAQY\RHPCAPTCTSV*STTSCHI/AS/RQOTERNO
1	ĺ		1 - 1
			SLLVPANPYHTAEIPDWLQVYARAPVKYDHILKWELFQLADLDT
			YQGMLKLLFMKELEQIVKMYEAYRQALLTELENRKQRQQWYAQQ
1			HGKNF
5860	2956	1270	TIRVEEFPLCPGGGKAQLSSASLLGAGLLLQPPTPPPLLLLLFP
1 2000	1 2,30	12,7	
1	1		LLLFSRLCGALAGPIIVEPHVTAVWGKNVSLKCLIEVNETITQI
1	1		SWEKIHGKSSQTVAVHHPQYGFSVQGEYQGRVLPKNYSLNDATI
1	1	1	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG
1		1	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFP
1			NETATIISOYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDI
1			
1	1		QYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDG
I	1	1	QWPDGLLASDNTLHFVHPLTFNYSGVYICKVT\NSPGSKEVTQK
1			VHPTFQDPSLPTYPPLPALQFQWASPSTA*TSRD\LATEP*KIA
1		1	PSPLSTL\ATIKGWTQLPTIIA+CSGVGALFIV\LVKCFGLGIF
1	1		1
1	1		CYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDBLDPYPDSV
([KKENKNPVNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDL
1			KMGMKFVSDEHYDENEDDLVSHVDGSVISRREWYV
5861	2051	1305	EVCACVQAFWLVASSGDDSQGDKCGCEVGSWVGSMRVVMARLL
1 3001	2331	1 200	
1		1	SEGEQGIPTACAAFAQQPAG/BPRRGLAGVGEGGPQCSWVNYRC
1			TLEFLVSLLGTDLARGRGNSASGPTAPADSKQL/ML*DVHRRVI
1			LE*RMNSGSPARDNAPSQRFCTNLSEGLRFGISPSWREALYGCH
			

SEG Predicted Predicted Predicted en Analon acid segment containing signal peptide (Analanine, Cocysteine, D-Aspartic Acid, &e Cocation Corresponding Cofired Contained Company Cofired Company Cofired Company Cofired Company Cofired Company Cofired Company Cofired Company Cofired Company Cofired Company Cofired Company Cofired Cofire	Deginning Cocation Corresponding Cocation Corresponding Cotation Corresponding Cofficial Committee Committ	020	December of the d	Predicted end	I have a sid a series and a series of the series of
Notation Corresponding Corresponding Continue Corresponding Corresponding Continue Corresponding Continue Corresponding Continue Corresponding Continue Corresponding Continue Corresponding Continue Corresponding Continue Corresponding Continue Corresponding Continue Corresponding Continue Corresponding Correspo	No: nucleotide location corresponding to first smino acid residue of residue of residue of amino acid residue of amino acid sequence	- 1			
location corresponding to first amino acid quence sequence A Sequence Sequence A Sequence	location corresponding to first amino acid amino acid amino acid residue of amino acid amino acid amino acid amino acid amino acid sequence sequence codon, /-possible nucleotide deletion, /-po	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
location corresponding to first amino acid quence sequence A Sequence Sequence A Sequence	location corresponding to first amino acid amino acid amino acid residue of amino acid amino acid amino acid amino acid amino acid sequence sequence codon, /-possible nucleotide deletion, /-po	NO:	nucleotide	location	Glutamic Acid. F=Phenylalanine, G=Glycine.
corresponding to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence code, sequence cod	to first amino acid residue of amino acid residue of amino acid amino acid sequence 5-Serine, T-Threonine, V-Valine, amino acid sequence 5-Serine, T-Threonine, V-Valine, amino acid sequence 5-Serine, T-Threonine, V-Valine, why Typophan, V-Tyrosine, X-unknown, *- Codon, /-possible nucleotide deletion,				
to first amino acid residue of amino acid sequence ##TTYPLOPHAN, Y=TYPLOSINE, X=UNIKNOWN, *=SLOP Codon, /=possible nucleotide deletion, \[\lambda_{\text{possible}} \] ##TTYPLOPHAN, Y=TYPLOSINE, X=UNIKNOWN, *=SLOP Codon, /=possible nucleotide deletion, \[\lambda_{\text{possible}} \] ##TTYPLOPHAN, Y=TYPLOSINE, X=UNIKNOWN, *=SLOP Codon, /=possible nucleotide deletion, \[\lambda_{\text{possible}} \] ##TTYPLOPHAN, Y=TYPLOSINE, X=UNIKNOWN, *=SLOP Codon, /=possible nucleotide deletion, \[\lambda_{\text{possible}} \] ##TTYPLOPHAN, Y=TYPLOSINE, X=UNIKNOWN, *=SLOP Codon, /=possible nucleotide deletion, \[\lambda_{\text{possible}} \] ##TTYPLOSINE, Y=TYPLOSINE,	to first amino acid residue of amino acid sequence sequence sequence sequence sequence code, and acid sequence sequence code, and acid sequence code, acid	- 1	location		1
amino acid residue of amino acid sequence Sequence Sequence A Septence A Sequence A SPECINF, TETREORINE, VEYDOINE, X-MURROWN, **Stop Codon, /*possible nucleotide deletion, A SPECINFERT CODE RESIDENCIA RESIDENCIA RESID	amino acid residue of amino acid sequence	- 1	corresponding	to first	L-Leucine, M-Methionine, N-Asparagine,
amino acid residue of amino acid sequence Sequence Sequence A Septimo (Codon, /=possible nucleotide deletion, >possible nucleotide insertion) Sequence A SPECIAMESTANDERS (CODON, /=possible nucleotide deletion, >possible nucleotide insertion) SEGUENCE PERCLIPLE PUNCTADUP PROLIAL THOMOS SITUATION PRESENCE IN SEGUENCE SEGUENCE	amino acid residue of amino acid sequence	1	to first	amino acid	P=Proline O=Glutamine R=Arginine
residue of amino acid sequence Sequence	residue of amino acid sequence Codon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion) A PFFQLIMMER KVSPDYNMFRGTVPLKKIIVDDDDSKIMS PRISTRCPLIPLIPVSGTADVPFRQILALTGMCYRVILA, OLD DHEEPCODFRELIDHOLDKVHILFGASLGGFLAGKFRAY RVISLILLONSFORTS IFNUTWIANSFALMFRAIKKIV RASEAULTUGGFVDFMADALIPFWTREISIJGSSLASKRITINCQNSTV RDIPVTIMOFPQSALSTREAEMYKLYPRABRAHKKTO LCKSAEVALVVQIHL/R/RMSMSPTREDITMGPRAMKKIV PARABRAHKKTO LCKSAEVALVVQIHL/R/RMSMSPTREDITMGPRAMKTON SARAVSRPFPS PVLTVSGK PFFSKGSLIPLARFREDTMGPLMVLFCLLFLYFGLADSFP VNISGGTFLISIGNAPGSLLTYSCOOLYPSJASRICKS TEGATRSKAVCKPVRCAPAVSFENGIYTPELGSYPVO ECEDETILLOSKAVCKPVRCAPAVSFENGIYTPELGSYPVO ECEDETILLOSKAVCKPVRCAPAVSFENGIYTPELGSYPVO ECEDETILLOSKAVCKPVRCAPAVSFENGIYTPELGSYPVO ECEDETILLOSKAVCKPVRCAPAVSFENGIYTPELGSYPVO ECEDETILLOSKAVCKPVRCAPAVSFENGIYTPELGSYPVO ECEDETILLOSKAVCKPVRCAPAVSFENGIYTPELGSYPVO ECEDETILLOSKAVCKPVRCAPAVSFENGIYTPALGSYRVANGHIRATINGVKKS QIQKSAMASPATAVANGSIKHANAVGIRRAT NAVSVILTFASSPVANGHIRATINGVKKS QIQKSAMASPATAVANGSIKHANAVGIRRAT DOK'SSMAGSPETAVANGSAVCKPTLIKAVISOB DKAKAKAKAYANG SAKLEHLIRANGVANGKATALANSVILMANGVANGKATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANSVANGKATANAVGATALANS	ŀ			
amino acid sequence Codom, /=possible nucleotide insertion) A	amino acid sequence Codon. / =possible nucleotide deletion.		amino acid		
amino acid sequence Codom, /=possible nucleotide insertion) A	amino acid sequence Codon. / =possible nucleotide deletion.	F	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence	sequence A A A A A B FROLIMBEIX/SPINNERGT/PILKKII/UDDDSXIM PRISICPLIER PUSGTADVERGT (LALITOKEY) TUDDDSXIM PRISICPLIER PUSGTADVERGT (LALITOKEY) TUDDDSXIM PRISICPLIER PUSGTADVERGT (LALITOKEY) TUDDDSXIM RVISLILLOS FORTS INTOVIRANS FULMERARIMKITY GEVERMARIALIST (STATEMENT AND THE PUBLISH TO THE PUT IMMOVING SELENGTININOSSY RID FOUT TWO PUSGTADVERGE LASKININOSSY RID FOUT TWO PUSGTADVERGE LASKININOSSY RID FOUT TWO PUSGTADVERGE LASKININOSSY RID FOUT TWO PUSGTAD TO THE PUT THE PUSCTAD TO THE PUT THE PUT THE PUSCTAD THE PUT T	ŀ	amino acid		1
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DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFKNMVPQ QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRIISAHGC KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNFVEGTA RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQTHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD	DPSGDNLYLGIVLAAVVIITGCFSYYQEAKSSKIMESFK QALVIREGEKMQVNAEEVVVGDLVEIKGGDRVPADLRII KVDNSSLTGESEPQTRSPDCTHE\NPLKTRNITFFSNNF RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQI AVFLGVSFFILSLIGYTWLEAVIFLIGIIVANVPEGLL CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTL- TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/I NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVIRNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPI	1			
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RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQLITGV AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF+H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD	RGVVVATGDRTVMGRIATLASGLEVGKTPIAIEIBHFIQI AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLI CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLI TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF+H/I NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVI RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPI				
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AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLLATVTV CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTQNRM TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD	AVFLGVSFFILSLILGYTWLEAVIFLIGIIVANVPEGLL CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTL TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF+H/I NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVI RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPI				
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TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF*H/LLGFC NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD	TVAHMWFDNQIHEADTTEDQSGTSFDKSSHTWVALF+H/I NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVI RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPI				CLTLTAKRMARKNCLVKNLEAVETLGSTSTICSDKTGTLTONRM
NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD	NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVI RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPI			l	· ·
RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD	RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAP			l .	• · · · · · · · · · · · · · · · · · · ·
RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAPERILD	RNKKVAEIPFNSTNKYQLSIHETEDPNDNRYLLVMKGAP	1			NRPVFKGGQDNIPVLKRDVAGDASESALLKCIELSSGSVKLMRE
		1			
	RCSTILLQGKEQPLDEEMKEAFQNAYLELGGLGERVLGF6	-			1 ~
PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG	PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAV				PEEQFPKGFAFDCDDVNFTTDNLCFVGLMSMIGPPRAAVPDAVG
KCRSAGIKVIMVIGDHPITAKAIAKGVGIIFEGNETVEDIAARL					4 · · · · · · · · · · · · · · · · · · ·
			L	L	ACABAGIAVIMVIGURPITAKATAKGVGITFEGNETVEDIAARL

SEQ	Predicted	Predicted end	I having and account as held to the
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ſ	sequence	1 1 1	\=possible nucleotide insertion)
		 	NIPVSQVNPRDAKACVIHGTDLKDFTSEQIDEILQNHTEIVPAR
			TSPQQKLIIVEGCQRQGAIVAVTGDGVNDSPALKKADIGVAMGI
			AGSDVSKQAADMILLDDNFASIVTGVBEGRLIFDNLKKSIAYTL
			TSNIPEITPFLLFIMANIPLPLGTITILCIDLGTDMVPAISLAY
			EAAESDIMKRQPRNPRTDKLVNERLISMAYGQIGMIQALGGFFS
1			YFVILAENGFLPGNLVGIRLNWDDRTVNDLEDSYGQQWTYEQRK
			VVEFTCHTAFFVSIVVVQWADLIICKTRRNSVFQQGMKNKILIF
			GLFEETALAAFLSYCPGMDVALRMYPLKPSWWFCAFPYSFLIFV
1			YDEIRKLILRRNPGGWVEKETYY
5867	3	1485	LPGRRARGGRGLGWPPAQALDGSRMGKAKVPASKRAPSSPVAKP
İ			GPVKTLTRKKNKKKKRFWKSKAREVSKKPASGPGAVVRPPKAPE
		1	DFSQNWKALQEWLLKQKSQAPEKPLVISQMGSKKKPKIIQQNKK
			ETSPQVKGEEMPAGKDQEASRGSVPSGSKMDRRAPVPRTKASGT
			EHNKKGTKERTNGDIVPERGDIEHKKRKAK\GQPQPHPPR/IDI
		,	WFDDVDPADIEAAIGPEAAKIARKQLGQSEGSVSLSLVKEQAFG
			GLTRALALDCEMVGVGPKGEESMAARVSIVNQYGKCVYDKYVKP
1	[[TEPVTDYRTAVSGIRPENLKQGEELEVVQKEVAEMLKGRILVGH
i			ALHNDLKVLFLDHPKKKIRDTQKYKPFKSQVKSGRPSLRLLSEK
			ILGLQVQQAEHCSIQDAQAAMRLYVMVKKEWESMARDRRPLLTA
		}	PDHCSDDA+QSCPAAAAAPLQRQCDQSQGQITSPQSGNSGETFS
			ESWQRGVAWCY
5868	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
ľ	1		AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
			LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
}			CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
1			DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5869	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
			AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
			LESRV+T\MTLDGHNLPSLVCVITGKGPLRBYYSRLIHQKHFQH
			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
			CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
L	ļ		DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5870	2122	833	LTAGASHTQDASQSTSAKYPAAAQNL/CVTNAMREDLADIWYIR
			AVTVYDKPASFFKETPLDLQHRLFMKLGSMHSPFRARSEPEDPV
			TERSAFTERDAGSGLVTRLRERPALLVSSTSWTEDEDFSILLAA
ľ			LESRV*T\MTLDGHNLPSLVCVITGKGPLREYYSRLIHQKHFQH
			IQVCTPWLEAEDYPLLLGSADLGVCLHTSSSGLDLPMKVVDMFG
			CCLPVCAVNFKCLHELVKHEENGLVFEDSEELAAQLQMLFSNFP
			DPAGKLNQFRKNLRESQQLRWDESWVQTVLPLVMDT
5871	3	3465	FFFCRPLRLYSKTTGDRSAMAGAAGLTAEVSWKVLERRARTKRS
1	1		VLKLL*LSLRRL*LEPTI*NGLLT*CSRLSVFRFLKV\GSVYEP
			LKSINLPRPDNETLWDKLDHYYRIVKSTLLLYQSPTTGLFPTKT
			CGGDQKAKIQDSLYCAAGAWALALAYRRIDDDKGRTHELEHSAI
			KCMRGILYCYMRQADKVQQFKQDPRPTTCLHSVFNVHTGDELLS
1			YEEYGHLQINAVSLYLLYLVEMISSGLQIIYNTDEVSFIQNLVF
1			CV\ERVYRVP\DFG\VWGKREGKYY*/SGSTELHSSSVGLGKRQ
]]		L*KQFNGFNLFGNQGCSWSVIFVDLDAHNRNRQTLCSLLPRESR
1			SHNTDAALLPCISYPAFALDDEVLFSQTLDKVVRKLKGKYGFKR
			FLRDGYRTSLEDPNRCYYKPAEIKLFDGIECEFPIFFLYMMIDG
			VFRGNPKQVQEYQDLLTPVLHHTTEGYPVVPKYYYVPADFVEYE
			KNNPGSQKRFPSNCGRDGKLFLWGQALYIIAKLLADELISPKDI
			DPVQRYVPLKDQRNVSMRFSNQGPLENDLVVHVALIAESQRLQV
			FLNTYGIQTQTPQQVEPIQIWPQQELVKAYLQLGINEKLGLSGR
			PDRPIGCLGTSKIYRILGKTVVCYPIIFDLSDFYMSQDVFLLID
			DIKNALQFIKQYWKMHGRPLFLVLIREDNIRGSRFNPILDMLAA
			LKKGIIGGVKVHVDRLQTLISGAVVEQLDFLRISDTBELPEFKS
			FEELEPPKHSKVKRQSSTPSAPELGQQPDVNISEWKDKPTHEIL
L	<u> </u>		QKLNDCSCLASQAILLGILLKREGPNFITKEGTVSDHIERVYRR

-650	, _ , , , -		
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 -	\=possible nucleotide insertion)
	1	 	AGSQKLWSVVRRAASLLSKVVDSLAPSITNVLVQGKQVTLGAFG
	1		HEEEVISNPLSPRVIQNIIYYKCNTHDEREAVIQQELVIHIGWI
			ISNNPELFSGTLKIRIGWIIHAMEYELQIRGGDKPALDLYQLSP
			SEVKQLLLDILQPQQNGRCWLNRRQIDGSLNRTPTGFYDRVWQI
			LERTPNGIIVAGKHLPQQPTLSDMTMYEMNFSLLVEDTLGNIDQ
			PQYRQIVVBLLMVVSIVLERNPELEFQDKVDLDRLVKEAFNEFQ
	İ	1	KDQSRLKEIEKQDDMTSFYNTPPLGKRGTCSYLTKAVMNLLLEG
			EVKPNNDDPCLIS
5872	68	665	VQGYMYRFVIKINSCYSEKTSICRHRCCPELPATQPWPTPTVFF
			NIAIDSESLGCI\SFKLFADKV/PKRWKKNFVLLNTGEKVLGDK
		1	GPCFYRIIPG\LCQGGDFTHHNGTGGKSLYSKEFDDENFI/LKH
			TAPGVLSTANAGPTTNGSQFFICTAKTEDG*QHVVFGKVKDGMS
		1	IVEALERSGERNGKTSKKITAANCGOL
5873	2240	506	RRPPEGGSGGGRTTRARMPLPWSLALPLLLSWVAGGFGNAASAR
55,5]	500	HHGLLASARQPGVCHYGTKLACCYGWRRNSKGVCEATCEPGCKF
	1		GECVGPNKCRCFPGYTGKTCSQDVNECGMKPRPCQHRCVNTHGS
			YKCFCLSGHMLMPDATCVNSRTCAMINCQYSCEDTEEGPQCLCP
			SSGLRLAPNGRDCLDIDECASGKVICPYNRRCVNTFGSYYCKCH
			IGFELQYISGRYDCIDINECTMDSHTCSHHANCFNTQGSFKCKC
			KQGYKGNGLRCSAIPENSVKEVLRAPGTIKDRIKKLLAHKNSMK
			KKAKIKNVTPEPTRTPTPKVNLQPFNYEEIVSRGGNSHGG\KKG
			NEEKMKEGLEDEKREEKALKD*HRRERPFRG\DVFFPKVNEAGE
			FGLIL\VQRKALTSKLEHKADLNISVDCSFNHG\ICDW\KQDR\
			EDDFDW\NPADR\DNAI\GFY\MAVPGLWQGHK\KDIGRLKLLL
		1	PDLQPQSNFCLLFDYRLAGDKVGKLRVFVKNSNNALAWEKTTSE
		1	DEKWKTGKIQLYQGTDATKSIIFEAERGKGKTGEIAVDGVLLVS
	1		
	1		L CLCPDSLLSVDD
5974		3397	GLCPDSLLSVDD
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD
5874	2	3387	ACPRLARRRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGFSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGFSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGFSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGFSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSFFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSFFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMXTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL+AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREEEKMIPPTKPEIQAKAPSSLSDAVP
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL+AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN
5874	2	3387	ACPELARRERVESLERERGWLEARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLERSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETGGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV
5874	2	3387	ACPELARREREVESLERERGWLEARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLERSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLUKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGGTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTTDQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPFTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\QRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP
5874	2	3387	ACPELARREREVESLERERGWLEARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLERSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLUKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGGTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTTDQLVKRVIEGSLSPKBRTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPFTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\QRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSFKERTLLKEDPAYMFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE
5874	2	3387	ACPELARREREVESLERERGWLEARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALAETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREEEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIBGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTTLFLFL APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKNNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK
5874	2	3387	ACPELARRERVESLERERGWLEARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTTSSPCPSADIDMKDMGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESBYDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGBEAPA\PGRG
5874	2	3387	ACPELARRRERVESLERERGWLEARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLBFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLIKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTTSSPCPSADIDMKDMGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESBVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGBEAPA\PGRG
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGGTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\QRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTNPDLWFL\HDQNS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLMR GEAEFEDEPPPREAELESPEVMPEEEDEDDEGGERAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSFKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEGGEBAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPPG RGFSSKSLKVGMIPAPRRVCLIQEFKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK
5874	2	3387	ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GGAEFEDEPPREAELESPEVMPEEEDEDDEDGGERAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPRRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFC\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL
			ACPELARREREVESLERERGWLEARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREEEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIBGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEABFEDEPPPREAELESPEVMPEEEDEDDEDGGEBAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG GGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFO\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF
5874	296	1848	ACPELARRERVESLERERGWLEARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREEEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKFSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSFKPAGVDISEAPQTSSPCPSADIDMKNDGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAFFEDEPPPREAELESPEVMPEEEDEDDEDGGERAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL\ALGAPALFTGLLQVTCFPPG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTOQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA
			ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTRNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLKKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKFSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDDEDDEGGERAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPRRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFG\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP
			ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGGTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYMFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\QRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTNPDLWFL\HDQNS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLMG GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGERAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQRMGWKEGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFFGSLFPHAICLGDVDNDTLNELVVGDTTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK
			ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTRNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLKKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKFSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\HDQNSS\AFK FY\RKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDDEDDEGGERAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPRRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFG\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP
			ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGGTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYMFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\QRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTNPDLWFL\HDQNS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLMG GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGERAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQRMGWKEGHGLGSLGK GIR\SRSACTQQAAMGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFFGSLFPHAICLGDVDNDTLNELVVGDTTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK
			ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGLDLKNLRLPRRKMS FDIIDKSDVFSRFGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL NMLLDKGAVKTKNCFFEIIKPFDKYIMRLQDRLLKSVTPLLMAC NAYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREEEKMIPPTKPEIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIEGSLSPKERTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAPGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTNPDLWFL\HDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEDGGEBAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCNKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEEQRPVFKQHIPANTKVMLISDIDGDGCREL
			ACPRLARRRRVRSLRRRRGWLRARWSRGQNNMAARRITQETFD AVLQEKAKRYHMDASGEAVSETLQFKAQDLLRAVPRSRAEMYDD VHSDGRYSLSGSVAHSRDAGRESLRSDVFSGPSFRSSNPSISDD SYFRKECGRDLEFSHSNSRDQVIGHRKLGHFRSQDWKFALRGSW EQDFGHPVSQESSWSQEYSFGPSAVLGDFGSSRLIEKECLEKE\ SRDYDVDHSG\EA\DSVLRGS\SQVQA\RGRALNIVDQEGSLLG KGETQGLLTAKGGVGKLVTLRNVSTKKIPTVNRITPKTQGTNQI QKNTPSPDVTLGTNPGTEDIQFPIQKIPLGDLKNLRLPRRKMS FDIIDKSDVFSRRGIEIIKWAGFHTIKDDIKFSQLFQTLFELET ETCAKMLASFKCSLKPEHRDFCFFTIKFLKHSALKTPRVDNEFL OMNYELSVKMKTLSNPLDLALALETTNSLCRKSLALLGQTFSLAS SFRQEKIL*AVGLQDIAPSPAAFPNFEDSTLFGREYIDHLKAWL VSSGCPLQVKKABPEPMREBEKMIPPTKPBIQAKAPSSLSDAVP QRADHRVVGTIDQLVKRVIBGSLSPKBRTLLKEDPAYWFLSDEN SLEYKYYKLKLAEMQRMSENLRGADQKPTSADCAVRAMLYSRAV RNLKKKLLP\WQRRGLLRAQG\LRG\WKARRA\TTGTQTLLFLR APGLKHHGRQAFGLS\QAKPSLPDRND\AAKD\CPLDPV\GPSP QDPSLEASGPSPKPAGVDISEAPQTSSPCPSADIDMKDNGRTAE KLARFVAQVG\PEIEQF\SI\ENSTDNPDLWFL\EDQNSS\AFK FY\RKKVFELCPSICFTSSPHNL\HTGGGDTT\GSQESPVDLME GEAEFEDEPPPREAELESPEVMPEEEDEDDEGGEBAPA\PGRG GPSLEGSTPADGLPGEA\AEDDL/ALGAPALFTGLLQVTCFPFG RGFSSKSLKVGMIPAPKRVCLIQEPKVHEPVRIAYDRPRGRPMS KKKKPKDLDFAQQKL\TDK\NLGFQ\MLQKMGWKEGHGLGSLGK GIR\SRSACTQQAAWGGSGWGLSPSTCSLPLGSFTAKMAYSWQL IFVF LAALGGLPLWRLSRRGFREYLLGLSAPSALGGAMRSVSYVQRVA LEFSGSLFPHAICLGDVDNDTLNELVVGDTSGKVSVYKNDDSRP WLTCSCQGMLTCVGVGDVCRKGKNLLVAVSAEGWFHLFDLTPAK VLDASGHHETLIGEBQRPVFKQHIPANTKVMLISDIDGDGCREL VVGYTDRVVRAFRWEELGEGPBHLTGQLVSLKKWMLEGQVDSLS

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residue of amino acid eequence	1		1	
amino acid sequence Codon, /-possible nuclectide deletion Sequence	}	1		
Sequence _possible nucleotide insertion				W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
GLFALCTLOTTLEMENBERDKLIMSVOYDBOLFALEKCINVTO- NCHBEVVACANDOCTY I IDHNITYUVEPOUDBLIBATCAGLYACK RGRNSPCLVYVTENGLYVVEPVGENECTAGLYACK RGRNSPCLVYVTENGLYVVEPVGENECTHUKLLETEN-GT TACCESAMILITSEL-LVVCPTKRSETIOTSHISVILDFOASRIPS WTCLLAGSGPF-TPTLPPKCVFGSKCAAGSITKQ HTDLGVFSKVAGAAABEPQESETTOVAAMIKKIFGDHFIPOYBV HTCLLAGSGPF-TPTLPPKCVFGSKCAAGSITKQ HTDLGVFSKVAGAAABEPQESETTOVAAMIKKIFGDHFIPOYBV HERTTSILHILDSRRVRGRDVIVILDELKOKGASETSEAKTLQ DLIMESVAFSPANLSSTSGRIVAALVOSAVALETKOTSLASFIP AVNOLTSOLFRIKSSSTSGRIVAALVOSAVALETKOTSLASFIP AVNOLTSOLFRIKSSEELKIBELKERMINATATULEKCIGEDV KKABLALISTER \(\text{AVVONRQOMM} \) DELKAKSESFFFOIQAAGSOL, SARGO\DAFSVIGSVALIEMENTATULEKCIGEDV KKABLALISTER \(\text{AVVONRQOMM} \) DELKAKSESFFFOIQAAGSOL, SARGO\DAFSVIGSVALIEMENTATULEKCIGEDV KKABLALISTSOLAVALIEMENTEKOOTIPLIK KKLESYLD LIMP\NSSICSK-RIEBRAK\RGAGGGGVAGSTSTBELLISALBDLEV LSRELIEMLAISRNOKLLQAGESNOVUELLIHRINGSFFEIMKLA LINQKKIKHEMOVLEKERLGOGTOHTIVENGOTIPLIK KKLESYLD LSRELIEMLAISRNOKLLQAGESNOVUELLIHRINGSFFEIMKLA ALEMAKASSGRIKERLGOGGOMPTENGOTIPKOOTIPLIKATVOV AKEKLISSIEKAKGAISSEBII HYAHRISASNAVCAPLTIVICOD PERPYTTOLEMISGLIGOMNDFSTROMOHIQKOLKEABILATATVO AKEKLISSIEKAKGAISSEBII HYAHRISASNAVCAPLTIVICOD PERPYTTOLEMISGLIGOMNDFSTROMOHIQKOLKEABILATATVO AKEKLISSIEKAKGAISSEBII HYAHRISASNAVCAPLTIVICOD PERPYTTOLEMISGLOONNDFSTROMOHIQKOLKEABILATATVO AKEKLISSIEKAKGAISSEBII HYAHRISASNAVCAPLTIVICOD PERPYTTOLEMISCLOONNDFSTROMOHIQKOLKEABILATATVO AKEKLISSIEKAKGAISSEBII HYAHRISASNAVCAPLTIVICOD PERPYTTOLEMISCLOONNDFSTROMOHIQKOLKEABILATATVO TISINAMASSICKARAVANOOTIPLATATIVICOD PERPYTTOLEMISCLOONNDFSTROMOHIQHIQKOLAUPTVO TISINAMASSICKARAVANOOTIPLATATIVICOD PERPYTTOLEMISCLOONNDFSTROMOHIQHIQKOLAUPTVO PERPYTTOLEMISCLOONNDFSTROMOHIQHIQUADVONOHIPLOONNOHIPLO		l.	sequence	
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TACCRSMANILITS: *LPOPCPYKRSTIGTSHBYULPOASSIPPS WTCLIAGSOFP**PTTPIPPKOYSGICAAAGSITPS WTCLIAGSOFP**PTTPIPPKOYSGICAAAGSITPS WTCLIAGSOFP**PTTPIPPKOYSGICAAAGSITUATGHIPSOYSGICAAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGSITUATGHIPSOYSGICAAGAGSITUATGHIPSOYSGICAAGAGSITUAGAGSITUATGHIPSOYSGICAAGAGSITUAGAGSITUATGHIPSOYSGICAAGAGSITUATGHIPSOYSGICAAGAGAGAAAAGAAGAAAAGAAAAAGAAAAAAAAAA		t		
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S876				
NPRTTELIHHI.SERNEVRORDVYLVIEDLKKASEYESEAKVI.D DLLMESVNFSPANLSTGSRYIMALVIDSAVALETTOTISLISFIP AVNILTSDIFFRYEKSKSEEKKIELGEKERNIJATIVLEKKOLOGEV KKAELHASTER\AKVUNRKOM, DIFLKAKSEEFREGIOAGOGU SARGOLDASVYOGIVALIKAKSEEFREGIOAGOGU SARGOLDASVYOGIVALIKAKSEEFREGIOAGOGU SARGOLDASVYOGIVALIKAKSEEFREGIOAGOGU SARGOLDASVYOGIVALIKAKSEEFREGIOAGOGU SARGOLDASVYOGIVALIKAKSEEFREGIOAGOGU SARGOLDASVYOGIVALIKAKSEERREGIOAGOGU SARGOLDASVYOGIVALIKAKSEERREGIOAGOGU SARGOLDASVYOGIVALIKAKSEERREGIOAGOGU LIMP\NPSHICSK*RIEBERAK\REALA\SIEBELTRVS\MELIKALEDEV LSRELIEMIAISRNOKULQAGENOVUELUIHRIDGEFGEIMILA LINQKHHHENOVIEKSVEKKROSIOOLOQKUERASANACAPLITAVYOG RERPYPTILEHRASISIOOLOQKUERAJIATAVYOG AKELKISIEKARKGAISSEEITYAARISASNAVCAPLITAVOG RERPYPTILEHRASISIOOLOQKUERAJIATAVOGO RERPYPTILEHRASILGAGONOMESTIONVOHLAKKIRA CPCSTVS\/NGSQMTCR*INILLILLIKAKUGUI. SERTISTISIANAKOONOMESTIONVOHLAKUKANA RIKKENAYSVORYKASIITATRNIPPERKAYAVUEBUDIIAVDPFS FILSGSIHLLEEDOSLYCISAMNOOGVEHTEBULTIVVETION LIAWULKASIIYKEELEPKAPTPEKLIMDIMMMIRIMPEQRORGEGII PDVSRSYHFGIVOLAKKUMINOOGVEHTEBULTIVVETINTI LIAWULKASIIYKEELEPKAPTPEKLIMDIMMMIRIMPEQRORGEGII PDVSRSYHFGIVOLAKKUMINOOGVEHTEBULTIVVETINTI KKEAYSVEVHRILISEREVLDHSKINCEOSPILPTEGITVYAFIR MEKDOPPTIVOLAKULMINOOVEHAYYKKKIKENVOOLIKVUSELI KKEAYSVEVHRILISEREVLDHSKINCEOSPILPTEGITVYAFIR MEKDOPPTIVOLOKAKINIOOTENTAYYKKIKRIVOOLIKVUSIINTO ALIAMASSAAGOSSAAGNAGSPILLIPISTYSPICAATMASSOED GTINGASSAAGNAGSSAAGNAGSPILLIPISTYSPICAATMASSOED GTINGASSAAGNAGSSAAGNAGSPILLIPISTYSPICAATMASSOED GTINGASSAAGNAGSSAAGNAGSPILLIPISTYSPICAATMASSOED GTINGASSAAGNAGSSAAGNAGSPILLIPISTYSPICAATMASSOED GTINGASSAAGNAGSSAAGNAGSPILLIPISTYSPICAATMASSOED GTINGASSAAGNAGSSAAGNAGGOTILLIPISTACATAVASIA ALIAMVETYMEKINSTYNYELITTAASVIPTYTILITAASVIPTILIPISTYSPICATMASSOED TITTSYTTSTYTSILDIALPYTKAARNINSPIYTYPILLITAASVIPTILPISTYSPITAATACAA SUTYNKOKASSAAMPASAADATATAVASAAAOAAAAAAAAAAAAAAAAAAAAAAAAAAAA	5876	1122	224	
DLLMESWIPSPANLSSTGSRYLMALUDSAALETKOTSLASPIP AWNOLTSDLFYKKSKEEIK KIELKLERULPALKEKCQEDV KKARLHLSTER \ARVUNTROMM\DFIKAKSEERPEG\AGAGGOL SARGO\DASVOIGSLVALIRENWPRIKGOTIPK\KKLESYLD KKARLHLSTER \ARVUNTROMM\DFIKAKSEERPEG\AGAGGOL SARGO\DASVOIGSLVALIRENWPRIKGOTIPK\KKLESYLD LMP\NPSHCSK*RIEBAK\RELA\SITERATYS\MMEL 1907 GTIGWAASSSGEKEKERGGGGGVAGNSTRERLISALEDLEV LSRELIEMLA.SINOKLLGAGEROVUELLIHEOFQELMKLA LNQGKHHEMOVLEKSVEKROSIOQLGKQLKEASGILATAVYQ AKEKLKSIEKAKGAISSEEITHYAHRISAACPILTWYBGD PERPYPTDLEWRSGLIGGWNDFSTNOVWGHLPGDALA\/RRKIAR CPCSTVS\NSGSOMTCR*NITLILGKSVCGL PERPYPTDLEWRSGLIGGWNDFSTNOVWGHLPGDALA\/RRKIAR CPCSTVS\NSGSOMTCR*NITLILGKSVCGL PERPYPTDLEWRSGLIGGWNDFSTNOVWGHLPGDALA\/RRKIAR CPCSTVS\NSGSOMTCR*NITLILGKSVCGL PERPYPTDLEWRSGLIGGWNDFSTNOVWGHLPGDALA\/RRKIAR CPCSTVS\NSGSOMTCR*NITLILGKSVCGL PERPYPTDLEWRSGLIGGWNDFSTNOVWGHLPGDALA\/RRKIAR CPCSTVS\NSGSOMTCR*NITLILGKSVCGL PERPYPTDLEWRSGLIGGWNDFSTNOVWGHLPGDALA\/RRKIAR CPCSTVS\NSGSOMTCR*NITLILGKSVCGL PERPYPTDLEWRSGLIGGWNDFSTNOVWGHLPGDALA\/RRKIAR CPCSTVS\NSGSOMTCR*NITLILGKSVCGL PERPYPTDLEWRSGLIGGWNDFSTNOWGHLPGOTTAVIT\ ISINARVSGNYKASLITATNIT\PPERAKFAVVLEGULGIUNDFST LSGNYLRSGSYHGGVCISANDOGYBHTAEDPALLYVCHUNGL LSGWARSISVREELEPKWPTPERLAUMDMWARDEGRGRCGII PDVSRSYHFGIVGLANDOFSRNOCESPERGTYAPIT MEKODDDFTTWTQLAKCLHINDLDVRGNIRGLWRLERKWHPLVV GVPASPYSUKVERSEPPSVTPIJELPPPREGRAPAGETGTYAPIT MEKODDDFTTWTQLAKCLHINDLDVRGNIRGLWRLERKWHPLVV GVPASPYSUKVERSPSVTPIJELPPPREGRAPAGETGTYAPIT MEKODDDFTTWTQLAKCLHINDLDVRGNIRGLWRLERKWHPLVV GVPASPYSUKVERSPSVTPIJELPPPREGRAPAGETGTYAPIT MEKODDDFTTWTQLAKCLHINDLDVRGNIRGLWRLERKWHPLVV GVPASPYSUKVERSPSVTPIJELPPPREGRAPAGETGTYAPIT MEKODDDFTTWTQLAKCLHINDLDVRGRIRGLWRLERKWHPLVV GVPASPYSUKVERSPSVTPIJELSTLANDTYTVIJLATAVTY SITURGUNGSRSAGGERAPGKRRRLGFTANDLTAGNV ALAMAVEFTMEKGTHRUSSRAGSPTLLPFSFTRAADLTYTVILATAVTY SITURGUNGSRSSAGGERAFAGAAGASSTYPLLATAMATTYTIJACHATA AADABHANACABOTARATAYALAA AADABHANACABOTARATAYALAA AADABHANACABOTARATAYALAA AADABHANACABOTARATAYALAAA AADABHANACABOTARATAYALAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	3070	1122	224	
AVBILITSDLFTKTSKSEEIKIELEKLEKTATITULEKCIQEDV KKARAILISTER ÄAVDINRGAM) PIFIKAKSEEPREJOAAGBOIL SABGO(JAPSVPIGGIVALITEENPERLKOOTTELK\KKLESYID IMP\NBEHGES** RIEBAK\RELA\SIEBAK\RE	1	i		
KKAELHISTER ARVUDNERQIM DFLAKSSEEFFEG (DAAGBOL)				
SARQ\DAFSVPIGSLVALITENINPEKQCTTPLK\KKLESYLD LNP\NPSHCSK\RIEBAK\RELA\SIEBALTSKYS\NMEL 5877 2030 1907 GTLGKMAASSSGEKEKERLGGLGVAGGNSTRERLLSALEDLEV LSRRLIEMLAISR\KLLGAGEENQVLELLIHRGEFGELMKLA LNQKKHHEMOVLEKSVEKREDSIQQLGVERGAGILTAVYQ AKEKLKSIEKARKGAISSEEIIKYAHRISASNAVCAPLTWVEGG PRRYPYTDLEMRSGLLGGONNIPSTINGHEGDALA\RKTAR CPCSTVS\RGSQMTCR*INILLILGKSVCEL 5878 950 2113 GLWKCMGLGOPHTIRVOP\PTPRQGGGOVVEAVIAGNRENYLY RMLRSLLSAQGVSPQMITVFIDGYYEEPMDVVALFGLRGIGHT ISINARVSGHYKASLTATFRLFFEAKFAVVLEEDLDILAVDFFS FLSGSIHLLEEDDSLVCISANNDQGVEHTVVGOVLANVLEDLDIJAVDFFS FLSGSIHLLEEDDSLVCISANNDQGVEHTVVGOVLANVLOSHERNYLY RMLRSLLSAQGVSPQMITVFIDGYYEEPMDVVALFGLRGIGHT ISINARVSGHYKASLTATFRLFFEAKFAVVLEEDLDIJAVDFFS FLSGSIHLLEEDDSLVCISANNDQGVEHTVVGOVLANVDSL KKEAYEVEVHELLSEASVLDHISKNFCEDSPLDTVEETMVGS LGWVLARSLYKEELJEKWPTEKLMONDMWREMBEGRGRECTI PDVSRSYHEG IVGLNNNGYHEAYFKKHUTVGVOLLNVDSL KKEAYEVEVHELLSEASVLDHISKNFCEDSPLDDTVEHTVGFVCL GVPASPYSVKKPBSVTFIFLEPSPFRAATNASSDED GTNGGASSGRAGENGEAGGKRRIGFLATAANLTSDED GTNGGASGREGEDREAGKRRIGFLATAANLTYDIAMTAGKUL ALANVFYMEKGTHRGLYKSIQKTLKFPQTFALLEIVHCLIGIV PTSVIVTGYQVSSRIFMWLITHSIRVGINGELWTLYLLIGIUV PTSVIVTGYQVSSRIFMWLITHSIRVGINGELWTLYLLIGIUV PTSVIVTGYQVSSRIFMWLITHSIRVGINGELWTLYLLIGIUV YFHNLLQRRKVLHG\0\6-1\6-1\chinox\0-1\chinox\0-1\0-1\0-1\0-1\0-1\0-1\0-1\0-1\0-1\0-1	1			
IMP_NPSHCSK*RIEBAK_RELAS_ISBALTERUS_NMEL		l		
S877 2010 1907 GTLGMAASSSGEKERIAGGLGVAGGNSTERILISALEDLEVL LSRELIEMAL SERNGLIGHAGEROVLEGILINGGEROLMELY LSRELIEMAL SERNGKLOAGEROVLEGILINGGEROLMELY LNOCKIHHEMQVLEKEVEKRDSDIQQLQKQLKEABGILINTAVYQ AKEKLKSIEKARKGAISSEIIKYTÄHRISÄSNÄVQAPITWYPGD PERRYPYTDLEMRSGLIGGORMPSTINGVOHLDGDALA/RRKIAR CPCSTTWS/MSSQMTC*INIILILIQKSVCEL GLÜKKCMGLGGPHTÜRVOPFYPTRQOGGROVVPAVIAGNRPNYLY RNLESLLSAQOVSPOMITYFIDGYYEPHDVVALFGLIGGICHTT IS INNAVSGVYKASLITATYRILPERAFPULEGILDIAVDFFS PLSQSIHLLEEDDSLYCISAWNDQSYEHAEDDALLYRUETUNDEN LGWVLARSLYKEELBEKWPTEPEKLWOMMMREMEGGRGECII PDVSRSYHEGIVGINNAVFHEAPTKKHLVEEDDLIAVDFFS KKEAYSEVEVHELLSEAEVLDHSKNPCEOSFLPDTEGRGRECII PDVSRSYHEGIVGINNAVFHEAPTKKHLVEEDDLIAVDFFS KKEAYSEVEVHELLSEAEVLDHSKNPCEOSFLPDTEGRGRECII PDVSRSYHEGIVGLNAMPTOGVQLENNOSL KKEAYSEVEVHELLSEAEVLDHSKNPCEOSFLPDTEGRGRECII PDVSRSYHEGIVGLAKENDLOWSHAMPTOGVQLINDSL KKEAYSEVEVHELLSEAEVLDHSKNPCEOSFLPDTEGRGRECII PDVSRSYHEGIVGLAKENDLOWSHIPTVOGVLENNOSL KKEAYSEVEVHELLSEAEVLDHSKNPCEOSFLPDTEGRAFTAKSDED GTNGGASEAGEDREAPGKRRIGFLATANLTFYDIAMTAGKIVL ALAWKFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWKFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWKFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGATAGKTAAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAK				SARGQ\DAFSVPIQSLVALIRENWPRLKQQTIPLK\KKLESYLD
S877 2010 1907 GTLGMAASSSGEKERIAGGLGVAGGNSTERILISALEDLEVL LSRELIEMAL SERNGLIGHAGEROVLEGILINGGEROLMELY LSRELIEMAL SERNGKLOAGEROVLEGILINGGEROLMELY LNOCKIHHEMQVLEKEVEKRDSDIQQLQKQLKEABGILINTAVYQ AKEKLKSIEKARKGAISSEIIKYTÄHRISÄSNÄVQAPITWYPGD PERRYPYTDLEMRSGLIGGORMPSTINGVOHLDGDALA/RRKIAR CPCSTTWS/MSSQMTC*INIILILIQKSVCEL GLÜKKCMGLGGPHTÜRVOPFYPTRQOGGROVVPAVIAGNRPNYLY RNLESLLSAQOVSPOMITYFIDGYYEPHDVVALFGLIGGICHTT IS INNAVSGVYKASLITATYRILPERAFPULEGILDIAVDFFS PLSQSIHLLEEDDSLYCISAWNDQSYEHAEDDALLYRUETUNDEN LGWVLARSLYKEELBEKWPTEPEKLWOMMMREMEGGRGECII PDVSRSYHEGIVGINNAVFHEAPTKKHLVEEDDLIAVDFFS KKEAYSEVEVHELLSEAEVLDHSKNPCEOSFLPDTEGRGRECII PDVSRSYHEGIVGINNAVFHEAPTKKHLVEEDDLIAVDFFS KKEAYSEVEVHELLSEAEVLDHSKNPCEOSFLPDTEGRGRECII PDVSRSYHEGIVGLNAMPTOGVQLENNOSL KKEAYSEVEVHELLSEAEVLDHSKNPCEOSFLPDTEGRGRECII PDVSRSYHEGIVGLAKENDLOWSHAMPTOGVQLINDSL KKEAYSEVEVHELLSEAEVLDHSKNPCEOSFLPDTEGRGRECII PDVSRSYHEGIVGLAKENDLOWSHIPTVOGVLENNOSL KKEAYSEVEVHELLSEAEVLDHSKNPCEOSFLPDTEGRAFTAKSDED GTNGGASEAGEDREAPGKRRIGFLATANLTFYDIAMTAGKIVL ALAWKFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWKFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWKFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIQKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGLYKSIGKTHAULTFYDIAMTAGKIVL ALAWHFYMEKGTHRGATAGKTAAKAKAKAKAKAKAKAKAKAKAKAKAKAKAKAK	1			LMP\NPSHCSK*RIEBAK\RELA\SIEABLTRRVS\MMEL
LSRELIEMLAISROKLLIOAGEENQVIELLIHROGE FOELMKLA LNOKSIHHRMQVLEKEKROSIOJOKOLKEABQILATAVYO AKEKLKSIEKARKGAISSEEIIKYAHRISASNAVCAPLTWYPGD PRRYPTDLEMRSGLLGQMNNPSTNGVNSHLPGDALA/RRIAR CPCSTVS/NSGMCTGC**INIILICKSYCEL 5878 950 2113 GLWKCMGLGOPHTHRVQD*PTPRQGGPQVVVAVAIGNRPNYLY RMLSSLLSAQGSPQMTVPJIGVTEGWVALGGIGHTP ISIKNAVSGHYKASLTATTNIPPEAKFAVVLEEDLDIAVDFS FLSQSIHLLEEDDSLYCISAMNDQGYBHTAEVDFWALPGLRGGHTP ISIKNAVSGHYKASLTATTNIPPEAKFAVVLEEDLDIAVDFS FLSQSIHLLEEDDSLYCISAMNDQGYBHTAEVDFALLYRVETMPG GWYLRSIYYKEELEPKWPTPEKLUMMMMRMPEQRRGRGCII PDVSRSYHGTVGLIMMGGYPHEAYFKKHKWNTVPGVGLRNVDSL KKEHYEVEVHRLISESAVLDHSKNYDCSPIPDTEGHTYVAPIR MEKDDPTTWTOLAKCLHINDLDVGNIRGLWELPFKKNHFLVV GVPASPYSVKKP PSYTIPLEPPP PKEGAPGAPPGOT 5879 3 981 RLTEAAANGSGSRAAGWAGSPPTLLIPLSPTSPRCAATMASSDED GTINGGASEAGEDREAPCKRRIGFLATAWLTFTD IAMTAGHLVIL ALAWVRYTWEKGTHRGLYKSIGKTLKFULIVPUVAGGELLTIY PTSVIVTGVOVSSRIFMVMLITHSIKPIQNEESVUFFLVAMTVT EITRYSFYTFSLLDHLEYFIKMARITHILVPUVAGGELLTIY AALPHVKKTOMFSIRLPNKYNVSPDYYYPLLITMASYIPLFPQL YFRHLQRRKVUHO\G*-L*KRNK*SLQTRCFFQNNQDYLSBES NNKNKQLCEISWIVWELKI 5880 1138 1324 SLMCLWAGGLGLGFSSONPLORAGILARPRERAEGTFSALTACSA SVTSKOKSSGMWPSASADRDSPVLPRPPGVQLPSGTGWVLSD *KKRGRCSS/MLSQPOHEREKEVVLLRRSMAEGERARASDVL CRSLANETHQLRPTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVGSVIEKLQEENRILKGKVTHVEDLANKMQRYN ASRDEVVRGLHAQLRGLQIPHEPELMRREISRINRQLEEKINDC AEVKGELAASRTARDAARRVQMEGOLAFKDGWRSTADRER AQSRIQELEEKVABLHOVSNKQDSREPDAGRHAGSKTAKYLA ADALELMVPGGWRSGTGSQOPEPPABGGHPGAAQRGGDLQCPH CLQCTSDEOGEELLRIVABCCQ 5881 26 441 GGTHSPPTEABRAQHLTMCTTRILFILVAAATGTHAQVOLLOGS SVKKGRASVNSCYVSTGYTLTKLSMWAVQAPGKGLE*MGPPD LQOVFTIYPQKFQGRVSTTIKLSMWAVQAPGKGLE*MGPPD LQOVFTIYPQKFQGRVSTTIKLSMWAVQAPGKGLE*MGPPD LQOVFTIYPQKFQGRVSTTIKLSMWAVQAPGKGLE*MGPPD LQOVFTIYPQKFQGRUGELLGULDALANAAVRGOE RYKROZBLELGULGQUERALANARROE RYKROZBLELGULGQUERALANARROE RYKROZBLELGULGQUERALANARROE RYKROZBLELGULGQUERALARARROE REMIGLARGGSLLSSISSEIRTILGSCSGAMNIFLIRRRQAVRGKLG ELVDGLUVPSALVYAELERPYTEPEPLOGLIDAKAANARROE ARGTAACADVRGVLDRALVYAEVLERSKNITF	5877	2030	1907	GTLGKMAASSSGEKEKERLGGGLGVAGGNSTRERLISALEDLEV
LNOCKIHHEMOVLEKEVEKRDSDIQOLOKOKLEKEGILATAVYO AREKLKSIKRAKGAISEELIYYAHRISASNAVCAPLTWUPGD PRRPYPTDLEMRSGLLGQMNNPSTNGVNGHLPGDALA/RRKIAR CPCSTVS/NGSQMTCR*INIILILOKSVCEL 5878 950 2113 GUMKMOLOGPHTHEVOP*PTFRQGPQVV9VAVIAGNRPNYLY RMLRSLLSAQGVSPQMTTVFIDGYYEEPMDVVALPGLRGIQHTF ISINANAVGHYKASLLATFINLPPEAKFAVVLEEDLDIAVDFS PLSQSIHLLEEDDSLYCISAMNDQGYEHTAEDPALLYRVETMOR LGWVLRRSLYKEELEPRWPTPEKLMDMMMRMPBGRRGRECII PDVSRSYHFGIVGLINMGVSYHEAPKKRNTVPGVGLRGNVDSL KKEAYEVEVHRLLSEABVLDHSKNPCEDSFLPDTEGHTYVAFIR MEKDDDFTHTWOLAKCLHINDLDVSGNIRGLWRLFRKKNHFLVV GVPASPYSVKKPPSVTPIFLEPPPKEEGAPQAPEOT 5879 3 981 RLITBAAAAGSGSRAAGMAGSPPTLLPLSFTSFRCAATHASSDED GTNGGASEAGEDREAPGKRRIGFLATAULTFUIMTTGMLVL AIAWVRYMEKGTHRGLYKSIGKTLKFPOTPALLBIVHCLIGIV PTSVIVTGVOVSSIE HAVMLLTHSILGVRESVVLDFLVAMTVT EITRYSFYTFSLLDHLPYFIKMARYNFFILLYVOVGAGELLTIY AAAPHVKKTGMFSIRLENKYNVSPDYYYPFLLITMASYIPLEPQL YFHMLRGRKVLHG\GV-L*KRNIK*SQMSESVLDHSPSF NNNNKQLCEISWIWFLKI 5880 1138 1324 SLWCLVAGGLGGPSSONPLORAGILARPREARGTFSALTACSA SVTSKGKSSSGMWPSAASDRDSPVLRPPGPVQLPSGTGWTLSD *KKKRGRCSS/MISQPCHEREKEVVLLRRSMAEGERARAASDVL CRSLAMETHQLRFLTIATHAMCHLALDERQHAJRWGRSP DQSSHTDGHTSVGSVIEKLQEENRLLKGKVTHVEDLNAKWGRND ASRDEVVRQLIAQRIGLIPHPEELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALBRVQMLEORGHADRGRGBD DQSSHTDGHTSVGSVIEKLQEENRLLKGKVTHVEDLNAKWGRND ARSHEVVRQLIAQRIGLIPHPEELMRKEISRLNRQLEEKINDC AEVKQELAASRTARDAALBRVQMLEOQILAYKDDFMSERADRER AQSRIQELEEKVASLLHQVSWRDOSREPDAGRIHAGSKTAKYLA ADALELMVPGGWRPGTSGOQPEPPAEGPAAQRGGDLQCPH CLQCFSDEGGELLRHVABCCC GGHPFSFTEAPRAQHLTMDCTWRILFLVAAATGTHAQVOLLQSG SEVKKGASVWVSCYVSGYTLTKLSMINVRQAPGKGLE*MGPPD LQDVETITPQKFGQRVSMTEETSTETTQ/AYLELSSLRSEDTAV HHCATDTV FRENCULPSALVYSSLVENGELDITTSBEGDL*LINGGE RTRRD*QLPEAGGPGLQEDLQLGELDITTSBEGDL*LINGGE ELVDGLVVPSALVYALLEAPPVEPRPTEGQSLAALANRGOE ARGTAACADVRGVLDRLRVKAVTKIREFILOKIYSFKPMINYQ IPQTALLKYRFFYGFLLGNERBATAKEIRRGAVERGEL ARGTAACADVRGVLDRLRVKAVTKIREFILOKIYSFKPMINYQ IPQTALLKYRFFYGFLLGNERBATAKEIRRGRVERKSPLISKIYLSYYR SYLGELMVYGYEVARKDOLMSVEDTAKRGFFSKSELKSNITF	Ì		1	
AKEKLKSIEKARKGAISSEEIIIYAHRISASNAVCAPLIWVEGD PREPPYDTLEMRSGLIGGMNDPSTAVGHLPGDALA/RRKIAR CPCSTVS/NGSQMTCR+INIILILQKSVCBL 5878 950 2113 GLWKCMGLGSPHTHEVOP+PTERQGGPO\VPVALIGNERPHYLY RMLSSLLSAQOSPGMTVTVFIDGYTSPEPMVVALIGNERPHYLY ISIKNARVSQHYKASLTATENIPPERKEAVVLEGRIGHTE ISIKNARVSQHYKASLTATENIPPERKEAVVLEGRIGHTE ISIKNARVSQHYKASLTATENIPPERKEAVVLEGRIGHTE ISIKNARVSQHYKASLTATENIPPERKEAVVLEGRIGHTE ISIKNARVSQHYKASLTATENIPPERKEAVVLEGRIGHTE ISIKNARVSQHYKASLTATENIPPERKEAVALGRIGHTE ISIKNARVSQHYKASLTATENIPPERKEAVALGRIGHTE ISIKNARVSQHYKASLTATENIPPERKEAVALGRIGHTENDPALLIKYETMPG LGWVLRRSLYKEELEPKWPTPEKLIMDMMWRMPEQREGRECII PDVSRSYHGIVGLINMAGYFHEAYFKKAKKENTYDGYOLENVOSI. KKEAYSVEVHRLISEASVLDHSKRYCEESPILPDTECHTYVAFIE MEKDDDFTTWTQLAKCLHIMDLDVRGNIRGIKMELIFEKKNHFLVV GVPASPYSVKKPPSVTIPILEPPPERGAGRAPEOT 5879 3 981 RLTEBAANGSGSRAAGWAGSPPTLIPLSFFFERCAATHASSDED GTINGGASEAGEDREAPGKREIFILTATAMLTFYITIMTAGKULVI ALAMVRYYMEKGTHRGLYKSIGKTLKFQTFALLEIVCLIGIV PTSVIVTGYOVSSRIFMVMLITHSIKPTJTMATGAULVI SITKYSFYTSSLLDHLYPITIKARATHFQTFALLEIVCLIGIV PTSVIVTGYOVSSRIFMVMLITHSIKPTJTMATAGHLTI AALPHVKKTGMFSIRLENYXNVSPPYYPFLLITMAGSYTDLFPQI YFHMLRGRRKVLHG\G*L*KRMIK*SLQTRCFFQNNDPYLSPSPF NNNKKQLCEISMIVMFLKI SLMCLVAGGLGLGFSSGNPLQRAGILARPRERAGTFSALTACSA SVTISKAKSSGMWPSASPDBSPVYLERPFGGVQLPSGTGWVLSD *KKKRGCSS/WLSQPOHEREKEVVLLRRSMABGERABAADUL CRELAMETHQLERFILTATAHMCCHLAKQLERQHAQRNVGERSP DQSEHTDGHTSVQSVIEKLQEENRILKQLEKYINDLESKINGLEKIND ASKDEVVRGHAGLGCLQIPHEPELMKREISRINGLEEKING ASKOLEBERVNASCYVSGTTIKISMINQLEKKINGLEEKIND ARVKGLAASRTARDBAABRRVQMLEGOLLAYKDDMESRADRER AQSRIGELBERVASLHHOVSHKQDSREPDAGRHAGSKTAKYLA ADALELMYPGGWRPGTSGOOPEPPABGGHPGAAQRGGDLQCH CLQCFSDEQGEELLRHVABCCQ 5881 26 441 GGTHFSPTEARFAQHLIMDCTRRILFILVAAATGTHAQVOLLOGS SEVKKEGASVWSCYVSGTTIKISMINVQAPAGGGLE*MGPPD LQOVFTTYPQKPGGRVGSTTIKISMINVQAPAGGALE*MGPPD LQOVFTTYPQKPGGRVGSTTIKISMINVQAPAGGALE*MGPPD LQOVFTTYPQKPGGRVGSTITKISMINVQAPAGGALE*MGPPD LQOVFTTYPQKPGGRVGSTITKISMINVQAPAGGALE*MGPPD LQOVFTTYPQKPGGRVGSTITKISMINVQAPAGGALE*MGPPD RYSKOVBLESLQQIERVGSTIDVIGSSENIALBINQTTATGOVOLLOGS SEVKEGASIVNSCYVSGTTIKISMINVQ			1	
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RMLRSLLSAQOVSPQMITVFIDGYYEPMDVVALFGLRGIGHTT ISINARVSQHYASLITATFNLFPERKEMDVVALEGULDIAVDFFS FLSQSIHLLEEDDSLYCISAMNDQGYEHTAEDPALLYRVTMPG LGWYLRRSLYKEELEPKWPTPEKLUMDUMMEMPEQRRGECII PDVSRSYHFGIVGLINNNGYFHRAYFKKHKPRTVPCVQLRNYDSL KKEAYEVEVÜRLLSEABVLDHSKNPCEDSPLPDTEGHTYVAFIR MEKDDDFTTWTQLAKCLHIWDLDVRGNIHRGUWRLFRKKNHFLVV GVPASPYSVKKPPSVTFIFLEPPKEEGAPGAPEGT S879 3 981 RLTSAAAASGSSRAGGMAGSPPTLLDLSSTSPRCAATMASSDED GTNGGASEAGEDREAPGKRRRIGFLATAWLTFYDIAMTAGWLVL AIAMVRFYMEKGTHRGLYKSIGKTLKFFQTFALLEIVHCLIGIV PTSVIVTGVQVSSRIFMWALITHSIKPIQNBESVVLFLVAWTVT LEITRYSFYTFSLLDHLPYFIKANFFILIPYGVAGELLTIY AALDHVKKTGMFSIRLPNKYNVSPDYYYFLLITMASYIPLFPQL YFFMLKGRGKVLHGGG-L-KRMIK-SLQTRCFFGNNDDYLSPSF NNKNKQLCEISMIVWFLKI S880 1138 1324 SLWCLVAGGIGLGFSSONFLQRAGILARPERGRTFSALTACSA SVTSKKSSSGMWPSAASDRDSPVPLRPPBFVQLPSGTGWVLSD -KKKRGRCSS/WLSQPQHEREKEVVLLRRSMABGERRARASDVL CRSLANETHQLRRTLTATAHMCQHLAKCLDERQHAQRNVGERSP DQSEHTDGHTSVGSVIELUGEBRLKKGVXTHVEDLNAKWQRYN ASRDEYVRGLHAQLRGLQIPHEPELMRKEISRLNRQLEEKINDC AEVKQBLAASRTARDAALBRVQMLEQGILAYNDDFMSERADRER AQSRIQLEEKVASLLHQVSWRDOSREPDAGRIHAGSKTAKYLA ADALELMVPGGREPGTGSQQPEPPAEGHPGAQAQRGQGDLQCPH CLQCFSDEQGEELLRAVABCCQ SGVKRGASSVMVSCVVSGYTLTKLSMHWYGAPGKGLE-MGPPD LQDVETIYPQKFQGRVSMTEETSTETTQ/AYLELSLRSEDTAV HHCATDTV 5882 2407 2216 SGCVENLYSHSLEYNPEWISVQSAVAPAQLAINSDGDL*LHSGE RTRRD-QLPEAGGGLQBPLQGEILDFTLDETVDGVVDLR MEQMLGAPQSDLSSISSEIRTLQSGCSAMNIRLRNRQAVRGKLG MECMLGAPGSDLSSISSEIRTLQSGCSAMNIRLRNRQAVRGKLG FLYDGLVVPSALVATAILBEPUTPERPELGQELDAKAANREGE ARGTAACADVRGVLDRIKKVAVTKIREPILDKIYSFRKPMTNYQ IPQTALLKYFFFYQFLLGSGRBARKUREPTETVTTLYSYFRKPMTNYQ IPQTALLKYFFFYQFLLGRURGREARAKGIPEYYETLLSKYLLYYY	5000	250		
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No:	SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
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location	L .		ł	Glutamic Acid. F=Phenylalanine C-Clusine
Loleucine, M-Methionine, N-Apparagine, perioduc of first amino acid residue of amino acid sequence S-Serine, T-Threonine, V-Valine, amino acid sequence S-Serine, T-Threonine, V-Valine, amino acid sequence S-Serine, T-Threonine, V-Valine, amino acid sequence S-Serine, T-Threonine, V-Valine, which is sequence S-Serine, T-Threonine, V-Valine, which is sequence S-Serine, T-Threonine, V-Valine, which is sequence S-Serine, T-Threonine, V-Valine, which is sequence S-Serine, T-Threonine, V-Valine, which is sequence S-Serine, T-Threonine, V-Valine, which is sequence S-Serine, T-Threonine, V-Valine, which is sequence S-Serine, T-Threonine, V-Valine, which is sequence S-Serine, T-Threonine, V-Valine, which is sequence S-Serine, T-Threonine, V-Valine, which is sequence S-Serine, D-Serine, V-Valine, which is sequence S-Serine, D-Serine, V-Valine, W-Valine	,		1	H=Histidine I=Isoleucine V-Ivoine
to first amino acid residue of amino acid sequence PETELICANYOSIDE, X-UNKINOW, *=stop Codon, /=possible nucleotide deletion, /=possible nucleotide insertion) PETELICANYOSIDE nucleotide insertion PETELICANYOSIDE NUCLEOLIDERPHYTERYASPSSAL SINOTIPNERTMOLLOGLOVEVENYURVARASPSSARGOLVPI, NNYDMMIGJUMB ** ERRADDSKEVESPOOLNARSPESPESTARGOLVPI, NNYDMMIGJUMB ** ERRADDSKEVESPOOLNARSPESTARGOLVPI, NNYDMMIGJUMB ** ERRADDSKEVESPOOLNARSPESTARGOLVPI, NNYDMMIGJUMB ** ERRADDSKEVESPOOLNARSPESTARGOLVPI, NNYDMMIGJUMB ** ERRADDSKEVESPOOLNARSPESTARGOLVPI, NNYDMMIGJUMB ** ERRADDSKEVESPOOLNARSPESTERGEPEPP PETELOGVOKOGOSVOSISSINDRINGISTITTEIRELBANGVOLVAR SOPOLRALPARAELINIHHLMVELKKIKPR FERENOVKOGOSVOSISSINDRINGISTITTEIRELBANGVOLVAR EETRELAGOHEDDSLINOKEEDEMER NRODYEMELASLARAN MKSSEPGSGLILISTYSGLOVENIELERRIVININGVENDLOG ELSKIRGERISTELBERESELERE ERRIVER NRADSPESTARGAREPSESTAR	ì			LaLeucine Mamethionine Nacharagine
amino acid residue of amino acid sequence source source sequence source sequence seq			1	Paproline OrGlutamine Pancinine
residue of amino acid sequence				S=Serine TaThreonine Valline
amino acid sequence Codon, /-possible nucleotide insertion		4		W-Truntonhan V-Turnging V-Valley
Sequence Sequence	1	1	1	Codon /-possible muslestide deletide
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I PSTSDTKSDTATGGESAGHATSSQEPSGCSDQRPAEDLNIRV. RLTKKLEERREEKRKEEQREIKKEI ERRKTGKEMLDYKRYQE. ELTKRMLEERNREKAEDRAARER IKQOIALDRAERAARPATKK EVEAAKAALLAKQAEMEVKRESYARERSTVARIQFRLPDGSSI TNQFPSDAPLEEARQFAAQTVGNTYGHFSLATMFPRREFIKEDL KKKLLDLELAPSASVVLLP/ALFINF*AGRPTASIVHSSGDII CKKKLLDLELAPSASVVLLP/ALFINF*AGRPTASIVHSSGDII TLUSTVLYPFLAIMRLISNFLPSNPPPTQTSVRVTSSEPPNPA SSKSEKREPVRKVLEKRGDDFKKEGKIYRLRTQDDGEDENNTI NGRSTQQM AAGGRESRLSRSMPTGFSKSPSGVRCCG\RR\AMEDKDEFLDI YMFRQIIAVVLGVIMGVLPLRGFELGIAGFCLINAGVIYLYFSI YLQIDEEYGGTWELTKEGFMTSPA/IVHGHLDHLLHCHPL*LI VYSSQVLPIQSKGPS 5886 86 1341 PFRGRALTLKKQFPGVAPPSLGTCHKSDPGRPAAQSQPPSPGG GTFGLLSFRMWTRITWTLKKHFVGYPTNSDFELKTSELPPLKN EVLLEALFLTVDPYMRVAAKRLKRGDTMMGQQVAKVVESKNVAI PKGTIVLASFGWTTHSISDCKDLEKLLTEMPDTIPLSLAIGTW MPGLTAYFGLEIGLGVKGGFTVMVNAAAGAVGSVVGGJAKLKG KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLBETLKKASPDGY DCYPDNVGGEFSNTVIGQMKKFGRIAICGAISTTNRTGPLPPGG PPBIGIYGELERMEFVVYFNYGNGDARGKALDLKRWULELPYFVI D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFF NMPAAFMGMLKGDNLGKTIVKA PAGCGGCGATATCPFGGFPMOSLGDEAARSPAAPGGAPGLIGLER RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRPGPPGLGGFF PARGLPQSRTL/FVLCVCDLSPAQCDINCCCDEDCSSVDFSVFS ACSPVVTGDSQFCSGKAVIYSLNFTANPPGRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLMABSY VSFITKLDIFTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTONNB AAPLVNQAVKCTRKINLGGETEALSMAPYSSPBILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVMAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLIGTVSSVVVPLQQKFEHHFLG ENYNGPVFTGNFOYSVVCPLQQKFEHHFLG ENYNGPVFTGNFOYSVVPLQQKFEHHFLG ENYNGPVFTGNFOYSVVPLQQKFEHHFLG ENYNGPVFTGNFOYSVVPLQQKFEHHFLG ENYNGPVFTGNFOYSVVPLQQKFEHHFLG ENYNGPVFTGNFOYSVVPLQQKFEHHFLG ENYNGPVFTGNFOYSVVPLQQKFEHHFLG ENYNGPVFTGNFOYSVVPLQQKFEHHFLG ENYNGPVFTGNFOYSVVPLQQKFEHHFLG ENYNGPVFTGNFOYSVVPLQQKFEHHFLG ENYNGPVFTGNFOYSVVPLQQGKFEHHFLG ENYNGPVFTGNFOYSVVPLQQGKFEHHFLG ENYNGPVFTGNFOYSVVPLQQGKFEHHFLG ENYNGPTGNFOYSVVPLGAAGFOPHKGSGIIQTTNRYGGLTI	1			
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GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFELKTSELPPLKNG EVLLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVESKNVAI PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVG MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGG KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLBETLKKASPDGY DCYPDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGFE PPEIGIYQELRMEAFVVYRMGGDARQKALKDLLKWVLELPYFVI D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCFCRGPRWDSLGDEAARSPAAFGGAPGLLGLEE RPDRCHPGGDDGPQLHRGSPG\SPSELSRRPGPPBGLGGPE PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNF AAFLVNQAVKCTRKINLEGCEEIEALSMAFYSSPEILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGGLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ				VYSSQVLPIQSKGPS
EVLLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVESKNVAI PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVC MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVQQIAKLKGG KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLBETLKKASPDGY DCYPDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGFI PPEIGIYQELRMEAFVVYRWQGDARQKALKDLLKWVLELPYFVI D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSIGDEAARSPAAPGGAPGLLGLRE RPDRCHPGGDDRGPQLHRGSPG\SPSELSRRPGPPGLPGLQFPE PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNABSY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGGLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ	5886	86	1341	PFRGRALTLKKQPRPGVAPPSLGTCHKSDPGRPAAQSQPPSPGS
EVLLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVESKNVAI PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVC MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVQQIAKLKGG KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLBETLKKASPDGY DCYPDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGFI PPEIGIYQELRMEAFVVYRWQGDARQKALKDLLKWVLELPYFVI D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSIGDEAARSPAAPGGAPGLLGLRE RPDRCHPGGDDRGPQLHRGSPG\SPSELSRRPGPPGLPGLQFPE PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNABSY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGGLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ				GTFGLLSFRMVRTKTWTLKKHFVGYPTNSDFELKTSELPPLKNG
PKGTIVLAS PGWTTHS I SDGKDLEKLLTEWPDTIPLS LALGTWO MPGLTAY FGLLE I CGV KGGETVMVNAAAGAVGS VVGQIAKLKGG KVVGAVGS DEKVAYLQKLG FDVVFNY KTVESLEETLKKAS PDGY DCYPDNVGGEF SNTVIGQMKKFGRIAICGAIS TYNRTGPLPP GFE PPEIGIY QELRMEA FVVYRWGGDARQKALKDLLKWVLELPY FVI D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEG FE NMPAA FMGMLKGDNLGKTIVKA PPEGROCRATRC FCREPR FWDSLGDEAARS PAAPGGAPGLIGLEE RPDRCHPGGDDGPQLHRGS PG SPSELS RRPGP PGLOG PFE PAPGLP GSRTL / PVLCVCDLS PAQCDINCCCD PDCS SVDF SVFS ACSVPVVTGDS GFCSQKAVIYS LNFTANP PQRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL / NENNFDTLMKTS DGFTLNAES YVSFTTKLDIPTAAKYEYGVPLQTSDS FLRFPSSLTS SLCTDNNF AAFLVNQAVKCTRKINLEGCE I EALSMAFYSS PEILRVPDS FR KVPITVQS IVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLS FVLGTVSS VVVPLQQKFEIHFLQ ENTOPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGGLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ	1			EVLLEALFLTVDPYMRVAAKRLKEGDTMMGQQVAKVVESKNVAL
MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGC KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLBETLKKASPDGY DCYPDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGE PPEIGIYQELRMEAFVVYRWQGDARQKALKDLLKWVLELPYFVI D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLRE RPDRCHPGGDDRGPQLHRGSPG\SPSELSRRPGPPGLPGLQGPE PAPGLPQSRTL\PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKXI\NENNFDTLMKTSGFTLNABSY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNF AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPBILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVW LEVKYSLTYTDAGEVTKAALSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGGLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ				PKGTIVLASPGWTTHSISDGKDLEKLLTEWPDTIPLSLALGTVG
KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLBETLKKASPDGY DCYPDNVGGEFSMTVIGQMKKFGRIAICGAISTYNRTGPLPPGF PPEIGIYQELRMEAFVVYRNQGDARQKALKDLLKWVLELPYFVI D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAPGGAPGLLGLFE RPDRCHPGGDDRGPQLHRGSPG\SPSELSRRPGPPGLQGFE PAPGLPQSRTL\PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKXI\NENNFDTLMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPBILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFIQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ	1		ĺ	MPGLTAYFGLLEICGVKGGETVMVNAAAGAVGSVVGQIAKLKGC
DCYPDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGE PPEIGIYQELRMEAFVVYRWQGDARQKALKDLLKWVLELPYFVI D+LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAFGGAPGLLGLRE RPDRCHPGGDDRGPQLHRGSPG\SPSELSRPGPPPGLPGLQGPE PAPGLPQSRTL\PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL\NENNFDTLMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNP AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPEILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ				KVVGAVGSDEKVAYLQKLGFDVVFNYKTVESLBETLKKASPDGY
PPEIGIYQELRMEAFVVYRWQGDARQKALKDLLKWVLELPYFVI D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAFGGAPGLLGLRE RPDRCHPGGDDRGPQLHRGSPG\SPSELSRPPGPPGLPGLQGPF PAPGLPQSRTL\PVLCVCDLSPAQCDINCCCDPDCSSVDFSVPS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL\NENNFDTLMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNF AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPBILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGGLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ	1		ľ	DCYPDNVGGEFSNTVIGQMKKFGRIAICGAISTYNRTGPLPPGP
D*LQANTLVYKSMKSAKPSLEYISEKLVSG\KIQYKEYIIEGFE NMPAAFMGMLKGDNLGKTIVKA APGCRGCRATRCPCRGPRWDSLGDEAARSPAAFGGAPGLLGLRE RPDRCHPGGDDRGPQLHRGSPG\SPSELSRRPGPPGLPGPGP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNABSY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNF AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPBILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ				
NMPAAFMGMLKGDNLGKTIVKA 5887 1937 104 APGCRGCRATRCPCRGPRWDSIGDEAARSPAAPGGAPGLIGLRE RPDRCHPGGDDDRGPQLHRGSPG/SPSELSRRPGPPBLPGLQGPE PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNABSY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNF AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPBILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGGLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ				
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RPDRCHPGGDDRGPQLHRGSPG/SPSELSRRGPPGLPGLQGFP PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDFDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCHHITN*NLHYPLLIQXXI/NENNFDTLMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNF AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPBILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGGLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ	5887	1937	104	
PAPGLPQSRTL/PVLCVCDLSPAQCDINCCCDPDCSSVDFSVFS ACSVPVVTGDSQFCSQKAVIYSLNFTANPPQRVFELVDQINPSI FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNARSY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNF AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPBILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ				
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FCIHITN*NLHYPLLIQKYL/NENNFDTLMKTSDGFTLNAESY VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNF AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPBILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGGLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ				ACSVPVVTGDSOFCSOKAVIYSLNETANPPOPVEFLUDOTNET
VSFTTKLDIPTAAKYEYGVPLQTSDSFLRFPSSLTSSLCTDNNF AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPBILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ				FCIHITN*NIHYPLLIOKYI, /NENNEDTI METCOCETI NADOV
AAFLVNQAVKCTRKINLEQCEEIEALSMAFYSSPBILRVPDSRK KVPITVQSIVIQSLNKTLTRREDTDVLQPTLVNAGHFSLCVNVV LEVKYSLTYTDAGEVTKADLSFVLGTVSSVVVPLQQKFEIHFLQ ENTQPVPLSGNPGYVVGLPLAAGFQPHKGSGIIQTTNRYGQLTI LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ				
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LHSTTEQDCLALEGVRTPVLFGYTMQSGCKLRLTGALPCQLVAQ		1		
				KVKSLLWGQGFPDYVAPFGNSQGP/ADMLDWVPIHFITQSFNRK
				DSCQLPGALVIEVKWTKYGSLLNPQAKIVNVTANLISSSFPEAN
				SGNERTILISTAVTFVDVSAPAEAGFRAPPAINARLPFNFFFPF
V	L			V

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	Amino actu segment containing signal peptide
			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
İ	sequence	Jequeee	\=possible nucleotide insertion)
5888			
2000	375	2302	LLCRTPGVAMQRADSEQPSKRPRCDDSPRTPSNTPSAEADWSPG
	1		LELHPDYKTWGPEQVCSFLRRGGFEEPVLLKNIRENEITGALLP
			CLDESRFENLGVSSLGERKKLLSYIQRLVQIHVDTMKVINDPIH
	1		GHIELHPLLVRIIDTPQFQRLRYIKQLGGGYYVFPGASHNRFEH
		<u> </u>	SLGVGYLAGCLVHALGEKQPELQISERDVLCVQIAGLCHDLGHG
		[PFSHMFDGRFIPLARPEVKWTHEQGSVMMFEHLINSNGIKPVME
		1	QYGLIPEEDICFIKEQIVGPLESPVEDSLWPYKGRPENKSFLYE
	j	1	
		1	IVSNKRNGIDVDKWDYFARDCHHLGIQNNFDYKRFIKFARVCEV
			DNELRICARDKEVGNLYDMFHTRNSLHRRAYQHKVGNIIDTMIT
	1	ł	DAFLKADDYIEITGAGGKKYRISTAIDDMEAYTKLTDNIFLEIL
		1	YSTDPKLKDAREILKQIEYRNLFKYVGETQPTGQIKIKREDYES
}			LPKEVASAKPKVLLDVKLKAEDFIVDVINMDYGMQEKNPIDHVS
		ł	FYCKTAPNRAIRITKNQVSQLLP\EKFAEQ\LIRVYCKKVDRKS
			LYA\ARQYFVQW\CADR\NFT\KPQDGRCY*PPTP*HPQKKGW\
1			NDSTFSPKIPTRLPRRLPKSRV\QLFKDDPM
5889	1831	731	
1 3003	1031	/31	LPAACGRPVTARPRQAPEGRSGRPRDLDPYPPQVFPPRPDRVAI
		1	VTGGTDGIGYSTAKHLARLGMHVIIAGNNDSKAKQVVSKIKEET
			LNDKET*VLLCCPGWLCLWNSSDPPTSASRGAGTTGVHHHFLLK
		l.	FGIFIL\DLASMTSIRQFVQKFKMKKIPLHVLINNAGVMMVPQR
		1	KTRDGFEEHFGLNYLGHFLLTNLLLDTLKESGSPGHSARVVTVS
1	1		SATHYVAELNMDDLQSSACYSPHAAYAQSKLALVLFTYHLQRLL
į.			AABGSHVTANVVDPGVVNTDLYKHVFWATRLAKKLLGWLLFKTP
Ĭ	ſ	ĺ	DEGAWTSIYAAVTPELEGVGGRYLYNKKETKSLHVTYNQKLQQQ
1		i	LWSKSCEMTGVLDVTL
5890	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
		200	GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
1	1	1	
1		ł	LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
1	1		ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
	i		PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
			RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
			KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
			AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
			LVRQIP\NTAIMMATYELVVYLLNG
5891	1322	200	FRRGWSAAGRAVPVAFCSRISASSPRRPRGAVRLQSGTEAACRS
			GRPDPRPASAAGGHAGERMSQRDTLVHLFAGGCGGTVGAILTCP
	Į.		LEVVKTRLQSSSVTLYISEVQLNTMAGASVNRVVSPGPLHCLKV
		1	· · · · · · · · · · · · · · · · · · ·
1	1]	ILEKEGPRSLFRGLGPNLVGVAPSRAIYFAAYSNCKEKLNDVFD
1		İ	PDSTQVHMISAAMAGFTAITATNPIWLIKTRLQL*/SQGTAGKR
1			RMGAFECVRKVYQTDGLKGFYRGMSASYAGISETVIHFVIYESI
1	1		KQKLLEYKTASTMENDEESVKEASDFVGMMLAAATSK\LVATTI
1	1		AYPHEVVRTRLREEGTKYRSFFQTLSLLVQEEGYGSLYRGLTTH
1	1		LVRQIP\NTAIMMATYELVVYLLNG
5892	1764	379	VVLRVCGRLSVNSAVSSRTGGWSAGLTCAMORLOVVLGHLRGPA
			DSGWMPQAAPCLSGAPHASAADVVVVHGRRTAICRAGRGGFKDT
1	1		TPDELLSAVMTAVLKDVNLRPEQLGDICVGNVLQPGAGAIMARI
1	Į.		AQFLSDIPETVPLSTVNRQCSSGLQAVASIAGGIRNGSYDIGMA
			l I
			CGVESMSLADRGNPGNITSRLMEKEKARDCLIPMGITSENVAER
1	1		FGISREKQDTFALASQQKAARAQSKGCFQAEIVPVTTTVHDDKG
	1		TKRSITVTQDEGIRPSTTMEGLAKLKPAFKKDGSTTAGNSSQVS
J]		DGAAAILLARRSKAEELGLPILGVLRSYAVVGVPPDIMGIGPAY
}			AIPVALQKAGLTVSDVDIFEINE\AFASQAAYCVEKLRLPP*EG
	[*TPLGGASGP*GHPLGLHWGHVQVITLAQ*S*SARGKRAYRSGC
]	PCAIGSWNGSPLPVFEYPWGT
5893	3	1653	ILSKRRCQKAKTKELMAKKVAVIGAGVSGLISLKCCVDEGLEFT
l			CFERTEDIGGVWRFKENVEDGRASIYQSVVTNTSKEMSCFSDFP
I	['	MPEDFPNFLHNSKLLEYFRIFAKKFDLLKYIQFQTTVLSVRKCP
1	1		
			DFSSSGQWKVVTQSNGKEQSAVFDAVMVCSGHHILPHIPLKSFP
	1		GMERFKGQYFHSRQYKHPDGFEGKRILVIGMGNLGSDIAVELSK
			NAAQVFISTRHGTWVMSRISEDGYPWDSVFHTRFRSMLRNVLPR
}			TAVKWMIBQQMNRWFNHENYGLBPQNKYIMKEPVLNDDVPSRLL
L	_		CGAIKVKSTVKELTETSAIFEDGTVEENIDVIIFATGYSFSFPF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ĺ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	
		1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
İ	'		LEDSLVKVENNMVSLYKYIFPAHLDKSTLACIGLIQPLGSIFPT
1			AELQARWVTRVFKGLCSLPSERTMMMDIIKRNEKRIDLFGESQS
ĺ	ĺ		QTLQTNYVDYLDELALEIGAKPDFCSLLFKDPKLAVRLYFGPCN
			SY*YRLVGPGQWEGARNAIFTQKQRILKPLKTRALKDSSNFSVS
			FLLKILGLLAVVVAFF\CQLQWS
5894	174	1673	RYSPKKVLQNKESSLKLGMATALVSAHSLAPLNLKKEGLRVVRE
			DHYSTWEQGFKLQGNSKGLGQEPLCKQFRQLRYEETTGPREALS
			RLRELCQQWLQPETHTKEHILELLVLEQFLIILPKBLQARVQEH
ļ			HPESREDVVVVLEDLQLDLGETGQQVDPDQPKKQKILVEEMAPL
1			KGVQEQQVRHECEVTKPEKEKGEETRIENGKLIVVTDSCGRVES
ł	1		
			SGKISEPMEAHNEGSNLERHQAKPKEKIBYKCSEREQRFIQHLD
			LIEHASTHTGKKLCESDVCQSSSLTGHKKVLS*ERKVIQC\HGV
			LGKAFQRSSHLVRHQKIHLGEKPYQCNECGKVFSQNAGLLEHLR
}			IHTGEKPYLCIHCGKNFRRSSHLNRHQRIHSQEEPCECKECGKT
1			FSQALLLTHHQRIHSHSKSHQCNECGKAFSLTSDLIRHHRIHTG
•			EKPFKCNICQKAFRLNSHLAQHVRIHNEEKPYQCSECGEAFRQR
			SGLFQHQRYHHKDKLA
5895	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGB
			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
			EATELQPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
			FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
			EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPOO
1			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
l	i		RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
			DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
1			TVEQLRCEHCARF\LADRF4EGVCPFCGYEEARGDQCDKCGKLI
,			
			NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
	<u> </u>		PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
	,		GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPBQVDLYQ
	ĺ		FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
			K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
			LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
			GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
			QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
			LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
1	J		LMDEVTKQGNIVRELKAQKADKNEVAAEVAKLLDLKKQLAVAEG
			KPPEAPKGKKKK
5896	2967	86	HPSLLGAIPFYPPPSSPWPPPLYLFWNSHRKSRHFINQRGIHGE
1			MRLFVSDGVPGCLPVLAAAGRARGRAEVLISTVGPEDCVVPFLT
			RPKVPVLQLDSGNYLFSTSAICRYFF\LLSGWEQDDLTNQWLEW
			EATELOPTLSAALYYL\VVQGKKG\EDVLGSVRRTLTHIDHSLS
			RQ\NCPFLAGETESLADIVLWGALYPLLQDPAYLPEELSALHSW
1			FQTLSTQ\EPCQR\AARRLVLKQ\QGVLALR\PYLQKQPQPSPA
j	j		EGKGLSPIEPEEEELATLSEEEIAMAVTAWEKGLESLPPLRPOO
			NPVLPVAGERNVLITSALPYVNNVPHLGNIIGCVLSADVFARYS
			RLRQWNTLYLCGTDEYGTATETKAL\EEGLTPQEICDKYHIIHA
	Į.		DIY\RWFNISFDIFGRTTTPQQ\TKIT\QDIFQQLLKRGFVLQD
			TVEQLRCEHCARF\LADRFVEGVCPFCGYEEARGDQCDKCGKLI
	İ		NAVELKKPQCKVCRSCPVVQSSQHLFLDLPKLEKRLEEWLGRTL
			PGSDWTPNAQFITPFFGFREWPSKPRWQ*TRDLK\WGNPGTP*E
	J		GFEDK\VFYVWFDATIGYLSITANYTDQWERWW\KNPEQVDLYQ
			FM\AKDNVPFHSLVFPSSALGAEDNYTL\VSHLIATEYLNYEDG
			K\FSKSRGVGVFRDM\AHDTGIPPDISRFYL\LYIRPEGK\DSA
			FSWTDLLLKNNS\ELLNNLGNFINRA\GMFVSKFFGG\YVPEMV
			LTPDDQRLLA\HVTLELQHYHQ\LLEKVRIRDALRSILTIS\RH
			GNQYI\QVNEPW\KRIKGSEADRQRAGTVTGLAVNIAALLSVML
			QPYMPTVSATIQAQLQLPPPACSILLTNFLCTLPAGHQIGTVSP
			LFQKLENDQIESLRQRFGGGQAKTSPKPAVVETVTTAKPQQIQA
			· · · · · · · · · · · · · · · · · · ·

SEQ Predicted Predicted end Amino acid segment conta ID beginning nucleotide (A=Alanine, C=Cysteine,	ining signal peptide
	Diagramia laid
NO: nucleotide location Glutamic Acid, F=Phenyla	D=Aspartic Acid, K=
location corresponding H=Histidine I=Isoleucin	danine, G≅Giycine,
	e, K=Lysine,
, , , , , , , , , , , , , , , , , , , ,	
and the second s	
residue of amino acid W=Tryptophan, Y=Tyrosine	, X=Unknown, *=Stop
amino acid sequence Codon, /=possible nucleo	tide deletion,
sequence \=possible nucleotide in	
LMDEVTKQGNIVRELKAQKADKNE	VAAEVAKLLDLKKQLAVAEG
KPPEAPKGKKKK	
5897 2967 86 HPSLLGAIPFYPPPSSPWPPPLYL	FWNSHRKSRHFINORGTHGE
MRLFVSDGVPGCLPVLAAAGRARG	
RPKVPVLQLDSGNYLFSTSAICRY	
EATELQPTLSAALYYL\VVQGKKG	/ EDIG COURTE MITTERS C
RQ\NCPFLAGETESLADIVLWGAL	
FQTLSTQ\EPCQR\AARRLVLKQ\	QGVLALR/PYLQKQPQPSPA
EGKGLSPIEPEEELATLSEEEIA	
NPVLPVAGERNVLITSALPYVNNV	
RLRQWNTLYLCGTDEYGTATETKA	L\EEGLTPQEICDKYHIIHA
DIY\RWFNISFDIFGRTTTPQQ\T	KIT\QDIFQQLLKRGFVLOD
TVEQLRCEHCARF\LADRFVEGVC	PFCGYEEARGDOCDKCGKLT
NAVELKKPQCKVCRSCPVVQSSQH	
PGSDWTPNAQFITPFFGFREWPSK	
GFEDK\VFYVWFDATIGYLSITAN	
FM\AKDNVPFHSLVFPSSALGAED	
K\FSKSRGVGVFRDM\AHDTGIPP	DICDEAL/ L'ALDEGAN DOS
FSWTDLLLKNNS\ELLNNLGNFIN	DISKFIL (BIIKPEGK (DSA
I TO DO DE LA NOTA DE CONTROL DE LA CONTROL DE LA CONTROL DECENTROL DE CONTROL DECENTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL DE CONTROL	RA (GMF VSRFFGG (YVPEMV
LTPDDQRLLA\HVTLELQHYHQ\L	LEKVRIRDALRSILTIS\RH
GNQYI\QVNEPW\KRIKGSEADRQ	
QPYMPTVSATIQAQLQLPPPACSI	
LFQKLENDQIESLRQRFGGGQAKT	
LMDEVTKQGNIVRELKAQKADKNE	VAABVAKLLDLKKQLAVAEG
KPPEAPKGKKKK	
5898 2967 86 HPSLLGAIPFYPPPSSPWPPPLYL	FWNSHRKSRHFINQRGINGE
MRLFVSDGVPGCLPVLAAAGRARG	RAEVLISTVGPEDCVVPFLT
RPKVPVLQLDSGNYLFSTSAICRY	FF\LLSGWEODDLTNOWLEW
EATELQPTLSAALYYL\VVQGKKG	EDVLGSVRRTLTHIDHSLS
RQ\NCPFLAGETESLADIVLWGAL;	
FQTLSTQ\EPCQR\AARRLVLKQ\(
EGKGLSPIEPEEEKLATLSEEKIA	
NPVLPVAGERNVLITSALPYVNNV	
RLRQWNTLYLCGTDEYGTATETKAI	STEE CONTROLL INC.
DIY\RWFNISFDIFGRTTTPQQ\TI	KIT/QDIFQQLLKRGFVLQD
TVEQLRCEHCARF\LADRFVEGVCI	
NAVELKKPQCKVCRSCPVVQSSQHI	
PGSDWTPNAQFITPFFGFREWPSKI	
GFEDK\VFYVWFDATIGYLSITANY	
FM\AKDNVPFHSLVFPSSALGAEDN	
K\FSKSRGVGVFRDM\AHDTGIPPI	DISRFYL\LYIRPEGK\DSA
FSWTDLLLKNNS\ELLNNLGNFINF	AAGMFVSKFFGG\YVPEMV
LTPDDQRLLA\HVTLELQHYHQ\LI	EKVRIRDALRSILTIS\RH
GNQYI\QVNEPW\KRIKGSEADRQF	
QPYMPTVSATIQAQLQLPPPPACSII	
LFQKLENDQIESLRQRFGGGQAKTS	
LMDEVTKQGNIVRELKAQKADKNEV	
KPPEAPKGKKKK	
5899 326 1078 NCPKSKEPNGVRAPSLPSPLRAAMA	T COUNTY OT VINAS BEES
The the training of the same	COCOL KIMBADAMANIEO
EANEKAEEIDAKAEBEFNIEKGRLV	
QQKKILMSTMRNQARLKVLRARNDI	
BIRDOT FRUIT DATE	KCKP/QDLLLVEAAVQKAI
EVYQGLLDKLVLQGLLRLLEPVMIV	
PEYMTISQKHVEV\QIDKEA*LAVE	
PEYMTISQKHVEV\QIDKEA*LAVE TLESRLDLSAKQKMPEIRMALFGAN	TNRKFFI
PEYMTISQKHVEV\QIDKEA*LAVE	TNRKFFI
PEYMTISQKHVEV\QIDKEA*LAVE TLESRLDLSAKQKMPEIRMALFGAN	TNRKFFI RMWYHRLSHLHSRLQDLLK
PEYMTISQKHVEV\QIDKEA*LAVE TLESRLDLSAKQKMPEIRMALFGAN 5900 64 1409 KAASRDSPCLEFCFLCGVSSHDLQH GGVIYPALPQPNFKSLLPLAVHHH	TNRKFFI RMWYHRLSHLHSRLQDLLK TASKSLTCAWQQHEDHFEL
PEYMTISQKHVEV\QIDKEA*LAVE TLESRLDLSAKQKMPEIRMALFGAN 5900 64 1409 KAASRDSPCLEFCFLCGVSSHDLQH GGVIYPALPQPNFKSLLPLAVHWHH KYANTVMRFDYVWLRDHCRSASCYN	TNRKFFI RMWYHRLSHLHSRLQDLLK TASKSLTCAWQQHEDHFEL SKTHQRSLDTASVDLCIKP
PEYMTISQKHVEV\QIDKEA*LAVE TLESRLDLSAKQKMPEIRMALFGAN 5900 64 1409 KAASRDSPCLEFCFLCGVSSHDLQH GGVIYPALPQPNFKSLLPLAVHWHH KYANTVMRFDYVWLRDHCRSASCYN KTIRLDETTLFFTWPDGHVTKYDLN	TNRKFFI RMWYHRLSHLHSRLQDLLK TASKSLTCAWQQHEDHFEL SKTHQRSLDTASVDLCIKP WLVKNSYEGQKQKVIQPRI
PEYMTISQKHVEV\QIDKEA*LAVE TLESRLDLSAKQKMPEIRMALFGAN 5900 64 1409 KAASRDSPCLEFCFLCGVSSHDLQH GGVIYPALPQPNFKSLLPLAVHWHH KYANTVMRFPYVWLRDHCRSASCYN KTIRLDETTLFFTWPDGHVTKYDLN LWNAEIYQQAQVPSVDCQSFLETNE	TNRKFFI RMWYHRLSHLHSRLQDLLK TASKSLTCAWQQHEDHFEL SKTHQRSLDTASVDLCIKP WLVKNSYEGQKQKVIQPRI GLKKFLQNFLLYGIAFVEN
PEYMTISQKHVEV\QIDKEA*LAVE TLESRLDLSAKQKMPEIRMALFGAN 5900 64 1409 KAASRDSPCLEFCFLCGVSSHDLQH GGVIYPALPQPNFKSLLPLAVHWHH KYANTVMRFDYVWLRDHCRSASCYN KTIRLDETTLFFTWPDGHVTKYDLN	ITNRKFFI RMWYHRLSHLHSRLQDLLK TASKSLTCAWQQHEDHFEL SKTHQRSLDTASVDLCIKP WLVKNSYEGQKQKVIQPRI GLKKFLQNFLLYGIAFVEN MWYFTSDFSRGDTAYTKLA

			I will all a second and a second asset as
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID NO.	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
<u> </u>	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	Bequestee	 	OKAPEEFELLSKSAI\KHEYIEDVGECHQPHDWDWAQS*ISTHG
			/YKELYLIRYNNYDRAVINTVPYDVVHRWYTAHRTLTIELRRPE
ļ			NEFWVKLKPGRVLFIDNWRVLHGRECFTGYRQLCGCYLTRDDVL
ļ		Ĭ	NTARLLGLQA
5901	1	2121	VAIEQTSLKMMQAVGGAPARPTGEYICNQCGAKYTSLDSFQTHL
			KTHLDTVLPKLTCPQCNKEFPNQESLLKHVTIHFMITSTYYICE
1			SCDKQFTSVDDLQKHLLDMHTFVFFRCTLCQEVFDSKVSIQLHL
			\AVKHSNEKKVYRCTSCNWDFRNETDLQLHVKHNHLENQGKVHK
			CIFCGESFGTEVELQCHITTHSKKYNCKFCSKAFHAIILLEKHL
	ļ		REKHCVFETKTPNCGTNGASEQVQKEEVELQTLLTNSQESHNSH
			DGSEEDVDTSEPMYGCDICGAAYTMETLLQNHQLRDHNIRPGES
	1		AIVKKKAELIKGNYKCNVCSRTFFSENGLREHMQTHLGPVKHYM
\			CPICGERFPSLLTLTEHKVTHSKSLDTGNCRICKMPLQSEEEFL
			EHCQMHPDLRNSLTGFRCVVCMQTVTSTLELKIHGTFHMQKTGN
ļ			GSAVQTTGRGQHVQKLYKCASCLKEFRSKQDLVKLDINGLPYGL
			CAGCVNLSKSASPGINVPPGTNRPGLGQNENLSAIEGKGKVGGL
			KTRCS*LATFKF*VLKVELPEPHPKPFHRGVSRPDSNSTQLKTP
			QVSPMPRISPSQSDEKKTYQCIKCQMVFYNEWDIQVHVANHMID
Ì			EGLNHECKLCSQTFDSPAKLQCHLIEHSFEGMGGTFKCPVCFTV
			FVQANKLQQHIFSAHGQEDKIYDCTQCPQKFFFQTELQNHTMTQ
			HSS
5902	712	209	LKNRRRSRPSIRQSIGSTSVSRWLTSLFTYLDHTADVQ*V*REF IPLKPRQ*ED*MFQSWLHAWGDTLEEAFEQCAMAMFGYMTDTGT
			VEPLQTVEVETQGDDLQSLLFHFLDEWLYKFSADEFFIP\GWGE
			EFSLSKHPQGTEVKAITYSAMQVYNEENPEVFVIIDI
	2106	735	DTPGPSLPSTTAPFSLRSLSFPSRPSYLLPGDPQPLQGRGLPTT
5903	2106	/35	PALFALSAVPGGAASPMPPSGLRLLPLLLPLLWLLVLTPGRPAA
			GLSTCKTIDMELVKRKRIEAIRGQILSKLRLASPPSQGEVPPGP
			LPEAVLALYNSTRDRVAGESAEPEPEPEADYYAKEVTRVLMVET
			HNEIYDKFKOSTHSIYMFFNTSELREAVPEPVLLSRAELRLLRL
			KLKVEOHVELYOKYSNNSWRYLSNRLLAPSDSPEWLSFDVTGVV
	i		ROWLSRGGEIEGFRLSAHCSCDSRDNTLQVDINGFTTGR\RGDL
-			ATIHGMNRPFLLLMATPLERAQHLQS\SRHRQAL\DTNY\CFSF
			HGGRNCLRC/VHC+HLIFRKDL\GW\KWI\HE\PKGYHANFC\L
			GPCPYIWSLDTQYSKVLALYNQ\HKPG\ASAAP\CCVPQALEP\
1			LPIVYY\VGRKPKVEQLSNMIVRSCKCS
5904	3	1126	MMEEIENAINTFKEEQRLIYEELIKEEKTTNNELSAISRKIDTW
			ALGNSETEKAFRAISSKVPVDKVTPSTLPEEVLDFEKFLQQTGG
1			ROGAWDDYDHONFVKVRNKHKGKPTFMEEVLEHLPGKTQDEVQQ
			HEKWYQKFLALEERKKESIQIWKTKKQQKREEIFKLKEKADNTP
-			VLFHNKQEDNQKQKEBQRKKQKLAVEAWKKQKSIEMSMKCASQL
			KEEEEKEKKHQKERQRQFKLKLLLESYTQQKKEQEEFLRLEKEI
1		1	REKAEKAEKRKNAADEISRFQERDLHKLELKILDRQAKEDEKSQ
			KQRRLAKLKEKVENNVSRDPSRLY/NTHQRLGRTNQKDRTNRLW
		1	ATSTYPT*GYSNLETRNTEKSMR
5905	287	2912	MASFPPRVNEKEIVRLRTIGELLAPAAPFDKKCGRENWTVAFAP
			DGSYFAWSQGHRTVKLVPWSQCLQNFLLHGTKNVTNSSSLRLPR
1			QNSDGGQKNKPREHIIDCGDIVWSLAFGSSVPEKQSRCVNIEWH
	1		RFRFGQDQLLLATGLNSGRIKIWDVYTGKLLLNLVDHTGVVRDL
			TFAPDGSLILVSASRDKTLRVWDLRDDGN\MMKVLRGHQNWVY\
			SCAFSPDSSMLCSVGASKAVVAAILV*LRLCWHHSHTGATMVLS WAERVASLATGLGATFTIG*SNLAFVLQGVLYVHRCWSMSTFCF
			SFFLFFFFKVISPTVKYH*LLSKLIFQFYGIGSLTSETNLM*SI
		1	WLSNGFSVLFFGILSDSRDILRL*FNLKFVLIFF*K*CIVSVQK
			KKKPKRIALLOEERLS+DKPPSSHLI+OTEVNIRILFRAILHS*
			LLIPRI*NCI*TYS*IIDPFYIQMTYDRG*FGKNKMVKF*FIEM
1			*LYYFHKIAFSFCNVV*HPCCLPKKFHLAVNILFACSICFSS*A
			QVGDPSLL*TSDYLKGRCQWSNNLLTLRFLSVYFFKNLVVSGKK
			REGGL*YLTLFISVYFS*LVFGINGFQYSFVVKLHCLYFMFRLI
i .	1	i	
	1	l .	FKTTFNKNI*NKICMSALINLKIDFNLIMILESIFFKEELIINA.
			FKLTFNRNI*NRICMSALINLKTDFNLTMTLSIFFKLLIIYNA* YNLN*I*QF*YKMCHFVLCMSE*SYNICLFIAGF\LWNMDKYTM

SEO	Predicted	Predicted end	I have a second of the second
ID	beginning	nucleotide	
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
j	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	Parcoline, Q=Glutamine, R=Arginine
	amino acid	residue of	S=Serine, T=Threonine, V=Valine
1	residue of	amino acid	W=Tryptophan, Y=Tvrosine Y-Unknown + Ch-
J	amino acid sequence	sequence	Codon, /=possible nucleatide deletion
	sequence	ļ <u>.</u>	\=possible nucleotide insertion\
į			IRKLEGHHHDVVACDFSPDGALLATASYDTDVVIMDDUNGDTVA
			EFGHLEPPPTPIFAGGANDRWVRSVSFSHDGLEVAGI ADDVAVD
			FWKIDEDYPVQVAPLSNGLCCAFSTDGSVI.AAGTUDGGVVENAM
5906	146	2038	PRQVPSLQHLCRMSIRRVMPTQEVQELPIPSKLLEFLSYRI
		2030	REGAGSGRMASGA\YNPYIEIIEQPRQRGMRFRYKCEGRSAGSI
			PGEHSTDNNRTYPSIQIMNYYGKGKV\RITLVTK\NDPYKPHPH
1		1	DLVGKDCRD\GYYEAEFGQE\RRP\LFFQN\LGIRCVKKKEVKE
1		İ	A\IITR\IKAGINPFDVP*KQLNDIEDCDLDVVRLWFRVFLPDG HGNL\TTALPPV\VSSPIYDNRAPNTAELRVCRVNKNCGSVRGG
			DEIFLLCDKVQKDDIEVRFVLNDWEAKGIFSQADVHRQVAIVFK
	1		TPPYCKAITEPVTVKMQLRRPSDQEVSESMDFRYLPDEKDTYGN
ł			NAKKUKITLLIFUKLCODHVETGFRHVDODGLELLTGCDDDDT 3.0
		1	USAGITVNFPERPRPGLLGSIGEGRYFKKEDNI FCUDARGIENA
1			TGVSSQAESYYPSPGPISSGLSHHASMADI.Deccurevaupmpn
			SGNTNPLSSFSTRTLPSNSOGIPPFIRIPVGNDLNACNA CLIANT
1	Í		ADDIVGMEASSMPSADLYGISDPNMISNCSVNMMTTSSDEWCER
İ			DNPRLLSMNLENPSCNSVLDPRDLROLHOMSSSSMSAGANSMTT
İ			VFVSQSUAFEGSDFSCADNSMINESGPSNSTNDNSUUPVODGOV
5907	99	1873	SGIGSMQNEQLSDSFPYEFFQV
ł		2075	TYLLSSWSS**NLDTKIKSQVKV/RKGHKKISWPYPQPAKQNGK
	i		KATSKVPSAPHFVHPNDHANREAELKKKWVEEMREKQQAAREQE RQKRRTIESYCQDVLRRQEEFEHKEEVLQELNMFPQLDDEATRK
			AYYKEFRKVVEYSDVILEVLDARDPLGCRCFQMEEAVLRAQGNK
			KLVLVLNKIDLVPKEVVEKWLDYLRNELPTVAFKASTQHQVKNL
			NRCSVPVDQASESLLKSKACFGARNIMRVT.GNVCBI.CBURNING
1 1			VGVVGLPNVGKSSLINSLKRSRACSVGAVPGTTKEMOEUVI DVE
			TRULDAPGIVPGPNSEVGTILRNCVHVOKLADDVTDVETTIODC
			NLBEISNYYGVSGFOTTEHFLTAVAHRIGKKKKCGLVCOROARK
1 1			AVLADWVSGKISFYIPPPATHTLPTHISAETVKEMTEVEDIEDE
			EQANEDIMECLATGESDELLGDTDPLEMETYLLUCDMUVIADAT [
	ļ		ENKTTVYKIGDLTGYCTNPNRHOMGWAKRNUDHDDVCNGMTDVG
	j		SVDRRSVLQRIMETDPLQQGQALASALKNKKMOKPADKIAGKI
5908	247	975	SDSMMSALDLSGNADDGVGD
1	1	575	HCGIKKRGEGSGSPSPASGGFQLGCQIPEPSLPSEEETHPHTRA
	ĺ		HTRTLRATLTRRPPRSHSTRLRFPMPLDGDGGLASWK/PMRER*
1 1		ľ	GWRRPAKAAGASLGVAATGKRGCRMSKRYLQKATKGKLLIIIFI
1			VTLWGKVVSSANHHKAHHVKTGTCEVVALHRCCNKNKIEERSQT VKCSCFPGQVAGTTRAAPSCVDASIVEQKWWCHMQPCLEGEECK
			VLPDRKGWSCSSGNKVKTTRVTH
5909	1	5002	PAIPGSTIIWAPGSHSAARADGRHGSLPSQSQAPGALCGARAPP
1			SSNLKADKSMI CAOARAGKNLYHNRFI GI AAMARDERNEGET DR
1		İ	CREPIRISINPOGFHNMDLRGGPHDGVTIDpgTgDTDLITTGDGD
	İ]	STLMGRSSYYSIGHSQDLVIHWDIKEEVDAGDWIGMVLIDERG C
1 1		ł	ENFLDYKNRGVNGSHRGOIIWKIDASSYFVEDETKICEKYVNGV
]			SGALRATTPSVTVKNSAAPIFKSIGADETVOGOGGEDDITERRIC
1 1	Ì	ŀ	DFQAMGLKKGMFFNPDPYLKISIOPGKHSTFDAT.DUUGOEDDGV
1	ļ	ī	11GNTVNP1WQAEOFSFVSLPTDVLETEVKDKFAKCDDIIVDD
	İ	1	GRESMPVQRLLERHAIGDRVVSYTIGRRI.PTDUVCGOLOEDERT
1 1			TSSIHPDDEEISLSTEPESAQIQDSPMNNLMESGSGEPRSEAPE
			SSESWKPEQLGEGSVPDRPGNQSIELSRPAEEAAVITEAGDQGM
			VSVGPEGAGELLAQVQKDIQPAPSAEELAEQLDLGREASALLLE
			DGEAPASTKEEPLEEEATTQSRAGREEBEKEQEEEGDVSTLEQG EGRLOLRASVKRKSPRCSI DVSELETILLAS
		1	EGRLQLRASVKRKSRPCSLPVSELETVIASACGDPBTPRTHYIR IHTLLHSMPSAQGGSAAEEEDGAEEESTLKDSSEKDGLSEVDTV
		1.	AADPSALEEDREEPEGATPGTAHPGHSGGHFPSLANGAAQDGDT
]	HPSTGSESDSSPRQGGDHSCEGCDASCCSPSCYSSSCYSTSCYS
			SSCYSASCYSPSCYNGNRFASHTRFSSVDSAKISESTVFSSQDD
			EEEENSAFESVPDSMQSPELDPESTNGAGPWODEL & A DSCHUED
		1 '	SPEGLESPVAGPSNRREGECPILHNSOPVSOLPSI.PPFHUHVDT
	j	•	IDEPLIPATION EARIDSHGRVFYVDHVNRTTTWODDTA A TROOMS
		1	RSGSIQQMEQLNRRYQNIQRTIATERSEEDSGSQSCEQAPAGGG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	1	1	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ		1	
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		1	
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence ·		\=possible nucleotide insertion)
	 		GGGGSDSEABSSQSSLDLRREGSLSPVNSQKITLLLOSPAVKFI
ļ	1		
	1		TNPEFFTVLHANYSAYRVFTSSTCLKHMILKVRRDARNFERYQH
i	l		NRDLVNFINMFADTRLELPRGWEIKTDQQGKSFFVDHNSRATTF
			IDPRIPLONGRLPNHLTHROHLORLRSYSAGEASEVSRNRGASL
	1	ł ·	LARPGHSLVAAIRSQHQHESLPLAYNDKIVAFLRQPNIFEMLQE
	· F	Í	
	k	Į.	ROPSLARNHTLREKIHYIRTEGNHGLEKLSCDADLVILLSLFEE
1	1	l .	EIMSYVPLQAAFHPGYSFSPRCSPCSSPQNSPGLQRASARAPSP
	1		YRRDFEAKLRNFYRKLEAKGFGQGPGKIKLIIRRDHLLBGTFNO
	!	İ	_
ļ	1		VMAYSRKELQRNKLYVTFVGEEGLDYSGPSREFFFLLSQELFNP
1	1	ļ	YYGLFEYSANDTYTVQISPMSAFVENHLEWPRFSGRILG\LALI
	1		HQYLLDAFFT\RPFYKALL\RLPC\D\LSDLEYLDEEFHQSLQW
	l .	1	
1	1	1	MKDNNITDILDLTFTVNBEVFGQVTERELKSGGANTQVTEKNKK
1	1	1	EYIBRMVKWRVERGVVQQTEALVRGFYEVVDSRLVSVFDARELE
1	[1	LVIAGTAEIDLNDWRNNTEYRGGYHDGHLVIRWFWAAVERFNNE
1	1	1	QRLRLLQFVTGTSSVPYEGFAAPPWEPMGLRRFLP*KKWGKITS
1	1	1	
i	<u>i</u> .	L	LPPRG\HTCLQPDWDLPTVSPRTPMLYEK\LLTA\VEETSTPGT
5910	1526	446	VAEFAAMEPGRTQIKLDPRYTADLLEVLKTNYGIPSACFSQPPT
		i	AAQLLRALGPVELALTSILTLLALGSIAIFLEDAVYLYKNTLCP
1		İ	IKRRTLLWKSSAPTVVSVLCCFGLWIPRSLVLVEMTITSFYAVC
1			
1		i .	FYLLMLVMVEGFGGKEAVLRTLRDTPMMVHTGPCCCCCPCCPRL
l l		I	LLTRKKLQ\R*CWALSNTPS*R*R*PWWACFSSPTASMTQQTFL
1			RGAQLYGSTLSSA/CSTLLALWTLGIISRQARLHLGEQNMGAKF
		1	· · · · · · · · · · · · · · · · · · ·
1		1	ALFQVLLILTALQPSIFSVLANGGQIACSPPYSSKTRSQVMNCH
ì			LLILETFLMTVLTRMYYRRKDHKVGYETFSSPDLDLNLKALRWM
1		1	AWTMKGCCTH
5911	109	595	QLPLAPCIQGKGLEMRSPKPQSFIIRSSHSGAGLLVKNPSTPVF
3311	109] 3,3	1 1
1			CGHRRGGAAFKYKPTPVVGPEQRPTGQKHMRGGVSLLSPRLECS
		1	GTISAHCNLRLPSSSNSPAPAS*LAGITGVCHHAQLIFVFLVET
	i	1	GFHHVGQAGLELL/NVVIHLPRPPKVLGLQA
F03.3	624		
5912	924	277	MILNKALMLGALALTTVMSPCGGEDIVADHVASYGVNLYQSYGP
1	i	1	SGQYSHEFDGDEEFYVDLERKETVWQLPLFRRFRRFDPQFALTN
	1	1	IAVLKHNLNIVIKRSNSTAATNEVPEVTVFSKSPVTLGQPNTLI
1	İ	f	CLVDNIFPPVVNITWLSNGHSVTEGVSETRPSSPKSDHFLLQDQ
	<u> </u>	L	VTSPSFPFE**DL*TAKVEQLGAWFEPLLKHWGABIPTTL
5913	46	1198	QLRMAGAEGAAGRQSELEPVVSLVDVLEEDEELENEACAVLGGS
1		1	DSEKCSYSOGSVKROALYACSTCTPEGEEPAGICLACSYECHGS
1	1	1	HKLFELYTKRNFRCDCGNSKFKNLECKLLPDKAKVNSGNKYNDN
1	1	1	
1		1	FFGLYCICKRPYPDPEDEIPDEMIQCVVCEDWFHGRHLGAIPPE
1		ł.	SGDFQEMVCQACMKRCSFLWAYAAQLAVTKIST\GMMDWCGTLM
İ		1	E*/DDQEVIKPENGRHQDSTLKEDVPEQGKDDVREVKVEQNSEP
1	! .	1	
		1	CAGSSSESDLQTVFKNESLNAESKSGCKLQELKAKQLIKKDTAT
1	1	1	YWPLNWRSKLCTCQDCMKMYGDLDVLFLTDEYDTVLAYENKGKI
i .		1	AQATDRSDPLMDTLSSMNRVQQVELIC/GIQ*FED
5914	960	124	NLGGSELPPEEALFIQVASMNQRRVDFYLASIEDMLVAI/GGRN
1 222	1 300	1	
1		1	ENGALSSVETYSPKTDSWSYVAGLPRFTYGHAGTIYKDFVYISG
	i		GHDYQIGPYRKNLLCYDHRTDVWEERRPMTTARGWHSMCSLGDS
		1	IYSIGGSDDNIESMERFDVLGVEAYSPQCNQWTRVAPLLHANSE
1	1		SGVAVWEGRIYILGGYSWENTAFSKTVQVYDREADKWSRGVDLP
J	}	1	1
1		1	KAIAGGSACFIAP*SLGQRTRKRKAKARGTRTGASDPSCASWDH
1	ŀ	1	PHRHLPGLCRPAATS
5915	1604	703	FPGRPTRPLKLGRRRKRARI IQAPHCHSPRPRTCPPGALQAPEA
1 -7	1 -55.	1	
1	1	1	PASRAEGPVAVVVNGHTEGPAPARSAPKEPPGLPRPLGSFPCPT
		1	PQEDFPALGGPCPPRMPPSPGFSAVVLLKGTPPPPPPGLVPPIS
1	1	1	KPPPGFSGLLPSPHP\PVSPAPPPPPPQK/RPRLLPAP/PGLPS
1	1		PRELPGEEPSAHPVHQGLPAERRGPLQRVQEPLRGVQTGPDLRS
1	1	1	
		<u> </u>	PVLQELPGPAGGEFPEGL**AAGPAAH
. 5916	256	633	SPRMWEIWGPWHRWESPSLEGEWPSRIPEPSPDSTKGTSGKGCR
1	1	1	TVTGAVHRHLNHVAGIIPWVLHSQLKPTAATAQDQWTSQQYPDH
	- }		
l		1	PTRLILQ*NQATADKNN*TTALLQPHQRL\VSPRMAEA
5917	1343	827	AHQILTYLEP/ICLVVNYNKILTVFLTKSVLEI*KFIHTPQTYR

SEQ	Predicted	Predicted end	Amino acid cogmont
ID	beginning	nucleotide	Amino acid segment containing signal peptid (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=H1Stidine, I=Isoleucine V-Lucine
	corresponding to first	to first	L=Leucine, M=Methionine N=Asparagine
	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine
	residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine
	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	bequence	Codon, /=possible nucleotide deletion,
			\=possible nucleotide insertion)
			F*NDFFGIKEVYVSRRLRKTSF/RLAVTFLEQAVVSKECVPVD FMEHLLPSLLSLASDPVPNVRVLLAKALRQMLLBKAYFRNAGN
			HLEVIEETILALQSDRDQDVSFFAALEPKRRNIIDTAVLEKQN
5918	13	1247	EGAQVARRESRRQWRAGRCGRGGGGRGAERTGGRGPPGRPRPL
			PGPARKGRRRMETPFYGDEALSGIGGGASGSGGTFASDODI ED
			APPTAAAGSMMKKDALTLSLSEOVAAAI.KDADADAGVDDA\ AD
			APSAAPPOGLLASPOLGLLKLASPELERIJIOSNGI.VTTTDTG
			QFLYPKVAASEEQEFAEGFVKALEDLHKONOLGAGDAAAAAA
			AGGPSGTATGSAPPGELAPAAAAPEAPVVA\NI.GGV\AGGCPGT
		*	RGGAAT\VAFAAEPVPFPPPPPPPGALGPRRP/RLALQGRRPQTV
	'		PDVP\SFGESP\PLSPIET\DTPRRI\KAKRKRL\RNPQIRAP
			PASRKLGAQSRALERESEDPS*SPEHGSLASTASLLREQVAQLE QKVLSHVNSGCQLLPQHQVPAY
5919	1	4254	TSVQCDSQCTPTSSQCSINMEHWISQAIHGSTTSTTSSSSTQSC
			GSGAAHRLADVMAQTHIENHSAPPDVTTYTSEHSIQVERPQGST
			GSRTAPKYGNAELMETGDGVPVSSRVSAKTOOLVNTTLED DED DE
			LKEFFVDDFEELLEVQQPDPNOPKPEGAOMLAMRGROLGUZTNM
			PPSLEAALQRWGTISPKAPCLTTMDTNGKPLYILTVGKLWTDEM
			LVAYSILHKLGTKQEPMVRPGDRVALVFPNNDPAAFMAAFVCCT
			LAEVVPVPIEVPLTRKDAGSOOIGFLIGSCGVTVALTSDACUVC
İ			LPKSPTGEIPQFKGWPKLLWFVTESKHLSKPPRDWF\PHIKDAN
İ			NDTAYIEYKTCK\DGSVLGVTVTRTALLTHCQALTQACGYTEAE
			TIVNVLDFKKDVGLWHGILTSVMNMMHVISIPYSLMKVMPLSWI QKVCQYKAKVACVKSRDMHWALVAHRDQRDINLSSLRMLIVADG
			ANPWSISSCDAFLNVFQSKGLRQEVICPCASSPEALTVAIRRPT
			DDSNQPPGRGVLSMHGLTYGVIRVDSEEKLSVLTVQDVGLVMPG
			AIMCSVKPDGVPQLCRTDEIGELCVCAVATGTSVYGLSGMTVNT
			FEVFAMISSGAPISEYPFIRTGLLGFVGPGGLVFVVGVMDGT MIT
ſ	Ì		VSGRRHNADDIVATALAVEPMKFVYRGRIAVFSVTVI.HDFD TVI
		ļ	VAEQRPDSTEEDSFQWMSRVLOAIDSIHOVGVVCLALUDANTU D
			KTPLGGIHLSETKQLFLEGSLHPCNVLMCPHTCVTNLPKPRQKQ
	1		PEIGPASVMVGNLVSGKRIAQASGRDLGQIEDNDQARKFLFLSE
			VLQWRAQTTPDHILYTLLNCRGAIANSLTCVQLHKRABKIAVML MBRGHLQDGDHVALVYPPGIDLIAAFYGCLYAGCVPITVRPPHP
1			QNIATTLPTVKMIVEVSRSACLMTTQLICKLLRSREAAAAVDVR
			TWPLILDTDD*PKKRPAQICKPCNPDTLAYLDFSVSTTGMLAGV
	j	1	KMSHAATSAFCRSIKLQCELYPSREVAICLDPYCGLGEVLWCLC
			SVISGHQSILIPPSELETNPALWLLAVSOVKVPDTECOVCYMEN
}		!	CTRGLGSQTESLKARGLDLSRVRTCVVVAEERPRIALTOSEGUI
			FRUIGLIPRAVSTSFGCRVNLAICLOGTSGPDPTTVVVDMPALD
ĺ	1		HDRVRLVERGSPHSLPLMESGKILPGVRIIIANPETKGPLGDSH
			LGEIWVHSAHNASGYFTIYGDESLQSDHFNSRLSFGDTQTIWAR
1	İ	ł	TGYLGFLRRTELTDANGERHDALYVVGALDEAMELRGMRYHPID IETSVIRAHKSVTECAVFTWTNLLVVVVELDGSEQRALDLVPLV
			TNVVLBEHYLIVGVVVVVDIGVIPINSRGEKQRMHLRDGFLADQ
			LDPIYVAYNM
5920	1381	1499	QLGAVAHAGVSRIPP*LFPPLHPTFLSLWCLHHKLP/HPPGASM
l			VRPPVVPRRPPAHISSVRQASTOVPRTVPHTORVANIGTOTTCP
			SGVGCCTPGRPLLPCKCSSAAHSTYRVOEPAVHTDGOEDT TACK
		ľ	LAAAPLHEQKQMIGERLYPLIHDVHTOLAGKITGMIJETDNEET
5921	727		LIMLESPESLHAKIDEAVAVLQAHQAMEOPKAYMH
_		157	VCPGTGGE*GLWGQLGGLPKETPLKPMDAFTGSGLKRKFDDVDV
}		1	GSSVSNSDDEISSSDSADSCDSLNPPTTASFTPTSILKRQKQLR
1	1	_ [:	RKNVRFDQVTVYYFARRQGFTSVPSQGGSSLGMAQRHNSVRSYT
			LCEFAQEQEVNHREILREHLKEEKLHAKKMKLTKNGTVESVEAD
			GLTLDDVSDEDIDVENVEVDDYFFLQFLPTKRRRALLRASGVHR IDAEEKQELRAIRLSREECGCDCRLYCDPEACACSQAGIKCQVD
		l i	RMSFPCGCSRDGCGNMAGRIEFNPIRVRTHYLHTIMKLELESKR
	ļ	1,5	2\GAAQQPQ*GALPDCOLOPDRSTGL*DPSWTGSKGLeptgra
	2475		AAATHLIILRVIENRGAEGKRK SYSNWGLFPSVFIQVPRSRTGNLKPIFLFYSYYE\CMETLKG\T
5922		495	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
,,,,,	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		1 1	
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
_			CLYNATOYKVCSPRNDRPDACYNPSEPAATTVFEIRTGLLLGDT
{			SKIITRTEEKEIPKQITLRFDACAAINSKKLEIGCGSLN*ERS*
1	ļ		RVENKYVCHESGVCKNCAYWPCVI*AT*KKNKNDSVYLQKGEAN
	j	1	PSCAAGHCNPLELIITNPLDPHWKKGERVTLGINRTGLKPQVVI
1		Į.	LIKGEVHKCSPKPVFQTFYEELNLPAPELLKKTKNLFLQLAENV
		i	IFLLNGTSCYVRGGTTIGDRWPWEA*ELVPTDPAPDIIPI*KAE
			ASNF*VLKTSIIRQYCIAREGKDFIIPVGKPNCIGQKLYNSTTK
1			TIT++DLNHTEKNPFSKFSKLKTA+AHAESH+DWTVPSGLY+IC
			RHRAYFRLPNKWADSCVIGTIKPSFFLLPIKMGELLGFSVYASR
}			EKKGIVIGNWKDNEWPRERIIQYYGPATWAQDGSWGYR/TP/VY
			MLNWIIRLQAILEIISNETGRALTVLAWQETQMRNAIYQNRLAL
]			DYLLVAEGGVCRKFNLTNCCLQINDQGQVVKNIVRDMTKLAHVP
			IQVWHKFDPESLFGKWFPAIGGFKTLIVGVLLVIRTCLLLPCVL
1			
			PLLFQMIKGIVATLVHQKTSAHVNYMNHYRSISQRDSKSEDESE
ļ <u>.</u>		L	NSH
5923	137	638	QLCGRRGQRFRTSIKRMHPI*RTCPNTNL/IILLSQENTQIRDL
			QQENRELWISLEEHQDALELIMSKYRKQMLQLMVAKKAVDAEPV
		,	LKAHQSHSAEIESQIDRICEMGEVMRKAVQVDDDQFCKIQEKLA
1			QLELENKELRELLSISSESLQARKENSMDTASQAIK
5924	274	2146	EKGKVKDAGAEQWISLSLSCKGSWETQFSNHLNSLTPPTSVRRM
			PLITTVTLLKMVARHHMKLLCSKAFSTQLQQKIFLHSQMGIHHQ
ì			SVCMKLKPNTSHIISILMGQPMALVQLETLAPLTIIIQKFQTQD
			HMKFWKNLPLHSHHLTPSVPQTVIPKKTGSPEIKLKITKTIQNG
ł			RELFESSLCGDLLNEVQASE\Q*NQSIESRKEKRKKSNKHDSSR
			SEERKSHKIPKLEPEEONRPNERVDTVSEKPREEPVLKEGSPSS
			ANTIFCSNNGSVHW\FKFQVGDLVWSKVGTYPWWPCMVSSDPQL
1			EVHTKINTRGAREYHVQFFSNQPERAWVHEKRVREYKGHKQYEE
			LLAEATKOASNHSEKOKIRKPRPORERAOWDIGIAHAEKALKMT
Ì	ļ		
1			REERIEQYTFIYIDKQPEEALSQAKKSVASKTEVKKTRRPRSVL
1		1	NTQPEQTNAGEVASSLSSTEIRRHSQRRHTSAEEEEPPPVKIAW
ļ	1	Į.	KTAAARKSLPASITMHKGSLDLQKCNMSPVVKIEQVFALQNATG
1		į.	DGKFIDQFVYSTKGIGNKTEISVRGQDRLIISTPNQRNEKPTQS
1			VSSPEATSGSTGSVEKKQQRRSIRTRSESEKSTEVVPKKKIKKE
			QVGFLHVES
5925	216	1911	MMTAESREATGLSPQAAQEKDGIVIVKVEEEDEEDHMWGQDSTL
1	1		QDTPPPDPEIFRQRFRRFCYQNTFGPREALSRLKELCHQWLRPE
1			INTKEQILELLVLEQFLSILPKELQVWLQEYRPDSGEEAVTLLE
1			DLELDLSGQQVPGQVHGPEMLARGMVPLDPVQESSSFDLHHEAT
1			QSHFKHSSRKPRLLQSRALPAAHIPAPPHEGSPRDQAMASALFT
	1		ADSQAMVKIEDMAVSLILEEWGCQNLARRNLSRDNRQENYGSAF
			PQGGENRNENEESTSKAETSEDSASRGETTGRSQKEFGEKRDQE
			GKTGERQQKNPEEKTRKEKRDSGPAIGKDKKTITGERGPREKGK
			GLGRSFSLSSNFTTPEEVPTGTKSHRCDECGKCFTRSSSLIRHK
1			IIHTGEKPYECSECGKAF\SLNS\NLVLHQRI\HTGEKPHECNE
	1		CGKAFSHSSNLILHQRIHSGEKPYECNECGKAFSQSSD\LTKHQ
			RIHTGEKPYECSECGKAFNRNSYLILHRRVHTREKPYKCTKCGK
			\AFTRSSTLTLHHRIHARERASEYSPASLDAFGAFLKSCV
5000	1	733	DRCLMLKQGSQPGSPPAT/CEPPAPPVYQAPCQSCPEPPGAHEP
5926	2	233	, , , , , , , , , , , , , , , , , , , ,
	 		SDSPHHTPVHPPPEHSAACPAPATCCPPPRSSMS
5927	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA
		1	YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
	}		KRRLEFIEKEKKQKDQIISLMKAEQMKRQBKERLERINRAREQG
		1	WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
			MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR
			KREAMQNKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV
		1	YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
			RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV
1			AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS
		1	SLTDTRETSEEMOKTNNAISSKREILRRLNENLKAQEDEKGKON
		-	LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL
		1 .	DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE
L			

SEO	Predicted	Predicted end	Amino
ID	beginning	nucleotide	Amino acid segment containing signal peptide
NO:	nucleotide	location	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
1.0.	location	i i	Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine.
]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence	_	\=possible nucleotide insertion)
		-	LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
	Ì		AIVDSPVETKSPEFSEASPOMSLKLEGNLEEPDDLETEILQEPS
-			GTNYDE\ SI DCTITDIMITCERNEMISHOOD DE TETLQEPS
			GTNKDE\SLPCTITDVWISEEKETKETQSADRITIQENEVSEDG
ļ			VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVQPEPFFHKVVHSE
-			HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
	i		LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLEIDEI
1			EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS
			EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEBWHSDNSD
			GEIASECECDSVFNHLEELRLHLEQEMGFEKFFEVYBKIKAIHB
	<u> </u>	_	DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYOEDNDE
5928	4146	1248	KHFSKFGSQALYQLKRPASGQNSISVMPAQKITKPAAKYGIPLA
			YKKYGDKKLHEKKPLQKHKQAHQTPEKRVNTGEERRKISEEAAR
			KRRLEFIEKEKKQKDQIISLMKAEQMKRQEKERLERINRAREQG
1			WRNVLSAGGSGEVKAPFLGSGGTIAPSSFSSRGQYEHYHAIFDQ
1			MQQQRAEDNEAKWKREIYGRGLPERQKGQLAVERAKQVEEFLQR
		ł	KREAMONKARAEGHMGILQNLAAMYGGRPSSSRGGKPRNKEEEV
			YLARLRQIRLQNFNERQQIKAKLRGEKKEANHSEGQEGSEEADM
			DDKK/ IECI KAHAMADAMI KROLEDIKOKEANHSEGGEGSEEADM
1			RRKK\IESLKAHANARAAVLKEQLERKRKEAYEREKKVWEEHLV
1	1		AKGVKSSDVSPPLGQHETGGSPSKQQMRSVISVTSALKEVGVDS
			SLTDTRETSBEMQKTNNAISSKREILRRLNENLKAQEDBKGKQN
1			LSDTFEINVHEDAKEHEKEKSVSSDRKKWEAGGQLVIPLDELTL
1			DTSFSTTERHTVGEVIKLGPNGSPRRAWGKSPTDSVLKILGEAE
	l .		LQLQTELLENTTIRSEISPEGEKYKPLITGEKKVQCISHEINPS
Ì			AIVDSPVETKSPEFSEASPOMSLKLEGNLEEPDDLETEILORPS
1	1		GTNKDE\SLPCTITDVWISEEKETKETQSADRITIOENEVSEDG
1	1		VSSTVDQLSDIHIEPGTNDSQHSKCDVDKSVOPEPFFHKVVHSE
1			HLNLVPQVQSVQCSPEESFAFRSHSHLPPKNKNKNSLLIGLSTG
•	-		LFDANNPKMLRTCSLPDLSKLFRTLMDVPTVGDVRQDNLBIDEI
1			EDENIKEGPSDSEDIVFEETDTDLQELQASMEQLLREQPGEEYS
			EEEESVLKNSDVEPTANGTDVADEDDNPSSESALNEEWHSDNSD
			GEIASECECDSVFNHLEBLRLHLEQEMGFEKFFEVYEKIKAIHE
]			DEDENIET CENTRONIT CHRISTIAN TO THE TENTRO T
5929	3	1558	DEDENIEICSKIVQNILGNEHQHLYAKILHLVMADGAYQEDNDE
	[-	1550	LDFSMTTQLPAYVAILLFYVSRASCQDTFTAAVYEHAAILPNAT
			LTPVSREEALALMNRNLDILEGAITSAADQGAHIIVTPEDAIYG
			WNFNRDSLYPYLEDIPDPEVNWIPCNNRNRFGQTPVQERLSCL\
			AKNNSIYVVANIGDKKPCDTSDPQCPPDGRYQYNTDVVF\DSQG
			KLVARYHKQNLFMGENQFNVPKEPEIVTFNTTFGSFGIFTCFDI
1			LFHDPAVTLVKDFHVDTIVFPTAWMNVLPHLSAVEFHSAWAMGM
1			RVNFLASNIHYPSKKMTGSGIYAPNSSRAFHYDMKTEEGKLLLS
1			QLDSHPSHSAVVNWTSYASSIEALSSGNKEFKGTVFFDEFTFVK
			LTGVAGNYTVCOKDLCCHLSYKMSENI PNEVVALGA FDGLUTUF
			GRYYLQICTLLKCKTTNLNTCGDSAETASTRFEMFSLSGTFGTO
1]		YVFPEVLLSENQLAPGEFQVSTDGRLFSLKPTSGPVLTVTLPGR
-			LYEKDWASNASSGLTAQARIIMLIVIAPIVCSLSW
5930	113	6082	RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK
1			KLVWIPSERHGFEAASIKEERGDEVMVBLAENGKKAMVNKDDIQ
1			KWNDDKEG KADDWA EL WOLVIER OF THE WAR KENERKAMANKDDIO
			KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF
			CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM
1	ļ		LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN
]			IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV
1			TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
			KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG
			PSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAOKL
	ļ		CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA
 	}		KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN
]			SEEOLCINYTHEKI OOL ENUMBER TOORISCHEELIN
			SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL
			DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ
]			GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
			NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT
			KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK
L			LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP

SEQ	Predicted	1 8 12 - 5 3	
ID		Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
I NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Í	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH
1		<u> </u>	LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR
			MCANYI KI BUMOMBURTURUN I OLUBBURTUR ARROY
		İ	NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK
	1		EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETBLFAEAEEM
			RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ
		1	DLEEQLDEEEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF
	1		IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE
	ĺ		RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL
			AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELOEDFES
İ			EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE
	t		QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR
			FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV
			QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEAEKKGIK
			FAKDAASLESQLQDTQELLQEETRQKLNLSSRIRQLEEEKNSLQ
			EQQEEEEEARKNLEKQVLALQSQLADTKKKVDDDLGTIESLEEA
			EVOSEBERARANDERQVIADQSQLADTRAKVUDDDLGTTESLEEA
	}		KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQELDDLTVDLD
			HQRQVASNLEKKQ\KKFDQLLAEEKSISARYAEERDRAEAEARE
			KETKALSLARALBEALBAKEEFERQNKQLRADMEDLMSSKDDVG
			KNVHELEKSKRALEQQV\EEMRTQLEELEDELQATEDAKLRLEV
			NMQAMKAQFERDLQTRDEQNEEKKRLLIKQVRELEAELEDERKQ
-			RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQAQMK
			DYQRELEEARASRDEIFAQSKESEKKLKSLEAEILQLQEELASS
			ERARRHAEQERDELADEITNSASGKSALLDEKRRLEARIAQLEE
1			ELEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAOKSDNAR
			QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLE
1			QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMEKA
ľ			NARMKQLKRQLEEAEEEATRANASRRKLQRELDDATEANEGLSR
	ł l		
	Į.		EVSTLKNRLRRGGPISESSSPSGPPOLHI.PGAGI.PI CODDTPOR
			EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFBAASIKEERGDEVMVELAENGKKAMVNKDDIO
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFBAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVONDNSSRFGKFIRINFDY
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENCKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVAASHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNYYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEAL KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNYYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFYEKLVOEO
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYRADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHINLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNYNFFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFYRCIIPNHEKRAGK
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYK KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQFPNRIVFOEFRORYEILTP
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFBAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIHYAGKVDYKADEWLMKNMDPLND NVATLHUGSSDRFVABLWKDVDRIVGLDOVTGMTTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGOSKIFFRRGVLAH
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATVERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIFFQAVCRGYLARKAFAKKOOOLSALKVIOR
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSFFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTROEBELOAKDEELLKVK
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKPQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAPAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLEEKNILAEOLOAETELFAFAFEM
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHINLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALDEECWFPKATDKTFVEKLVQEQ GSHSKPQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHERRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNOILONEKKMOAHIO
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNNYRFLSNGYIPPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKKKMEEILLLEDONSKF
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNNYRFLSNGYIPPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKMQAHIQ DLEEQLDEEEGARQKLQLEKVTAEAKKKMEEILLLEDONSKF
5931	113	6082	EVSTLYNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVVYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKK KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEEKTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNILAKIRNKQEVMISDLEE
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFBAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKPQKPRQLKDKADFCIHYAGKVDYKADEWLMKNMDPLND NVATLHLQSSDRFVABLWKDVDRIVGLDQVTGMTTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAPAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNOILQNEKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLODDIAELOAOIDBLKLOL
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTMRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIHYYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCMGVLEGIRICRGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGGSKIFFRAGVLAH LEEERDLKITDIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHQWWRVPTKVKPLLQVTRQBEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAGSSQLAEEEKAKNLAKIRNKQETMISDLEE
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGRARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGRISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCMGVLEGIRICRGGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFARAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNILAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDZIAELQAQIDELKLQL AKKEEELQGALARGDDBTLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAOOGELRTKRE
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHINLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNERLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKPQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVAELWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFPQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNOILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDBTLHKNNALKVVRELQQQLAELQEDFES EKASRNKAERQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALBEETKNHEAQIQDMRQRHATALEELSEDLEOAKR
5931	113	6082	EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHINLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHING FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFELN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHERRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEELQAKDEELLKVVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNGILQAQIBELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAOV
5931	113	6082	EVSTLYNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQAMPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNNYRFLSNGYIPIPGQ\QDKGNFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVPQEFRQRYEILTP NAIPKGFMDGKQACERMIRALBLDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEGLQAETELFAEAEEM RABLAAKKQELEEILHDLESRVEEEEERNQILQMEKKMQAHIQ DLEEQLDEBEGARQKLQLEEKVIAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDBTLHKNNALKVVRELQAQIAELQEDFES EKASNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSQLEQAKR FRANLEKNKGCLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEERAEKKGIK
5931	113	6082	EVSTLYNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASULHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLEGFNNYRFLSNGYIPIPGQ\QDKGHFRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKFQKPRQLKDKADFCIIHYAGKVDYKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVFQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVFTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGBLEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RARLAAKKQELEEILHDLESRVEEEEERNQILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASRNKAERQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE QEVAELKKALEEETKNHEAQIQDMRQRHATALEELSEQLEQAKR FKANLEKNKQGLETDNKELACEVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEEABKKGIK FANDAASLESQLQDTGELLQEETRQKLNLSSRIROLEFEKNSLO
5931	113	6082	EVSTLYNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE RGNCFWIVPFTMAQRTGLEDPERYLFVDRAVIYNPATQADWTAK KLVWIPSERHGFEAASIKEERGDEVMVELAENGKKAMVNKDDIQ KMNPPKFSKVEDMAELTCLNEASVLHNLKDRYYSGLIYTYSGLF CVVINPYKNLPIYSENIIEMYRGKKRHEMPPHIYAISESAYRCM LQDREDQSILCTGESGAGKTENTKKVIQYLAHVASSHKGRKDHN IPGE\LERQLLQANPILESFGNARTVQNDNSSRFGKFIRINFDV TGYIVGANIETYLLEKSRAVRQAKDERTFHIFYQLLSG\AGEHL KSDLLLBGFNNYRFLSNGYIPPGQ\QDKGNPRGDPGEAMHIMG FSHEEILSMLKVVSSVLQFGNISFKKERNTDQASMPENTVAQKL CHLLGMNVMEFTRAILTPRIKVGRDYVQKAQTKEQADFAVEALA KATYERLFRWLVHRINKALDRTKRQGASFIGILDIAGFEIFBLN SFEQLCINYTNEKLQQLFNHTMFILEQEEYQREGIEWNFIDFGL DLQPCIDLIERPANPPGVLALLDEECWFPKATDKTFVEKLVQEQ GSHSKPQKPRQLKDKADFCIIHYAGKVDYXKADEWLMKNMDPLND NVATLLHQSSDRFVABLWKDVDRIVGLDQVTGMTETAFGSAYKT KKGMFRTVGQLYKESLTKLMATLRNTNPNFVRCIIPNHEKRAGK LDPHLVLDQLRCNGVLEGIRICRQGFPNRIVPQEFRQRYEILTP NAIPKGFMDGKQACERMIRALELDPNLYRIGQSKIFFRAGVLAH LEEERDLKITDIIIFFQAVCRGYLARKAFAKKQQQLSALKVLQR NCAAYLKLRHWQWWRVPTKVKPLLQVTRQEEELQAKDEELLKVK EKQTKVEGELEEMERKHQQLLEEKNILAEQLQAETELFAEAEEM RABLAAKKQELEEILHDLESRVEEEEERNOILQNEKKKMQAHIQ DLEEQLDEBEGARQKLQLEKVTAEAKIKKMEEEILLLEDQNSKF IKEKKLMEDRIAECSSQLAEEEEKAKNLAKIRNKQEVMISDLEE RLKKEEKTRQELEKAKRKLDGETTDLQDQIAELQAQIDELKLQL AKKEEELQGALARGDDETLHKNNALKVVRELQAQIAELQEDFES EKASNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE EKASRNKAEKQKRDLSEELEALKTELEDTLDTTAAQQELRTKRE EKASRNKAEKQCLETDNKELAECVKVLQQVKAESEHKRKKLDAQV QELHAKVSEGDRLRVELAEKASKLQNELDNVSTLLEERBKKKLDAQV

SEQ ID NO:	Predicted beginning nucleotide location corresponding to first amino acid residue of amino acid	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion) KKKLLKDAEALSQRLEEKALAYDKLEKTKNRLQQELDDLTVDLD HQRQVASNLEKKQ\KKFDQLLAEEKSISARYABERRRAEAEARE KETKALSLARALEBALEAKEEFERQNKQLRADMEDLMSSKDDVG KNVHELEKSKRALEGQV\EEMRTQLEELEDELQATBDAKLRLEV NMQAMKAQFERDLQTRDEQNBEKKRLLIKQVRELEAELEDERKQ RALAVASKKKMEIDLKDLEAQIEAANKARDEVIKQLRKLQAQMK DYQRELEEARASRDEIFAQSKESEKKLKSLEABILQLQEELASS ERARHAEQERDELADEITNSASGKSALLDEKRLBARIAQLBE BLEEEQSNMELLNDRFRKTTLQVDTLNAELAAERSAAQKSDNAR QQLERQNKELKAKLQELEGAVKSKFKATISALEAKIGQLEEQLE QEAKERAAANKLVRRTEKKLKEIFMQVEDERRHADQYKEQMBKA NARMKQLKRQLEEAEEATRANASRRKLQRELDDATEANEGLSR EVSTLKNRLRRGGPISFSSSRSGRRQLHLEGASLELSDDDTESK TSDVNETQPPQSE
5932	33	572	RHLEEICFLFLQKGRKLKLSGPRWEEGKPRGTGGLWVKAEANMG FGATLAVGLTIFVLSVVTIIICPTCSCCCLYKTCRRPRPV\APP PHPP/PVVHAPYPQPPSVPPSYPGPSYQGYHTMPPQPGMPAAPY PMQYPPPYPAQPMGPPAYHETLAGGAAAPYPASQPPYNPAYMDA PKAAL
5933		3190	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK APSIGKMSTAKRTLSKKEQEELKKKEDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVNAAKEEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIBTKKPPLKKGEKEKKKSNLELFKEELKQI QEERDERHRTKGRLSRFEPPQSDSDGQRRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAFMNRDAERALKNLNGKMI MSFEMKLGMGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEFVVREGPMFEAMIMNREINNPMFRFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNPYLHGMSEEQ ETEAFVEEPSKKGALKEEQRDKLBEILRGLTPRKNDIGDAMVFC LNNAEAAEEIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHQSENFKQRVM TCFRAWEDWAIYPEPFLIKLQNIFLGLVNIIBEKETEDVPDDLD GAPIEEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD QHEESEEEENQNQEEESBDEEDTQSSKSEEHHLYSNPIKEEMTE SKFSKYSEMSEBKRAKLREIELKVMKFQDELESGKRPKKPGQSF QEQVEHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK DECTPTRKERKRRHSTSPSPSRSSSGRVKSPSPSRSERSRSER SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPRRSRRSRSSP KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLF
5934	1	3190	GTRKLKMADKTPGGSQKASSKTRSSDVHSSGSSDAHMDASGPSD SDMPSRTRPKSPRKHNYRNESARESLCDSPHQNLSRPLLENKLK AFSIGKMSTAKRTLSKKEQEELKKKBDEKAAAEIYEEFLAAFEG SDGNKVKTFVRGGVVNAAKBEHETDEKRGKIYKPSSRFADQKNP PNQSSNERPPSLLVIETKKPPLKKGEKEKKKSNLELFKEELKQI QEERDBRHKTKGRLSRFEPPQSDSDQGRSMDAPSRRNRSSGVL DDYAPGSHDVGDPSTT\NFYLGNI\NPQMNLKKCCCQEFGRFGP LASVKIMWPRTDEERARERNCGFVAPMNRRDAERALKNLNGKMI MSFEMKLGWGKAVPIPPHPIYIPPSMMEHTLPPPPSGLPFNAQP RERLKNPNAPMLPPPKNKEDFEKTLSQAIVKVVIPTERNLLALI HRMIEPVVREGPMFEAMIMNREINNPMFFLFENQTPAHVYYRW KLYSILQGDSPTKWRTEDFRMFKNGSFWRPPPLNYLHGMSBEQ ETAFVEEPSKKGALKEEQRDKLEEILRGLTPRKNDIGDAMVFC LNNAEAAEBIVDCITESLSILKTPLPKKIARLYLVSDVLYNSSA KVANASYYRKFFETKLCQIFSDLNATYRTIQGHLQSENFKQRVM TCFRAWEDWAIYPBPPLIKLQNIFLGLVNIIEEKBTEDVPDLD GAPIBEELDGAPLEDVDGIPIDATPIDDLDGVPIKSLDDDLDGV

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ĺ	to first	amino acid	D-Droline, Mamethionine, Nasparagine,
	amino acid		P=Proline, Q=Glutamine, R=Arginine,
•		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
}			PLDATEDSKKNEPIFKVAPSKWEAVDESELEAQAVTTSKWELFD
			QHEESEBEENQNQEEESEDBEDTQSSKSEEHHLYSNPIKEEMTE
ĺ			SKFSKYSEMSEEKRAKLREIELKVMKFQDELESGKRPKKPGQSF
			QEQVEHYRDKLLQREKEKELERERERDKKDKEKLESRSKDKKEK
	i		DECTPTRKERKRRHSTSPSPSRSSSGRRVKSPSPKSERSERSER
			SHKESSRSRSSHKDSPRDVSKKAKRSPSGSRTPKRSRSRSRSP
ļ	į		KKSGKKSRSQSRSPHRSHKKSKGKTNTGRKFFKKAVTYWKCDLF
ļ		i	LCPERSVF
5935	3	4493	SYWLSGWRLSRPPRQFWAGWRGIGRFGTMAPVHGDDCEIGASAL
			TGVYEEVDEEQYSKLVQARQDDDWIVDDDGIGYVEDGREIFDDD
			LEDDALDADEKGKDGKARNKDKRNVKKLAVTKPNNIKSMFIACA
1			GKKTADKAVDLSKDGLLGDILQDLNTETPQITPPPVMILKKKRS
1	}		IGASPNPFSVHTATAVPSGKIASPVSRKEPPLTPVPLKRAEFAG
			DDVQVESTEEEQESGAMEFEDGDFDEPMEVEEVDLEPMAAKAWD
			DDVQVESTEEEQESGAMEFEDGDFDEPMKVEKVDLEPMAAKAWD
1			KESEPAEEVKQEADSGKGTVSYLGSFLPDVSCWDIDQEGDSSFS
			VQEVQVDSSHLPLVKGADEEQVFHFYWLDAYEDQYNQPGVVFLF
İ			GKVWIESAETHVSCCVMVKNIERTLYFLPREMKIDLNTGKETGT
			PISMKDVYEEFDEKIATKYKIMKFKSKPVEKNYAFEIPDVPEKS
			EYLEVKYSAEMPQLPQDLKGETFSHVFGTNTSSLELFLMNRKIK
			GPCWLEVKKSTALNQPVSWCKVEAMALKPDLVNVIKDVSPPPLV
			VMAFSMKTMQNAKNHQNEIIAMAALVHHSFALDKAAPKPPFQSH
1			FCVVSKPKDCIFPYAFKEVIEKKNVKVEVAATERTLLGFFLAKV
			HKIDPDIIVGHNIYGFELEVLLQRINVCKAPHWSKIGRLKRSNM
J			PKLGGRSGFGERNATCGRMICDVEISAKELIRCKSYHLSELVQQ
			ILKTERVVIPMENIQNMYSESSQLLYLLEHTWKDA\KFILQIMC
1			ELNVLPLALQITNIAGNIMSRTLMGGRSERNBFLLLHAFYENNY
			IVPDKQIFRKPQQKLGDEDEEIDGDTNKYKKGRKKGAYAGGLVL
'			DPKVGFYDKFILLLDFNSLYPSIIQEFNICFTTVQRVASEAQKV
			TEDGEQEQIPELPDPSLEMGILPREIRKLVERRKQVKQLMKQQD
			LNPDLILQYDIRQKALKLTANSMYGCLGFSYSRFYAKPLAALVT
1			YKGREILMHTKEMVQKMNLEVIYGDTDSIMINTNSTNLERVFKL
			GNKVKSEVNKLYKLLEIDIDGVFKSLLLLKKKKYAALVVEPTSD
			GNYVTKQELKGLDIVRRDWCDLAKDTGNFVIGQILSDQSRDTIV
			ENIQKRLIEIGENVLNGSVPVSQFEINKALTKDPQDYPDKKSLP
		•	HVHVALWINSQGGRKVKAGDTVSYVICQDGSNLTASQRAYAPEQ
i			LQKQDNLTIDTQYYLAQQIHPVVARICEPIDGIDAVLIATGWEL
[]			\DPTQFKVHHYHKDEENDALLGGPAQLTDEEKYRDCERFKCPCP
	į		TCGTENIYDNVFDGSGTDMEPSLYRCSNIDCKASPLTFTVQLSN
			KLIMDIRRFIKKYYDGWLICEEPTCRNRTRHLPLQFSRTGPLCP
			ACMKATLQPEYSDKSLYTQLCFYRYIFDAECALEKLTTDHEKDK
			LKKQFFTPKVLQDYRKLKNTAEOFLSRSGYSEVNLSKLFAGCAV
			KS KS
5936	1124	139	
1 2230	4444	133	RGEEOFDAEFRRFACLGFGERLQEFSRLLRAVHRSRAWTCYLAI
			RMLMATCCPSPTTTACTGPWQRAPPLRLLVQKRRADSSGLAFAS
1			NSLQRRKKGLLLRPVAPLRTRPPLLISLPQDFRQVSSVIDVDLL
			PETHRRVRLHKHGSDRPLGFYIRDGMSVRVAPQG\LERVPGIFI
			SRLVRGGLAESTGLLAVSDEILEVNGIEVAGKTLNQVTDMMVAN
			SHN\LIVTVKPANQRNNVVRGASGRLTGPPSAGPGPAEPDSDDD
			SSDLVIENRQPPSSNGLSQGPPCWDLHPGCRHPGTRSSLPSLDD
			QEQASSGWGSRIRGDGSGFSL
5937	31	1600	PTSLLKSTVQLMCRLLQDKRYQCVYSLAEIFKVLASFYVILVIL
			YGLTSSYSLWWMLRSSLKQYSFEALREKSNYSDIPDVKNDFAFI
) .			LHLADQYDPLYSKRFSIFLSEVSENKLKQINLNNEWTVEKLKSK
1 1			LVKNAQDKIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPS
	İ		AVSQLVNLKELRVYHSSLVVDHPALAFLEENLKILRLKFTEMGK
			IPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNLRTLYL
			KSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKS
			LELISCDLERIPHSIFSLNNLHELDLRENNLKTVEEIISFQHLQ
	1		NLSCLKLWHNNIAYIPAQIGALSNLEQLSLDHNNIENLPLQLFL
			CTKLHYLDLSYNHLTFIPEEIQYL\SNLQYFAVTNNNIEMLPDG
			PIGETTAL AND AND A PROPERTY OF THE PROPERTY OF

050	I Dead at -2	Dradiated 3	
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
	 		LFQCKKLQCLLLGKNSLMNLSPHVGELSNLTHREPIG\NYLETL
1	l		PPELEGCQSLKRNCLIVEENLLNTLPLPVTERLQTCLDKC
5938	395	1865	
3336	395	1862	YKGEGFFCNQEARGERRKKKKAMSSPNIWSTGSSVYSTPVFSQK
			MTVWILLLLSLYPGFTSQKSDDDYEDYASNKTWVLTPKVPEGDV
			TVILNNLLEGYDNKLRPDIGVKPTLIHTDMYVNSIGPVNAINME
			YTIDIFFAQTWYDRRLKFNSTIKVLRLNSNMVGKIWIPDTFFRN
1			SKKADAHWITTPNRMLRIWNDGRVLYSLRLTIDAECQLQLHNFP
1	ł		MDEHSCPLEFSSYGYPREEIVYQWKRSSVEVGDTRSWRLYOFSF
			VGLRNTTEVVKTTSGDYVVMSVYFDLSRRMGYFTIQTYIPCTLI
1			VVLSWVSFWINKDAVPARTSLGITTVLTMTTLSTIARKSLPKVS
1	i		YVTAMDLFVSVCFIFVFSALVEYG\TLHYFVSNRKPSKDKDKKK
			KNPAPTIDIRPRSATIQMNNATHLQERDEEYGYECLDGKDCASF
			FCCFEDCRTGAWRHGRIHIRIAKMDSYARIFFPTAFCLFNLVYW
5939		1404	VSYLYL
5555	66	1404	IRPGYLKEVQENSPGHRAGLEPFFDFIVSINGSRLNKDNDTLKD
			LLKANVEKPVKMLIYSSKTLELRETSVTPSNLWGGQGLLGVSIR
1			FCSFDGANENVWHVLEVESNSPAALAGLRPHSDYIIGADTVMNE
1			SEDLFSLIETHEAKPLKLYVYNTDTDNCREVIITPNSAWGGEGS
			LGCGIGYGYLHRIPTRPFEEGKKISLPGQMAGTPITPLKDGFTE
			VQLSSVNPPSLSPPGTTGIEQSLTGLSISSTP\PAVSSVLSTGV
1			PTVP\LLPPQVNQSLTSVPPMESSYLHLPGLMPFTRQGLPNLPQ
i			PSTFNLPR\PTHSWPGVGLYQEFVKPGVLPPLSSMPPRNLPG\I
1			APLPLPSEFLPSFPLVPESSSAASSGELLSSLPPTSNAPSDPAT
į			TTAKADAASSLTVDVTPPTAKAPTTVEDRVGDSTPVSEKPVSAA
1			VDANASESP
5940	145	717	RRSASRSASPRQSAGTAVTTGTRAGGTCLAAAHHRMRWRADGRS
1		,	LEKLPVHMGLVITEVEQEPSFSDIASLVVWCMAVGISYISVYDH
			COTENDATED MEET ACCOUNT OF DOCUMENTAL STATEMENT OF THE PROPERTY OF THE PROPERT
Ì			QGIFKRNNSRLMDEILKQQQELLGLDCSKYSPEFANSNDKDDQV
			LNCHLAVKVLSPEDGKADIVRAAQDFCQLVAQKQKRPTDLDVDT
5041			LA/VYLVQMVVLILI
5941	13	6147	MCLGRMGASSPRSPEPVGPPAPGLPFCCGGSLLAVVVLLALPVA
i			WGQCNAPEW\LPFARPTNLTDEFEPPIGTYLNYECRPGYSGRPF
			SIICLKNSVWTGAKDRCRRKSCRNPPDPVNGMVHVIKGIQFGSQ
	1		IKYSCTKGYRLIGSSSATCIISGDTVIWDNETPICDRIPCGLPP
1	ł		TITNGDFISTNRENFHYGSVVTYRCNPGSGGRKVFELVGEPSIY
			CTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGILVSDNRSLFSL
			NEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPSCSRVCQPPPD
·			VLHAERTORDKDNFSPGQEVFYSCEPGYDLRGAASMRCTPOGDW
			SPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGAKVDFVCDEGF
			QLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSPPVIPNGRHTG
			KPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRCTSDPOGNG
1			VWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASDFPIGTSLKYE
1			CRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKTPPDPVNGMVH
1			VITDIQVGSRINYSCTTGHRLIGHSSAECILSGNAAHWSTKPPI
	Ì		CQRIPCGLPPTIANGDFISTNRENFHYGSVVTYRCNPGSGGRKV
1			FELVGKPSIYCTSNDDQVGIWSGPAPQCIIPNKCTPPNVENGIL
1			VSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQALNKWEPELPS
1			CSRVCQPPPDVLHAERTQRDKDNFSPGQEVFYSCBPGYDLRGAA
1	[SMRCTPQGDWSPAAPTCEVKSCDDFMGQLLNGRVLFPVNLQLGA
			KVDFVCDEGFQLKGSSASYCVLAGMESLWNSSVPVCEQIFCPSP
			PVIPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTI
{			RCTSDPQGNGVWSSPAPRCGILGHCQAPDHFLFAKLKTQTNASD
1			FPIGTSLKYECRPEYYGRPFSITCLDNLVWSSPKDVCKRKSCKT
1			PPDPVNGMVHVITDIQVGSRINYSCTTGHRLIGHSSAECILSGN
1			TAHWSTKPPICQRIPCGLPPTIANGDFISTNRENFHYGSVVTYR
[CNLGSRGRKVFELVGEPSIYCTSNDDQVGIWSGPAPQCIIPNKC
.			TPPNVENGILVSDNRSLFSLNEVVEFRCQPGFVMKGPRRVKCQA
			LNKWEPELPSCSRVCQPPPEILHGEHTPSHQDNFSPGQEVFYSC
			EPGYDLRGAASLHCTPQGDWSPEAPRCAVKSCDDFLGQLPHGRV
1			LFPLNLQLGAKVSFVCDEGFRLKGSSVSHCVLVGMRSLWNNSVP
L	L		VCEHIFCPNPPAILNGRHTGTPSGDIPYGKEISYTCDPHPDRGM

SEQ Predicted beginning nucleotide location nucleotide location nucleotide location corresponding to first amino acid segment containing signal per (A=Alanine, C=Cysteine, D=Aspartic Acid Glutamic Acid, F=Phenylalanine, G=Glyci H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valline, W=Tryptophan, Y=Tyrosine, X=Unknown, *= Codon, /=possible nucleotide deletion, \	Stop TPEQF ENLVWS HEGFRL HEFYSNN QVGVW RCQPG TTLSHQ
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence codon, /=possible nucleotide deletion, /=possible nucleotide deletion, responding sequence sequence codon, /=possible nucleotide deletion, /=possible nucleotide deletion, responding sequence sequence codon, /=possible nucleotide deletion, /=possible nucleotide deletion, responding sequence codon, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, repossible nucleotide insertion) codon, /=possible nucleotide deletion, /=possible nucleotide insertion repossible nucleotide deletion, repossible nucleotide insertion repossible nucleotide deletion, repossible nucleotide insertion repossible nucleotide deletion, repossible nucleotide insertion repossible nucleotide deletion, repossible nucleoti	TPEQF TPEQF TNLVWS TEGFRL TPYSNN QVGVW RCQPG TLSHQ
location corresponding to first amino acid residue of amino acid sequence PFASPTIPINDFEFPVGTSLNYECRPGYFGKMFSISCLE SVEDNCRRKSCGPPPEFFNGMYHINTDTQFGSTVNYSCN IGSPSTTCLVSGNNVTWDKKAPICELISCEPPPTISNGD RTSFHORTVVTYQCTTGRWGPKLPHCSRVCQPPPELLHGEH DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPR CDDFLGQLPHGRVLLPLNQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPAILNGRHTGFTLGDI VSYTCDPHDRGMTSLIFFTLGDI VSYTCDPHDRGMTSLIFFTLGDI GFIFTDQGIWSQLDHYCKEVNCSFPLFMIGISCEPM GDYVTLKCEDGYTLESSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	Stop TPEQF CNLVWS EEGFRL FYSNN OVGVW RCQPG TLSHQ
location corresponding to first amino acid residue of amino acid sequence This is a comes a	TPEOF CNLVWS EGFRL FYSNN OVGVW RCQPG TLSHQ
corresponding to first amino acid residue of amino acid sequence P=Proline, Q=Glutamine, N=Asparagine, Y=Valine, amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Codon, /=possible nucleotide deletion, \	TPEOF CNLVWS EGFRL FYSNN OVGVW RCQPG TLSHQ
to first amino acid residue of amino acid sequence P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *= Codon, /=possible nucleotide deletion, \text{ =possible nucleotide insertion} TFNIIGESTIRCTSDPHGNGWSSPAPRCELSVRAGHCK PFASPTIPINDFEFPVGTSLNYECRPGYPGKMFSISCLE SVEDNCRRKSCGPPPEPFNGMVHINTDTQFGSTVNYSCN IGSPSTTCLVSGNNVTWDKKAPICELISCEPPPTISNGD RTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDD SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEILFF FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEH DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPR CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI VSYTCDPHPDRRGMTFNLIGESTIRRTSSPHGNGVWSSPA PVGAACPHPPKIQGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMK GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	TPEOF CNLVWS EGFRL FYSNN OVGVW RCQPG TLSHQ
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *= Codon, /=possible nucleotide deletion, \ possible nucleotide insertion) TFNLIGESTIRCTSDPHGNGVWSSPAPRCELSVRAGHCK PFRASPTIPINDFEFPVGTSLNYECRPGYPGKMFSISCLE SVEDNCRRKSCGPPPEPFNGMVHINTDTQFGSTVNYSCN IGSPSTTCLVSGNNVTWDKKAPICELISCEPPPTISNGD RTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDD SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEILRF FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEH DNFSFGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPR CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKLQNGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFMMGISKELEMK GDYVTLKCEDGYTLEGSPWSQCQADDRNDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	TPEOF CNLVWS EGFRL FYSNN OVGVW RCQPG TLSHQ
residue of amino acid sequence W=Tryptophan, Y=Tyrosine, X=Unknown, *= Codon, /=possible nucleotide deletion, \	TPEOF CNLVWS EGFRL FYSNN OVGVW RCQPG TLSHQ
residue of amino acid sequence	TPEOF CNLVWS EGFRL FYSNN OVGVW RCQPG TLSHQ
amino acid sequence Codon, /=possible nucleotide deletion, =possible nucleotide insertion) TFNLIGESTIRCTSDPHGNGVWSSPAPRCELSVRACHCK	TPEOF CNLVWS EGFRL FYSNN OVGVW RCQPG TLSHQ
=possible nucleotide insertion	ENLVWS EEGFRL FYSNN OQVGVW RCQPG
TFNLIGESTIRCTSDPHGNGVWSSPAPRCELSVRAGHCK PFASPTIPINDFEFPVGTSLNYECRPGYFGKMFSISCLE SVEDNCRRKSCGPPPEPFNGWVHINTDTQFGSTVNYSCN IGSPSTTCLVSGNVTWDKKAPICEIISCEPPPTISNGD RTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDD SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRF FVMYGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEH DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPR CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIQGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTQGIWSQLDHYCKEVNCSFPLFWNGISKELEMK GDYYTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	ENLVWS EEGFRL FYSNN OQVGVW RCQPG
TFNLIGESTIRCTSDPHGNGVWSSPAPRCELSVRAGHCK PFASPTIPINDFEFPVGTSLNYECRPGYPGKMFSISCLE SVEDNCRRKSCCPPPEPFNGMVHINTDTQFGSTVNYSCN IGSPSTTCLVSGNNVTWDKKAPICELISCEPPPTISNGD RTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDD SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRF FVMYGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEH DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPR CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFWNGISKELEMK GDYYTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	ENLVWS EEGFRL FYSNN OQVGVW RCQPG
PFASPTIPINDFEFPVGTSLNYECRPGYFGKMFSISCLE SVEDNCRRKSCGPPPEPFNGMVHINTDTQFGSTVNYSCN IGSPSTTCLVSGNNVTWDKKAPICEIISCEPPPTISNGD RTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDD SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRF FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEH DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPR CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFWNGISKELEMK GDYYTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	ENLVWS EEGFRL FYSNN OQVGVW RCQPG
SVEDNCRRKSCGPPPEPFNGMVHINTDTQFGSTVNYSCN IGSPSTTCLVSGNNVTWDKKAPICEIISCEPPPTISNGD RTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDD SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRF FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEH DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPR CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMK GDYYTLKCEDGYTLEGSPWSQCQADDRNDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	TEGFRL DFYSNN DQVGVW TRCQPG TLSHQ
IGSPSTTCLVSGNNVTWDKKAPICEIISCEPPPTISNGD RTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDD SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRF FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEH DNFSFGQEVFYSCEPSYDLRGAASLHCTPQGDWSPRAPR CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGFPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMK GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	FYSNN QVGVW RCQPG TLSHQ
RTSFHNGTVVTYQCHTGPDGEQLFELVGERSIYCTSKDD SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRF FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEH DNFSFGQEVFYSCEPSYDLRGAASLHCTPQGDWSPRAPR CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGFPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMK GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	QVGVW RCQPG TLSHQ
SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRF FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEH DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPR CDPFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIQNGYJGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFWNGISKELEMK GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	RCQPG TLSHQ
SSPPPRCISTNKCTAPEVENAIRVPGNRSFFSLTEIIRF FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEH DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPR CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIQNGYJGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFWNGISKELEMK GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	RCQPG TLSHQ
FVMVGSHTVQCQTNGRWGPKLPHCSRVCQPPPEILHGEH DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPR CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFWNGISKELEMK GDYYTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	TLSHQ
DNFSPGQEVFYSCEPSYDLRGAASLHCTPQGDWSPEAPR CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFWNGISKELEMK GDYYTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	
CDDFLGQLPHGRVLLPLNLQLGAKVSFVCDEGFRLKGRS LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIJOGHYJIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMK GDYVTLKCEDGYTLEGSPWSQCQADDRNDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIJLKHRKGNNAHENPKEVAI	CTITIC
LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMK GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	באעוט.
LAGMKALWNSSVPVCEQIFCPNPPAILNGRHTGTPLGDI VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMK GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	
VSYTCDPHPDRGMTFNLIGESTIRRTSEPHGNGVWSSPA PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMK GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	
PVGAACPHPPKIQNGHYIGGHVSLYLPGMTISYTCDPGY GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMK GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	
GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMK GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	PRCEL
GFIFCTDQGIWSQLDHYCKEVNCSFPLFMNGISKELEMK GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	LLVGK
GDYVTLKCEDGYTLEGSPWSQCQADDRWDPPLAKCTSRT VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	
VGTLSGTIFFILLIIFLSWIILKHRKGNNAHENPKEVAI	
GGSSVHPRTIOTNEENSRVI.P	HLHSQ
	VCDVT
DK\AQMIRFEERTGYFSSTDLGRTASHYYIKYNTIETFN	
HKTEGDIFAIVSKAEEFDQIKVREEEIEELDTLLSNFCB	LSTPG
GVENSYGKINILLQTYINRGEMDSFSLISDSAYVAQNAA	RIVRA
LFEIALRKRWPTMTYRLLNLSKAIDKRLWGWASPLROFS	
MLTRLEEKKLTVDKLKDMRKDEIGHILHHVNIGLKVKQC	
SVMMEAFIQPITRTVLRVTLSIYADFTWNDQVHGTVGEP	WWIWV
EDPTNDHIYHSEYFLALKKOVISKEAQLLVFTIPIFEPL	PSQYY
IRAVSDRWIGAEAVCIINFOHLILPERHPPHTELLDLQP	_
LGCKAYEALYNFSHFNPVQTQIFHTLYHTDCNVLLGAPT	
VAAELAI FRVFNKYPTSKAVYIAPLKALVRERMDDWKVR	IEEKL
GKKVIELTGDVTPDMKSIAKADLIVTTPEKWDGVSRSWQ	NRNYV
OOVTILIIDEIHLLGEERGPVLEVIVSRTNFISSHTEKP	VRTVC
LSTALANARDLADWLNIKQMGLFNFRPSVRPVPLEVHIC	
HYCPRMASMNKPAFQAIRSHSPAKPVLIFVSSRRQTRLT	ALELI
AFLATEEDPKQWLNMDEREMENI I ATVRDSNLKLTLAFG	IGMHH
AGLHERDRKTVEELFVNCKVQVLIATSTLAWGVNFPAHL	VIIKG
TEYYDGKTRRYVDFPITDVLQMMGRAGRPQFDDQGKAVI	
KKDFYKKFLYEPFPVESSLLGVLSDHLNAEIAGGTITSK	CDALD
YITWTYFFRRLIMNPSYYNLGDVSHDSVNKFLSHLIEKS	LIELE
LSYCIEIGEDNRSIEPLTYGRIASYYYLKHQTVKMFKDR	LKPEC
STEELLS I LSDAREYTDLPVRHNEDHMNSELAKCLP IES	
DSPHTKAHLLLQAHLSRAMLPCPDYDTDTKTVLDQALRV	
DVAANQGWLVTVLNITNLIQMVIQGRWLKDSSLLTLPNI	ENHHL
HLFKKWKPIMKGPHARGRTSIECLPELIHACGGKDHVFS	SMVES
ELHAAKTKQAWNFLSHLPEINVGISVKGSWDDLVEGHNE	
LTADKRDDNKWIKLHADOEYVLOVSLORVHFGFHKGKPE	
PRFPKSKDEGWFLILGEVDKRELIALKRVGY1RNHHVAS	LSFYT
PEIPGRYIYTLYFMSDCYLGLDQQYD/NLSQRYTSESFC	TGOHO
GL	
5943 1 2274 DKPTRHKTYLSSSWAKMAAAEGPVGDGELWQTWLPNHVV	
EGLKNQSPTEAEKPASSSLPSSPPPQLLTRNVVFGLGGE	LFLWD
GEDSSFLVVRLRGPSGGG\EEPALSQYQRLLCINPPLFE	IYOVL
LSPTOHHVALIGIKGLMVLELPKRWGKNSEFEGGKSTVN	
VAERFFTSSTSLTLKHAAWYPSEILDPHVVLLTSDNVIR	
EPQTPTNVIILSEABEESLVLNKGRAYTASLGETAVAFD	FGPLA
AVPKTLFGQNGKDEVVAYPLYILYENGETFLTYISLLHS	PGN/I
WKAVGSIAHAS\AABDNYGYDACAVLCLPCVPNILVIAT	
YHCVVLEGEEEDDHTSEKSWDSRIDLIPSLYVFECVBLE	LALKT
ASGEDDPFDSDFSCPVKLHRDPKCPSRYHCTHEAGVHSV	
HKLHKFLGSDEEDKDSLQELSTRQKCFVEHILCTKPLPC	
	GLTWI
IRGFWIVPDILGPTMICITSTYECLIWPLLSTVHPASPP	GLTWI ROPAP
EDVEVAESPLRVLAETPDSFEKHIRSILQRSVANPAFLK	GLTWI ROPAP LLCTR
EDAEAMESTRATURITABLEMETRSIDGES AWARMENT	GLTWI ROPAP LLCTR
1	GLTWI ROPAP LLCTR ASEKD
IAPPPEECLQLLSRATQVFREGYILKQDLAKEEIQRRVK KKKOLEDLSYCREERKSLREMAERLADKYEEAKEKQEDI	GLTWI RQPAP PLLCTR ASEKD LLCDQ

SEO	Predicted	Predicted end	Amino pold
ID	beginning		Amino acid segment containing signal peptide
NO:		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lvsine.
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine.
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 4	\=possible nucleotide insertion)
	2040000		(=possible nucleotide insertion)
	ļ		KLLHSFHSELPVLSDSERDMKKELQLIPDQLRHLGNAIKQVTMK
		1	KDYQQQKMEKVLSLPKPTIILSAYQRKCIQSILKEEGEHIREMV
			KQINDIRNHVNF
5944	167	3428	FSIATFTDEPEVLTEPPSATTTTTIGISATWTTLAGSHGKRNNT
		1	ITTTSSKRKNRKNKITPENVQIIFDDPLPISYSQPEKVNGESKS
	İ	1	SSTSESGDSDNMRISSCSDESSNSNSSRKSDNHSPAVVTTTVSS
i		-	KKQPSVLVTFPKEERKSVSGKASIKLSETISEGTSNSLSTCTKS
		[GPSPLSSPNGKLTVASPKRGQKREEGWKEVVRRSKKVSVPSTVI
	1		SRVIGRGGCNINAIREFTGAHIDIDKQKDKTGDRIITIRGGTES
1		i	TRQATQLINALIKDPDKBIDELIPKNRLKSSSANSKIGSSAPTT
			TANNEL MCTIONERING CONCORDED TRANSCONDERING
ļ	1	,	TAANTSLMGIKMTTVALSSTSQTATALTVPAISSASTHKTIKNP
			VN\NVRPGFPVSFP\LAYPPPQFAHALLAAQTFQQIRPPRLPMT
	1		HFGGTFPPAQSTWGPFPVRPLSPARATNSPKPHMVPRHSNQNSS
			GSQVNSAGSLTSSPTTTTSSSASTVPGTSTNGSPSSPSVRRQLF
1			VTVVKTSNATTTTVTTTASNNNTAPTNATYPMPTAKEHYPVSSP
1			SSPSPPAQPGGVSRNSPLDCGSASPNKVASSSEQEAGSPPVVET
l			TNTRPPNSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
ĺ			EVRMTVPPLATSSAPVAVPSTAPVTYPMPQTPMGCPQPTPKMET
	Į i		PAIRPPPHGTTAPHKNSASVQNSSVAVLSVNHIKRPHSVPSSVQ
			LPSTLSTQSACQNSVHPANKPIAPNFSAPLPFGPFSTLFENSPT
ļ	1		SAHAFWGGSVVSSQSTPESMLSGKSSYLPNSDPLHQSDTSKAPG
i			FRPPLQRPAPSPSGIVNMDSPYGSVTPSSTHLGNFASNISGGQM
			YGPGAPLGGAPAAANFNRQHFSPLSLLTPCSSASNDSSAQSVSS
			GVRAPSPAPSSVPLGSEKPSNVSQDRKVPVPIGTERSARIRQTG
			TSAPSVIGSNLSTSVGHSGIWSFEGIGGNQDKVDWCNPGMGNPM
	1	'	IHRPMSDPGVFSQHQAMERDSTGIVTPSGTFHQHVPAGYMDFPK
			VGGMPFSVYGNAMIPPVAPIPDGAGGPIFNGPHAADPSWNSLIK
		•	MUSCOTENNICHOTENEGRANDERNAMENTO
5945	1461	197	MVSSSTENNGPQTVWTGPWAPHMNSVHMNQLG
33.13	1401	191	GVTHLFLFGKRKLRNGIAEDLKGQADFFFLLVSEAVVATGSPRA
			WLTCLILPLPGIIFSVLPKAMSRPLLITFTPATDPSDLWKDGQQ
			QPQPEKPESTLDGAAARAFYEALIGDESSAPDSQRSQTEPARER
1			KRKKRRIMKAPAAEAVAEGASGRHGQGRSLEAEDKMTHRILRAA
			QEGDLPELRRLLEPHEAGGAGGNINARDAFWWTPLMCAARAGQG
			AAVSYLLGRGAAWVGVCELSGRDAAQLAEEAGFPEVARMVRESH
		ŀ	GETRSPENRSPTPSLQYCENCDTHFQDSNHRTSTAHLLSLSQGP
			QPPNLPLGVPISSPGFKLLLRGGWEPGMGLGPRGEGRANPIPTV
			LKRDQEGLGYRSAPQPRVTHFPAWDTRAVAGRE\TPPRVATLSW
			REERRREE\KDRAWERDLRTYMNLEF
5946	541	1666	ILGSYSSIQPEEYS\SVVC\EVVLQDLLA\YVSPK\HSYLRDLP
			SEGSPQRVNSIDFV\EL\EHLQPDVLVHAVLRVVDF/TILTEAV
		}	YSYRGQKQKKVMLTVEQAQDQHYALVLWGPGAAW\YPQLQRKKG
	1		YIWEFKYLFVQCNYTLENLELHTTPWSSCECLFDDDIRAITFKA
			KFQKSAPSFVKISDLATHLEDKCSGVVLIKAQISELAFPITASQ
			KIALNAHSSLKSIFSSLPNIVYTGCAKCGLELETDENRIYKQCF
	1	1	SCLPFTMKKIYYRPALMTAIDGRHDVCIRVESKLIEKILLNISA
	 		DCLNRVIVPSSEITYGMVVADLFHSLLAVSAEPCVLKIQSLFVL
		1	DENSYPLOODEST LORY VADDE ROLLING STEVE
5947	3	1317	DENSYPLQQDFSLLDFYPDIVKHGANARL
• = /	- 1	1311	RGIPDRRRRGPIGRVNMDLENKVKKMGLGHEQGFGAPCLKCKEK
			CEGFELHFWRKICRNC\NVAKKSM/TVLLSNEEDRKVGKLFEDT
[İ	KYTTLIAKLKSDGIPMYKRNVMILTNPVAAKKNVSINTVTYEWA
	İ		PPVQNQALARQYMQMLPKEKQPVAGSEGAQYRKKQLAKQLPAHD
	1		QDPSKCHELSPREVKEMEQFVKKYKSEALGVGDVKLPCEMDAQG
1			PKQMNIPGGDRSTPAAVGAMEDKSAEHKRTOYSCYCCKLSMKEG
	1		DPAIYAERAGYDKLWHPACFVCSTCHELLVDMIYFWKNEKLYCG
			RHYCDSEKPRCAGCDELIFSNEYTQAENONWHLKHFCCFDCDSI
			LAGEI YVMVNDKPVCKPCYVKNHAVVCQGCHNAI DPEVQRVTYN
		ľ	NFSWHASTECFLCSCCSKCLIGQKFMPVEGMVFCSVECKKRMS
5948	39	3370	YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ
1			GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM
' F			VETETECHI. HD TCT EDDI ETTI EDDY DE OPROBLEMENT
į	[VEIEIEGRIHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP
			PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRIVEY

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
I	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ĺ	\=possible nucleotide insertion)
			SPPSAPRRPPVYYKFIEKSABELDNEVEYDMDEEDYAWLEIVNE
1			KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQQSLIDEDA
1			VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGQWLC/
			RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
]			E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
i			QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA
ł			YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
1			KKAKKAKKALAEPCAVLPTVCAPYIPPORLNRIANOVAIORKKO
ŀ			FVERAHSYWLLKRLSRNGAPLLRRLOSSLOSORSSOORENDEEM
			KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREOVKVEOVA
Į			MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI
j			KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
ł			FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
			RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG
			SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
1			GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESPGKRLDAGL
İ			TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSSNSPLCDSS
}			FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV
	1		GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWQ
			WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
			SRVHGEPTSDLSDID
5949	39	3370	YRERYPVSGGSVLRSALEVCWDFLSGLTEGSLLPEGFFSGPIDQ
			GNHYQMRRKGRCHRGSAARHPSSPCSVKHSPTRETLTYAQAQRM
			VEIEIEGRLHRISIFDPLEIILEDDLTAQEMSECNSNKENSERP
	i		PVCLRTKRHKNNRVKKKNEALPSAHGTPASASALPEPKVRTVEY
			SPPSAPRRPPVYYKFIEKSAEELDNEVEYDMDEEDYAWLEIVNE
			KRKGDCVPAVSQSMFEFLMDRFEKESHCENQKQGEQOSLIDEDA
			VCCICMDGECQNSNVILFCDMCNLAVHQECYGVPYIPEGOWLC/
1			RAHCLQSRARPADCVLCPNKGGAFKKTDDDRWGHV\VCALW\IP
			E\VGFANTVFIEPIDGVRNIPPARWKLT\CNLCKEKGR/VGACI
1			QCHKANCYTAFHVTCAQKAGLYMKMEPVKELTGGGTTFSVRKTA
	ļ		YCDVHTPPGCTRRPLNIYGDVEMKNGVCRKESSVKTVRSTSKVR
			KKAKKAKALAEPCAVLPTVCAPYIPPQRLNRIANQVAIQRKKQ
1			FVERAHSYWLLKRLSRNGAPLLRRLQSSLQSQRSSQQRENDEEM
1			KAAKEKLKYWQRLRHDLERARLLIELLRKREKLKREQVKVEQVA MELRLTPLTVLLRSVLDQLQDKDPARIFAQPVSLKEVPDYLDHI
1			KHPMDFATMRKRLEAQGYKNLHEFEEDFDLIIDNCMKYNARDTV
1			FYRAAVRLRDQGGVVLRQARREVDSIGLEEASGMHLPERPAAAP
			RRPFSWEDVDRLLDPANRAHLGLEEQLRELLDMLDLTCAMKSSG
			SRSKRAKLLKKEIALLRNKLSQQHSQPLPTGPGLEGFEEDGAAL
			GPEAGEEVLPRLETLLQPRKRSRSTCGDSEVEEESPGKRLDAGI,
			TNGFGGARSEQEPGGGLGRKATPRRRCASESSISSSNSPLCDSS
		i	FNAPKCGRGKPALVRRHTLEDRSELISCIENGNYAKAARIAAEV
	•		GQSSMWISTDAAASVLEPLKVVWAKCSGYPSYPALIIDPKMPRV
			PGHHNGVTIPAPPLDVLKIGEHMQTKSDEKLFLVLFFDNKRSWO
			WLPKSKMVPLGIDETIDKLKMMEGRNSSIRKAVRIAFDRAMNHL
5950	1156	7.7.	SRVHGEPTSDLSDID
2930	1166	373	ESRSLTMSTSQPGACPCQGAASRPAILYALLSSSLKAVPRPRSR
			CLCRQHRPVQLCAPHRTCREALDVLAKTVAFLRNLPSFWQLPPQ
			DORRLLOGCWGPLFLLGLAQDAVTFEVAEAPVPSILKKILLEEP
)	}		SSSGGSGQLPDRPQPSLAAVQWLQCCLESFWSLELSPKE\YACL
]			KGPILFNPDVPGLQAASHIGHLQQEAHWVLCEVLEPWCPAAQGR
5951	143	5449	LTRVLLTASTLKSIPTSLLGDLFFRPIIGDVDIAGLLGDMLLLR
		2443	WNVKPSLLVVQLFKFSDKEEHEQNDSISGKTGETGVEEMIATRK
į l			VEQDSKETVKLSHEDDHILEDAGSSDISSDAACTNPNKTENSLV GLPSCVDEVTECNLELKDTMGIADKTENTLERNKIBPLGYCEDA
			ESNRQLESTEFNKSNLEVVDTSTFGPESNILENAICDVPDQNSK
	ļ		QLNAIESTKIESHETANLQDDRNSQSSSVSYLESKSVKSKHTKP
[1	į	VIHSKQNMTTDAPKKIVAAKYEVIHSKTKVNVKSVKRNTDVPES
			QQNFHRPVKVRKKQIDKEPKIQSCNSGVKSVKNQAHSVLKKTLQ
	·		MILLY MILL STATE OF THE STATE O

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DQTLVQIFKPLTHSLSDKSHAHPGCLKEPHHPAQTGHVSHSSQK
			QCHKPQQQAPAMKTNSHVKEELEHPGVEHFKEEDKLKLKKPEKN
			LQPRQRRSSKSFSLDEPPLFIPDNIATIRREGSDHSSSFESKYM
			WTPSKQCGFCKKPHGNRFMVGCGRCDDWFHGDCVGLSLSQAQQM
			GEEDKEYVCVKCCAEEDKKTEILDPDTLENQATVBFHSGDKTME
			CEKLGLSKHTTNDRTKYIDDTVKHKVKILKRESGEGRNSSDCRD
			NEIKKWQLAPLRKMGQPVLPRRSSEEKSEKIPKESTTVTCTGEK
			ASKPGTHEKQEMKKKKV\EKGVLNVHPAASASKPSADQIRQSVR
		İ	HSLKDILMKRLTDSNLKVPEEKAAKVATKIEKELFSFFRDTDAK
			YKNKYRSLMFNLKDPKNNILFKKVLKGEVTPDHLIRMSPEELAS
	1		KELAAWRRENRHTIEMIEKEQREVERRPITKITHKGEIEIESD
			APMKEQEAAMEIQEPAANKSLEKPEGSEK\RKEEVDSMSKDTTS
			QHRQHLFDLNCKICIGRMAPPVDDLSPKKVKVVVGVARKHSDNE
	<u> </u>		AESIADALSSTSNILASEFFEEEKQESPKSTFSPAPRPEMPGTV
	I		EVESTFLARLNFIWKGFINMPSVAKFVTKAYPVSGSPEYLTEDL
			PDSIQVGGRISPQTVWDYVEKIKASGTKEICVVRFTPVTEEDQI
			SYTLLFAYFSSRKRYGVAANNMKQVKDMYLIPLGATDKIPHPLV
			PFDGPGLELHRPNLLLGLIIRQKLKRQHSACASTSHIAETPESA
			PPIALPPDKKSKIEVSTEEAPEEENDFFNSFTTVLHKQRNKPQQ
		ļ	NLQEDLPTAVEPLMEVTKQEPPKPLRFLPGVLIGWENQPTTLEL
		ĺ	ANKPLPVDDILQSLLGTTGQVYDQ\AQSVMEQNTVKBIPFLNEQ
			TNSKIEKTDNVEVTDGENKEIKVKVDNISESTDKSABIETSVVG
			SSSISAGSLTSLSLRGKPPDVSTEAFLTNLSIQSKQEETVESKE
			KTLKRQLQEDQENNLQDNQTSNSSPCRSNVGKGNIDGNVSCSEN
			LVANTARSPQFINLKRDPRQAAGRSQPVTTSESKDGDSCRNGEK
			HMLPGLSHNKEHLTEQINVEEKLCSAEKNSCVQQSDNLKVAQNS
			PSVENIQTSQAEQAKPLQEDILMQNIETVHPFRRGSAVATSHFK
			VGNTCPSEFPSKSITFTSRSTSPRTSTNFSPMRPQQPNLQHLKS
			SPPGFPFPGPPNFPPQSMFGFPPHLPPPPLLPPPGFG\FA\QNPM
			VPWPPVV\HLP\GQPQRMMGPLSQASRYIGPQNFYQVKDIRRPE
			RRHSDPWGRQDQQQLDRPFNRGKGDRQRFYSDSHHLKRERHEKE
			WEQESERHRRRDRSQDKDRDRKSREEGHKDKERARLSHGDRGTD
			GKASRDSRNVDKKPDKPKSEDYEKDKEREKSKHREGEKDRDRYH KDRDHTDRTKSKR
5952	3226	639	
3934	3226	639	PPARRSARDLPRALSMEAARPSGSWNGALCRLL\LVTL\AFLIF
			ASDACKNVTLHVPSKLDAEKLVGRVNLKECFTAANLIHSSDPDF
	\		QILEDGSVYTTNTILLSSEKRSFTILLSNTENQEKKKIFVFLEH
	1		QTKVLKKRHTKEKVLRRAKRRWAPIPCSMLENSLGPFPLFLQQV
	1	1	QSDTAQNYTIYYSIRGPGVDQEPRNLFYVERDTGNLYCTRPVDR EQYESFEIIAFATTPDGYTPELPLPLIIKIEDENDNYPIFTEET
			YTFTIFENCRYGTTYGOVCATDKDEPDTMHTRLKYSIIGOVPPS
			PTLFSMHPTTGVITTTSSQLDRELIDKYQLKIKVQDMDGQYFGL QTTSTCIINIDDVNDHLPTFTRTSYVTSVEENTVDVEILRVTVE
		1	DKDLVNTANWRANYTILKGNENGNFKIVTDAKTNEGVLCVVKPL
			NYEEKQQMILQIGVVNEAPFSREASPRSAMSTATVTVNVEDQDE
			GPECNPPIQTVRMKENAEVGTTSNGYKAYDPETRSSSGIRYKKL TDPTGWVTIDENTGSIKVFRSLDRBAETIKNGIYNITVLASDQG
			GRTCTGTLGIILQDVNDNSPFIPKKTVIICKPTMSSAEIVAVDP
		1	DEPIHGPPFDFSLESSTSEVQRMWRLKAINDTAARLSYQNDPPF
		ľ	GSYVVPITVRDRLGMSSVTSLDVTLCDCITENDCTHRVDPRIGG
	[GGVQLGKWAILAILLGIALFFCILFTLVCGASGTSKQPKVIPDD
	1		LAQQNLIVSNTEAPGDDKVYSANGFTTQTVGASAQGVCGTVGSG
		[I KNGGQETIEMVKGGHQTSESCRGAGHHHTLDSCRGGHTEVDNC
Enra	335		RYTYSEWHSFTQPRLGEESIRGHTLIKN
5953	330	811	PLLCNPDPGWYWWVKQESEISKESQEMDARPKLDLGFKEGQTIK
			LCIGNITNKKGGASKPRTARGGGLSLLPPPPGGKVTIPPPSS/V
			KLPSTNHVTPPSIPKSNHGGSDADILLDLDSPAPVTTPAPTPVS
5054	 		VSNDLWGDFSTASSSVPNQAPQPSNWVQF
5954	32	2130	PPPPPPKLANMADLEAVLADVSYLMAMEKSKATPAARASKRIVL
			PEPSIRSVMQKYLAERNEITFDKIFNQKIGFLLFKDFCLNEINE AVPQVKFYEEIKEYEKLDNEEDRLCRSRQIYDAYIMKELLSCSH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
			PFSKQAVEHVQSHLSKKQVTSTLFQPYIKEICESLRGDIFQKFM
			ESDKFTRFCQWKNVELNIHLTMNEFSVHRIIGRGGFGEVYGCRK
			ADTGKMYAMKCLNKKRIKMKQGETLALNERIMLSLVSTGDCPFI
			VCMTYAFHTPDKLCFILDLMNGGDLHYHLSQHGVFSBKEMRFYA
			TEIILGLEHMHNRFVVYRDLKFANILLDEHGHARIS\DLGLACD
	1		FSKKKPHASVGTHGYMAPEVLQKGTAYDSSADWFSLGCMLFKLL
			RGHSPFRQHKTKDKHBIDRMTLTVNVELPDTFSPELKSLLEGLL ORDVSKRLGCHGGGSQEVKEHSFFKGVDWQHVYLQKYPPPLIPP
			RGEVNAADAFDIGSFDEEDTKGIKLLDCDQELYKNFPLVISERW
			OOEVTETVYEAVNADTDKIEARKRAKNKOLGHEEDYALGKDCIM
			HGYMLKLGNPFLTQWQRRYFYLFPNRLEWRGEGESRQNLLTMEQ
	1	1	ILSVEETQIKDKKCILFRIKGGKQFVLQCESDPEFVQWKKELNE
	1		TFKEAQRLLRRAPKFLNKPRSGTVELPKPSLCHRNSNGL
5955	1726	444	KREREFRLAVCPLRYPSAYESSPGTELRECGLCRSGQBFADCRR
			PANRQDVLSGWINLPVLQLTKDPLKTPGRLDHGTRTAFIHHREQ
	1		VWKRCINIWRDVGLFGVLNEIANSEBEVFEWVKTASGWALALCR
	1		WASSLHGSLFPHLSLRSEDLIAEFAQVTNWSSCCLRVFAWHPHT
			NKFAVALLDDSVRVYNASSTIVPSLKHRLQRNVASLAWKPLSAS
			VLAVACQSCILIWTLDPTSLSTRPSSGCAQVLSHPGHTPVTSLA
			WAPSGGRLLSASPVDAAIRVWDVSTETCVPLPWFRGGGVTNLLW SPDGSKILATTPSAVFRVWEAOMWTCERWPTLSGRCOTGCWSPD
			GSRLLFTVLGEPLIYSLSFPERCGEGKG\ALEVQSQQRLWQICL
			ROOYRHOMVRRGLGERLTPWSGTPVGNVWLCL
5956	1705	139	GVGVRGARAMATVQEKAAALNLSALHSPAHRPPGFSVAQKPFGA
٥٥رد	1/03		TYVWSSIINTLQTQVEVKKRRHRLKRHNDCFVGSEAVDVIFSHL
			IQNKYFGDVDIPRAKVVRVCQALMDYKVFEAVPTKVFGKDKKPT
			FEDSSCSLYRFTTIPNQDSQLGKENKLYSPARYADALFKSSDIR
			SASLEDLWENLSLKPANSPHVNISATLSPQVINEVWQEETIGRL
		1	LQLVDLPLLDSLLKQQEAVPKIPQPKRQSTMVNSSNYLDRGILK
			AYSDSQEDEWLSAAIDCSEYLPDQMVVEISRSFPEQPDRTDLVK
			ELLFDAIGRYYSSREPLLNHLSDVHNGIARLLVNGKTEIALEAT
1			QLLLKLLDFQNREEFRRLLYFMAVAANPSEFKLQKESDNRMVVK
!			RIFSKAIVDNKNLSKGKTDLLVLFL\MDHQKDVFKIPGTL\HKI VS\VK\LMAIQNGRDPNRDAGYIYCQRIDQRDYSNNTEKTTKDE
i			LLNLLKTLDEDSKLSAKEKKK\LLGQFYKCHPDIFIEHFGD
5957	1479	451	ELOVAVAMDTLDRVVKPKTKRAKRFLEKREPKLNENIKNAMLIK
235/	14/3	451	GGNANATVTKVLKDVYALKKPYGVLYKKKNITRPFEDOTSLEFF
			SKKSDCSLFMFGSHNKKRPNNLVIGRMYDYHVLDMIELGIENFV
į			SLKDIKNSKCPEGTKPMLIFAGDDFDVTEDYRRLKSLLIDFFRG
		1	PTVSNIRLAGLEYVLHFTALNGKIYFRSYKLLLKKSGCRTPRIE
1			LEEMGPSLDLVLRRTHLASDDLYKLSMKMPKALKPKKKKNISHD
			TFGTTYGRIHMQKQDLSKLQTRKM\KGLKKRPAERITEDHEKKS
			KRIKKKLMELSQPLLFHCVLLKRIIKHQSIQSFL
5958	1	3138	AAALGMLLWFPACQAFNLDVEKLTVYSGPKGSYFGYAVDFHIPD
			ARTASVLVGAPKANTSQPDIVEGGAVYYCPWPAEGSAQCRQIPF
			DTTNNRKIRVNGTKEPIEFKSNQWFG\ATVKA\HKGKSCGPVAP
			LLFTWRNFLKPTPEKGPVGTCYVAIQNFSAYAEFSPCGNSNADP EGOGYCOAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA
1	1		EGQGYCQAGFSLDFYKNGDLIVGGPGSFYWQGQVITASVADIIA NYSFKDILRKLAGEKOTEVAPASYDDSYLGYSVAAGEFTGDSQQ
			ELVAGIPRGAONFGYVSIINSYDMTFIONFTGEQMASYFGYTVV
			VSDVNSDGLDDVLVGAPLFMEREFESNPREVGQIYLYLQVSSLL
1			FRDPQILTGTETFGRFGSAMAHLGDLNQDGYNDIAIGVPFAGKD
			QRGKVLIYNGNKDGLNTKPFPKFCQGVWASHAVPSGFGFTLRGD
}			SDIDKNDYPDLIVGAFGTGKVAVYRARPVVTVDAQLLLHPMIIN
1			LENKTCQVPDSMTSAACFSLRVCASVTGQSIANTIVLMAEVQLD
			SLKQKGAIKRTLFLDNHQAHRVFPLVIKRQKSHQCQDFIVYLRD
			ETEFRDKLSPINISLNYSLDESTFKEGLEVKPILNYYRENIVSE
}			QAHILVDCGEDNLCVPDLKLSARPDKHQVIIGDENHLMLIINAR
			NEGEGAYEAELFVMIPEEADYVGIERNNKGFRPLSCEYKMENVT
			RMVVCDLGNPMVSGTNYSLGLRFAVPRLEKTNMSINFDLQIRSS NKDNPDSNFVSLQINITAVAQVEIRGVSHPPQIVLPIHNWEPEE

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted		(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
ID	beginning	nucleotide location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide		H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 4	\=possible nucleotide insertion)
	Bequence	_	EPHKEEBYGPLVEHIYELHNIGPSTISDTILEVGWPFSARDEFL
	1		LYIFHIOTLGPLQCQPNPNINPQDIKPAASPEDTPELSAFLRNS
ļ	j		, · · - · · · · · · · · · · · · · · · ·
			TIPHLVRKRDVHVVBFHRQSPAKILNCTNIECLQISCAVGRLEG
	i	j	GESAVLKVRSRLWAHTFLQRKNDPYALASLVSFEVKKMPYTDQP
		1	AKLPEGSIAIKTSVIWATPNVSFSIPLWVIILAILLGLLVLAIL
			TLALWKCGFFDRARPPQEDMTDREQLTNDKTPEA
5959	1	1166	GTSGYAAQQLPSLLKEREFHLGTLNKVFASQWLNHRQVVCGTKC
3939	† +	1 1100	NTLFVVDVOTSQITKIPILKDREPGGVTQQGCGIHAIELNPSRT
		Ļ	LLATGGDNPNSLAIYRLPTLDPVCVGDDGHKDWIFSIAWISDTM
	!		
ļ			AVSGSRDGSMGLWEVTDDVLTKSDARHNVSRVPVYAHITHKALK
		1	DIPKEDTNPDNCKVRALAFNNKNKELGAVSLDGYFHLWKAENTL
1			SKLLSTKLPYCRENVCLAYGSEWSVYAVGSQAHVSFLDPRQPSY
		1	NVKSVCSRERGSGIRSVSFYEHIITVGTGQGSLLFYDIRAQRFL
1		1	EERLSACYGSKPRLAGENLKLTTG\KGWLNHDETWRNYFSDIDF
1		1	PPNAVYTHCYDSSGTKLFVAGGPLPSGLHGNYAGLWS
F		070	FVWSDGGPRPRRGPAVGAGAAHLSDPWAMTPGTANRATNPLNKE
5960	2853	870	LDWASINGFCEOLNEDFEGPPLATRLLAHKIQSPQEWEAIQALT
[
	ł	1	VLETCMKSCGKRFHDEVGKFRFLNELIKVVSPKYLGSRTSEKVK
			NKILELLYSWTVGLPEEVKIAEAYQMLKKQG\IVKSDPKLPDDT
	1		TFPLPPPRPKNVIFEDEEKSKMLARLLKSSHPEDLRAANKLIKE
		ļ	MVQEDQKRMEKISKRVNAIEEVNNNVKLLTEMVMSHSQGGAAAG
	· I	1	SSEDL\MKEL\YQRCBRMRPTLFPTGRVDTEDND\EALAEILQA
		ļ	NDNLTOVINLYKOLVRGEEVNGDATAGSIPGSTSALLDLSGLDL
l	1	l	PPAGTTYPAMPTRPGEQASPEQPSASVSLLDDELMSLGLSDPTP
1	i	1	PSGPSLDGTGWNSFQSSDATEPPAPALAQAPSMESRPPAQTSLP
ł	Ì	[ASSGLDDLDLLGKTLLQQSLPPESQQVRWEKQQPTPRLTLRDLQ
į.	i	1	NKSSSCSSPSSSATSLLHTVSPEPPRPPQQPVPTELSLASITVP
	-		LESIKPSNILPVTVYDQHGFRILFHFARDPLPGRSDVLVVVVSM
		ì	LSTAPQPIRNIVFQSAVPKVMKVKLQPPSGTELPAFNPIVHPSA
1	1		ITQVLLLANPQKEKVRLRYKLTFTMGDQTYNEMGDVDQFPPPET
	Ì	1	WGSL
F061	198	3147	SGEPRPEPGNMATCIGEKIEDFKVGNLLGKGSFAGVYRAESIHT
5961	198	3147	GLEVAIKMIDKKAMYKAGMVQRVQNEVKIHCQLKHPSILELYNY
1			T
	1	1	FEDSNYVYLVLEMCHNGEMNRYLKNRVKPFSENEARHFMHQIIT
	1		GMLYLHSHGILHRDLTLSNLLLTRNMNIKIADFGLATQLKMPHE
İ	1	1	KHYTLCGTPNYISPEIATRSAHGLESDVWSLGCMFYTLLIGRPP
1	ł	1	FDTDTVKNTLNKVVLADYEMPTFLSIEAKDLIHQLLRRNPADRL
i	1	i	SLSSVLDHPFMSRNSSTKSKDLGTVEDSIDSGHATISTAITASS
1	l		STSISGSLFDKRRLLIGQPLPNKMTVFPKNKSSTDFSSSGDGNS
1			FYTQWGNQETSNSGRGRVIQDAEERPHSRYLRRAYSSDRSGTSN
1		1	SQSQAKTYTMERCHSAEMLSVSKRSGGGENEERYSPTDNNANIF
1	1	}	NFFKEKTSSSSGSFERPDNNOALSNHLCPGKTPFPFADPTPQTE
1	1		TVQQWFGNLQINAHLRKTTEYDSISPNRDFQGHPDLQKDTSKNA
	1		WTDTKVKKNSDASDNAHSVKQQNTMKYMTALHSKPEIIQQECVF
			GSDPLSEQSKTRGMEPPWGYQNRTLRSITSPLVAHRLKPIRQKT
1			KKAVVSILDSEEVCVELVKEYASQEYVKEVLQISSDGNTITIYY
			PNGG\RGFPLA\DRPPSPT\DNISR\YSF\DNLPEKYWRKYQYA
			SRFVQLVRSKSPKITYFTRYAKCILMENSPGADFEVWFYDGVKI
1			HKTEDFIQVIEKTGKSYTLKSESEVNSLKEEIKMYMDHANBGHR
1			
			ICLALESIISEEERKTRSAPFFPIIIGRKPGSTSSPKALSPPPS
1	1		VDSNYPTRDRASFNRMVMHSAASPTQAPILNPSMVTNEGLGLTT
			TASGTDISSNSLKDCLPKSAQLLKSVFVKNVGWATQ\LTSGAVW
1			VQFNDGSQLVVQAGVSSISYTSPNGQ\TTR\YGENEKLPDYIKQ
1			KLOCLSSILLMFSNPTPNFH
5962	20	2447	RVCSSSASTASQAVMADAWEEIRRLAADFQRAQFAEATQRLSER
3962		2331	NCIEIVNKLIAQKQLEVVHTLDGKEYITPAQISKEMRDELHVRG
1			
			GRVNIVDLQQVINVDLIHIBNRIGDIIKSEKHVQLVLGQLIDEN
			YLDRLAEEVNDKLQESGQVTISELCKTYDLPGNFLTQALTQRLG
			RIISGHIDLDNRGVIFTEAFVARHKARIRGLFSAITRPTAVNSL
1			ISKYGFQEQLLYSVLEELVNSGRLRGTVVGGRQDKAVFVPDIYS
ı			RTQSTWVDSFFRQNGYLEFDALSRLGIPDAVSYIKKRYKTTQLL
,	1		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
j	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Bequence	\=possible nucleotide insertion)
	bequence		FLKAACVGQGLVDQVEASVEEAISSGTWVDIAPLLPTSLSVEDA
]			AILLQQVMRAFSKQASTVVFSDTVVVSEKF\INDCTELFRELMH
1			QKAEKEMKNNPVHLITEEDLKQISTLESVSTSKKDKKDERRRKA
1			TEGSGSMRGGGGGNAREYKIKKVKKKGRKDDDSDDESQSSHTGK
ı		į.	KKPEISFMFQDEIEDFLRKHIQDAPEEFISELAEYLIKPLNKTY
i			
			LEVVRSVFMSSTTSASGTGRKRTIKDLQEBVSNLYNNIRLFEKG
		}	MKFFADDTQAALTKHLLKSVCTDITNLIFNFLASDLMMAVDDPA
1		1	AITSEIRKKILSKLSEETKVALTKLHNSLNEKSIEDFISCLDSA
ł		1	AEACDIMVKRGDKKRERQILFQHRQALAEQLKVTEDPALILHLT
1			SVLLFQFSTHSMLHAPGRCVPQIIAFLNSKIPEDQHALLVKYQG
i			LVVKQLVSQSKKTGQGDYPLNNELDKEQEDVASTTRKELQELSS
<u> </u>			SIKDLVLKSRKSSVTEE
5963	62	1130	PWNPQDFPGNRGLMG\QKGEIGPP\GQQGKKGAPGMP\GLMGSN
1	1	1	GSPGQPGTPGSKGSKGEPGIQGMPGASGLKGEPGATGSPGEPGY
			MGLPGIQGKKGDKGNQGEKGIQGQKGENGRQGIPGQQGIQGHHG
-			AKGERGEKGEPGVRGAIGSKGESGVDGLMGPAGPKGQPGDPGPQ
1			GPPGLDGKPGREFSEQFIRQVCTDVIRAQLPVLLQSGRIRNCDH
Ì			CLSQHGSPGIPGPPGPIGPEGPRGLPGRDGVPGLVGVPGRP
ł			GVRGLKGLPGRNGEKGSQGFGYPGEQGPPGPPGPEGPPGISKEG
Ĭ			PPGDPGLPGKDGDHGKPGIQGQPGPPGICDPSLCFSVIARRDPF
			RKGPNY
5964	3	2147	SCRTRGRLSPLQPREAGSSRGSRARSEPPRPGGMEEACQVQTTK
			RGDPHELRNIFLQYASTEVDGERYMTPEDFVQRYLGLYNDPNSN
1			PKIVQLLAGVADQTKDGLISYQEFLAFESVLCAPDSMFIVAFQL
			FDKSGNGEVTFENVKEIFGQTIIHHHIPFNWDCEFIRLHFGHNR
i			KKHLNYTEFTQFLQELQLEHARQAFALKDKSKSGMISGLDFSDI
			MVTIRSHMLTPFVEENLVSAAGGSISHQVSFSYFNAFNSLLNNM
Ì			ELVRKIYSTLAGTRKDAEVTKEEFAQSAIRYGQATPLEIDILYQ
			LADLYNASGRLTLADIERIAPLAEGALPYNLAELQRQQSPGLGR
			PIWLQIAESAYRFTLGSVAGAVGATAVYPIDLVKTRMQNQRGSG
1		f	SVVGELMYKNSFDCFKKVLRYEGFFGLYRGLIPQLIGVAPEKAI
			KLTVNDFVRDKFTRRDGSVPLPAEVLAGGCAGGSQVIFTNPLEI
ļ			VKIRLQVAGEITTGPRVSALNVLRDLGIFGLYKGAKACFLRDIP
1			FSAIYFPVYAHCKLLLADENGHVGGLNLLAAGAMAG\VPAASLV
			TPADVIKTRLQVAARAGQTTYSGVIDCFRKIL\REEGPSAFWKG
ł		ł	TAARVFRSSPQFG\VTLVTYELLQRGFYIDFGGLKPAGSEPTPK
E			SRIADLPPANPDHIGGYRLATATFAGIENKFGLYLPKFKSPSVA
			VVQPKAAVAATQ
5965	1	1498	MVTWLYRFLPTSNMAAKLRSLLPPDLRLQFWLHARLQKCFLSRG
			CGSYCAGAKASPLPGKMAMGLMCGRRELLRLLQSGRRVHSVAGP
1			SQWLGKPLTTRLLFPAAPCCCRPHYLFLAASGPRSLSTSAISFA
			EVQVQAPPVVAATPSPTAVPEVASGETADVVQTAAEQSFAELGL
1			GSYTPVGLIQNLLEFMHVDLGLPWWGAIAACTVFARCLIFPLIV
1		1	TGQREAARIHNHLPEIQKFSSRIREAKLAGDHIEYYKASSEMAL
		1	YQKKHGIKLYKPLILPVTQAPIFISFFIALREMANLPVPSLQTG
			GLWWFQDLTVSDPIYILPLAVTATMWAVLELGAETGVQSSDLQW
1			MRNVIRMMPLITLPITMHFPTAVFMYWLSSNLFSLVQVSCLRIP
			AVRTVLKIPQRVVHDLDKLPPREGFLESFKKGWKNAEMTRQLRE
1			REQRMRNQLELAARGPLRQTFTHNPLLQPGKDNPPNIPSS\SSS
	1		SSKPKSKYPWHDTLG
5966	102	1925	RSKQVMARLTKRRQADTKAIQHLWAAIEIIRNQKQIANIDRITK
		1	YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE
1			GYWLPGDBIDWETENHDWYCFBCHLPGEVLICDLCFRVYHSKCL
			SDEFRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
			RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE
			FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC
1			KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMQKE
1			DNQVDVRFFGHHHQRAWIPSENIQDITVNIHRLHVKRSMGWKKA
}			CDELELHQRFLREGRFWKSKNEDRGEEEAESSISSTSNEQLKVT
			CEPRAKKGRRNQSVEPKKEEPEPETEAVSSSQEIPTMPQPIEKV
			SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF
	1	<u> </u>	,

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
110.	location		U-Wighiding T Including W Island
1	1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			KDRMKSDHKRETERVVREALEKLRSEMEEEKRQAVNKAVANMQG
			EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC
1			EEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
5967	102	1925	
3967	102	1925	RSKQVMARLTKRRQADTKAIQHLWAAIEIIRNQKQIANIDRITK
			YMSRVHGMHPKETTRQLSLAVKDGLIVETLTVGCKGSKAGIEQE
1	İ		GYWLPGDEIDWETENHDWYCFECHLPGEVLICDLCFRVYHSKCL
1			SDEFRLRDSSSPWQCPVCRSIKKKNTNKQEMGTYLRFIVSRMKE
			RAIDLNKKGKDNKHPMYRRLVHSAVDVPTIQEKVNEGKYRSYEE
	t		FKADAQLLLHNTVIFYGADSEQADIARMLYKDTCHEL\DELQLC
1			KNCFYLANARPDNWFCYPCIPNHELDWAKMKGFGFWPAKVMOKE
i			DNQVDVRFPGHHHQRAWIPSENIQDITVNIHRLHVKRSMGWKKA
1	1		CDELELHQRFLREGRFWKSKNEDRGEEEAESSISSTSNEQLKVT
1			QEPRAKKGRRNQSVEPKKEEPEPETEAVSSSQEIPTMPQPIEKV
	[SVSTQTKKLSASSPRMLHRSTQTTNDGVCQSMCHDKYTKIFNDF
	ļ		
1			KDRMKSDHKRETERVVREALEKLRSEMEEEKRQAVNKAVANMQG
1	Į.		EMDRKCKQVKEKCKEEFVEEIKKLATQHKQLISQTKKKQWCYNC
F.C.C.			EEEAMYHCCWNTSYCSIKCQQEHWHAEHKRTCRRKR
5968	81	1288	VRFPRRGGAPPTVLTPGRQQGVFLGPQRPGSEPDIPARGQPHPP
}	İ		RPVGVSTSAQAQVQPPAMHRRRLALGLGFCLLAGTSLSVLWVYL
1			ENWLPVSYVPYYLPCPEIFNMKLHYKREKPLQPVVWSQYPQPKL
			LEHRPTQLLTLTPWLAPIVSEGTFNPELLQHIYQPLNLTIGVTV
			FAVGN/HFLESAEEFFMRGYRVHYYIFTDNPAAVPGVPLGPHRL
1			LSSIPIQGHSHWEETSMRRMETISQHIAKRAHREVDYLFCLDVD
1			MVFRNPWGPETLGDLVAAIHPSYYAVPRQQFPYERRRVSTAFVA
			DSEGDFYYGGAVFGGQVARVYEFTRGCHMAILADKANGIMAAWR
İ			EESHLNRHFISNKPSKVLSPEYLWDDRKPQPPSLKLIRFSTLDK
ĺ			DISCLRS
5969	1126	503	
3303	1120	303	DVGFNIKRKRCDLDVFLESPRKPSGRRDRAPEKQRRIAANKCLC
ĺ			TGVREGEPPS/TTSQKVKEAGRDFTYLIVVLFGISITGGLFYTI
			FKELFSSSSPSKIYGRALEKCRSHPEVIGVFGESVKGYGEVTRR
1			GRRQHVRFTEYVKDGLKHTCVKFYIEGSEPGKQGTVYAQVKENP
			GSGEYDFRYIFVEIESYPRRTIIIEDNRSQDD
5970	316	4712	SQDNIGHRLLQKHGWKLGQGLGKSLQGRTDPIPIVVKYDVMGMG
			RMEMELDYAEDATERRRVLEVEKEDTEELRQKYKDYVDKEKAIA
1	}		KALEDLRANFYCELCDKQYQKHQEFDNHINSYDHAHKQRLKDLK
			QREFARNVSSRSRKDEKKQEKALRRLHELAEQRKQAECAPGSGP
			MFKPTTVAVDEEGGEDDKDESATNSGTGATASCGLGSEFSTDKG
			GPFTAVQITNTTGLAQAPGLASQGISFGIKNNLGTPLQKLGVSF
			SFAKKAPVKLESIASVFKDHAEEGTSEDGTKPDEKSSDQGLQKV
1			GDSDGSSNLDGKKEDEDPQDGGSLASTLSKLKRMKREEGAGATE
1			PEYYHYIPPAHCKVKPNFPFLLFMRASEQMDGDNTTHPKNAPES
			I .
			KKGSSPKPKSCIKAAASQGAEKTVSEVSEQPKETSMTEPSEPGS
			KAEAKKALGGDVSDQSLESHSQKVSETQMCESNSSKETSLATPA
1			GKESQEGPKHPTGPFFPVLSKDESTALQWPSELLIFTKAEPSIS
			YSCNPLYFDFKLSRNKDARTKGTEKPKDIGSSSKDHLQGLDPGE
			PNKSKEVGGEKIVRSSGGRMDAPASGSACSGLNKQEPGGSHGSE
			TEDTGRSLPSKKERSGKSHRHKKKKKKKKKKSSKHKRKHKADTEEK
1			SSKAESGEKSKKRKKKKKKKKKKSSAPADSERGPKPEPPGSGSPA
1			PPRRRRRAQDDSQRRSLPAEEGSSGKKDEGGGGSSSQDHGGRKH
1			KGELPPSSCQRRAGTKRSSRSSHRSQPSSGDEDSDDASSHRLHQ
1			KSPSQYSEEEEEEDSGSEHSRSRSRSGRRHSSHRSSRRSYSSSS
1			DASSDQSCYSRQRSYSDDSYSDYSDRSRRHSKRSHDSDDSDYAS
1			†
1			SKHRSKRHKYSSSDDDYSLSCSQSRSRSRSHTRERSRSRGRSRS
			SSCSRSRSKRRSRSTTAHSWQRSRSYSRDRSRSTRSPSQRSGSR
1			KRSWGHESPEERHSGRRDFIRSKIYRSQSPHYFRSGRGEGPGKK
			DDGRGDDSKATGPPSQNSNIGTGRGSEGDCSPEDKNSVTAKLLL
			EKIQSRKVERKPSVSEEVQATPNKAGPKLKDPPQGYFGPKLPPS
			LGNKPVLPLIGKLPATRKPNKKCEESGLERGEEQEQSETEEGPP
			GSSDALFGHQFP\SEETTGPLLDPPPEESKSGEVTADHPVAPLG
1			PPAHFDCYLGDPTISHNYLPDPSDGNTLESLDSSSQPGPVESSL
			LPIAPDLEHFPSYAPPSGDPSIESTDGAEDA\SLAPLESOPITF
			The state of the s

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	F-FIGITIE, QEGIUCAMINE, K=Arginine,
	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	sequence	sequence	Codon, /=possible nucleotide deletion,
	bequence		\=possible nucleotide insertion)
1		ļ.	TPEEMEKYSKLQQAAQQHIQQQLLAKQVKAFPASAALAPATPAL
			QPIHIQQPATASATSITTVQHAILQHHAAAAAAAIGIHPHPHPQ
			PLAQVHHIPQPHLTPISLSHLTHSIIPGHPATFLASHPIHIIPA
			SAIHPGPPTFHPVPHAALYPTLLAPRPAAAAATALHLHPLLHPI
5000	 		FSGQDLQHPPSHGT
5971	53	2149	SFLYFVGVDMDNPIGNWDGRFDGVQLCSFACVESTILLHINDII
1			PESVTQERRPPKLAFMSRGVGDKGSSSHNKPKATGSTSDPGNRN
ŀ			RSELFYTLNGSSVDSQPQSKSKNTWYIDEVAEDPAKSLTEISTD
	•		FDRSSPPLQPPPVNSLTTENRFHSLPFSLTKMPNTNGSIGHSPL
i			SLSAQSVMEELNTAPVQESPPLAMPPGNSHGLEVGSLAEVKENP
			PFYGVIRWIGOPPGLNEVLAGLELEDECAG\CTDGTF/REGTRY
			FTCALKKALFVKLKSCRPDSRFASLQPVSNOIERCNSLAIWRAY
1			LSEVVEENTPTQKWEKEGLEIMIG\KKKGIOGHYNSCYLDSTLF
			CLFAFSSVLDTVLLRPKEKNDVEYYSETOELLRTEIVNPLRIYG
1			YVCATKIMKLRKILEKVEAASGFTSEEKDPEEFLNILFHHILRV
			EPLLKIRSAGQKVQDCYFYQIFMEKNEKVGVPTIQQLLEWSFIN
1			SNLKFAEAPSCLIIQMPRFGKDFKLFKKIFPSLELNITDLLEDT
			PROCRICGGLAMYECRECYDDPDISAGKIKQFCKTCNTQVHLHP
1 1			KRLNHKYNPVSLPKDLPDWDWRHGCIPCONMELFAVLCIETSHY
			VAFVKYGKDDSAWLFFDSMADRDGGQNGFNIPQVTPCPEVGEYL
			KMSLEDLHSLDSRRIQGCARRLLCDAIYVPCTQSPTMSLYK
5972	440	1761	ILLAGSPSPRDQCSQRQSSGGDKELVTRGCTFSTAVVSPSAMTQ
			EPFREELAYDRMPTLERGRQDPASYAPDAKPSDLQLSKRLPPCF
1 1	1		SHKTWVFSVLMGSCLLVTSGFSLYLGNVFPAEMDYLRCAAGSCI
. !			PSAIVSFTVSRRNANVIPNFQILFVSTFAVTTTCLIWFGCKLVL
1			NPSAININFNLILLLLELLMAATVIIAARSSEEDCKKKKGSMS
			DSANILDEVPFPARVLKSYSVVEVIAGISAVLGGIIALNVDDSV
, ,	i		SGPHLSVTFFWILVACFPSAIASHVAAECPNKCLVEVLIAISSL
1			TSPLLFTASGYLSFSIMRIVEMFKDYPPAIKPSYDVLLLLLLV
			LLLQA/GPQHGHRHPVRALQGQCKAAGCILGHPERPAGAPGWGG
			GQEPPEGVRQGESLESRRGANGPVTPRRGNRVAAPSLAPGMETH
			NP
5973	65	· 2007	NGDGKDLFGHIWAWRSNGIISNFRRSPHAGMAEDEPDAKSPKTG
1			GRAPPGGAEAGEPTTLLQRLRGTISKAVQNKVEGILQDVQKFSD
[]			NDKLYLYLQLPSGPTTGDKSSEPSTLSNEEYMYAYRWIRNHLEE
			HTDTCLPKQSVYDAYRKYCESLACCRPLSTANFGKIIREIFPDI
l i			KARRLGGRGQSKYCYSGIRRKTLVSMPPLPGLDLKGSESPEMGP
	1		EVTPAPRDELVEAACALTCDWAERILKRSFSSIVEVARFLLQQH
1	İ		LISARSAHAHVLKAMGLAEEDEHAPRERSSKPKNGLENPEGGAH
			KKPERLAOPPKDLEARTGAGPLARGERKKSVVESSAPGANNLOV
			NALVARLPLLLPRAPRSLIPPIPVSPPILAPRLSSGALKVATLP
1		i	LSSRAGAPPAAVPIINMILPTVPALPGPGPGPGRAPPGGLTQPR
		1	GTENREVGIGGDQGPHDKGVKRTAEVPVSEASGQAPPAKAAKQD
			I EDTASDAKRKRGRPLKKSGGSGERNSTPLKSAAAMESAQSSRL
			PWETWGSGGEGNSAGGAERPGPMGEAEKGAVLAQG\QGDGTVSK
	j		GGRGPGSQHTKEAEDKIPLVPSKVSVIKGSRSQKEAFPLAKGEV
			DTAPQGNKDLKEHVLQSSLSQEHKDPKATPP
5974	4293	2200	LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\BID
			LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR
		İ	TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQQNGSV\S
•		1	DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQQELR
İ			EKRAQDVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC
1			VCVRKRPLNKKETQMKDLDVITIPSKDVVMVHEPKQKVDLTRYL
			ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG
		1	QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK
ſ	1	İ	LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLQE
	}		PEVKCVEDVI. KI. TDI CNCCDEGCOTORANTICORONIA CONTROLLO
- 1			REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR
1	i		KGKLHGKFSLIDLAGNERGADTSSADRQTRLEGAEINKSLLALK
1			ECIRALGRNKPHTPFRASKLTQVLRDSFIGENSRTCMIATISPG
			MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPNQI\DD
			LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM

		15	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:			
l .	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į.	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
-		•	
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
į.	amino acid	sequence	Codon, /=possible nucleotide deletion,
[1	Bequence	•
1	sequence		\=possible nucleotide insertion)
			EEQVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYATQLE
1	ļ.	į	AILEQKIDILTBLRDKVKSFRAALQEEEQASKQINPKRPRAL
	·		
5975	4293	2200	LGLQMHTTSGRIHQAMVTSLNEDNESVTVEWIENGDTKGK\EID
1		İ	LESIFSLNP\DL\VPDGEIEPSP\ETPPPPASSAKVNKIVKNRR
ĺ	1		TV\ASIKNDPPS\RDNRVVGSARARPSQFPEQFSSAQONGSV\S
1			,
Į.	l .	1	DISPVQAAKKEFGPPSRRKSNCVKEVEKLQEKREKRRLQQQELR
(EKRAODVDATNPNYEIMCMIRDFRGSLDYRPLTTADPIDEHRIC
1			VCVRKRPLNKKETOMKDLDVITIPSKDVVMVHEPKOKVDLTRYL
1	İ	1	
}	}	1	ENQTFRFDYAFDDSAPNEMVYRFTARPLVETIFERGMATCFAYG
			QTGSGKTHTMGGDFSGKNQDCSKGIYALAARDVFLMLKKPNYKK
		1	LELQVYATFFEIYSGKVFDLLNRKTKLRVLEDGKQQVQVVGLQE
		1	
ŀ	ļ	1	REVKCVEDVLKLIDIGNSCRTSGQTSANAHSSRSHAVFQIILRR
Ì		1	KGKLHGKFSLIDLAGNERGADTSSADRQTRLEGAEINKSLLALK
1	1	L	ECIRALGRNKPHTPFRASKLTQVLRDSPIGENSRTCMIATISPG
ľ		1	MASCENTLNTLRYANRVKELTVDPTAAGDVRPIMHHPPNOI\DD
1		1	
1		i	LETQWGVGSSPQRDDLKLLCEQNEEEVSPQLFTFHEAVSQMVEM
1		1	EEQVVEDHRAVFQESIRWLEDEKALLEMTEEVDYDVDSYATQLE
	1	1	AILEOKIDILTELRDKVKSFRAALQEEEQASKQINPKRPRAL
			VHHLHLTRVSVVVNLDIILRIAOOMGIKTLNLVLG\LKRA\LEF
5976	20	2949	
ł	1	1	PEVSWMEVKDPNMKGAMLTNTGKYAIPTIDA\EAYAIGKKEKPP
	l .		FLPEEPSSSSEEDDPIPDELLCLICKDIMTDAVVIPCCGNSYCD
	Ì	l .	BCIRTALLESDEHTCPTCHQNDVSPDALIANKFLRQAVNNFKNE
1			17
l	ì	1	TGYTKRLRKQLPSPPPPIPPPRPLIQRNLQPLMRSPISRQQDPL
1		1	MIPVTSSSTHPAPSISSLTSNQSSLAPPVSGNPSSAPAPVPDIT
1		1	ATVSISVHSEKSDGPFRDSDNKILPAAALASEHSKGTSSIAITA
	1		LMEEKGYQVPVLGTPSLLGQSLLHGQLIPTTGPVRINTARPGGG
(['	
	1		RPGWEHSNKLGYLVSPPQQIRRGERSCYRSINRGRHHSERSQRT
	1		QGPSLPATPVFVPVPPPPLYPPPPHTLPLPPGVPPPQFSPQFPP
1	1		GQP\PPAGYSVPPPGFPPAPANLSTPWVSSGVQTAHSNTIPTTQ
1			APPLSREEFYREORRLKEEEKKKSKLDEFTNDFAKELMEYKKIO
1			
1	l .	ľ	KERRRSFSRSKSPYSGSSYSRSSYTYSKSRSGSTRSRSYSRSFS
	i		RSHSRSYSRSPPYPRRGRGKSRNYRSRSRSHGYHRSRSRSPPYR
	1		RYHSRSRSPQAFRGQSPNKRNVPQGETEREYFNRYREVPPPYDM
			l "
ļ	ŀ		KAYYGRSVDFRDPFEKERYREWERKYREWYEKYYKGYAAGAQPR
	Į.		PSANRENFSPERFLPLNIRNSPFTRGRREDYVGGQSHRSRNIGS
i	1	1	NYPEKLSARDGHNQKDNTKSKEKESENAPGDGKGNKHKKHRKRR
[1	1	KGEESEGFLNPELLETSRKSREPTGVEENKTDSLFVLPSRDDAT
1	1	1	
I	1		PVRDEPMDAESITFKSVSEKDKRERDKPKAKGDKTKRKNDGSAV
ļ	1	1	SKKENIVKPAKGPQEKVDG\DVRDLLDLNL\QLKKPKEETPKDL
1	1	1	TILNHHLPLRRMKKSL\EPP\EKLTLNQQK\TPRNKTSQRGKSE
I	1		EGLFORCOIRKANN
<u> </u>		ļ	
5977	1363	1336	FLEDRGQVLSHFQCLSLHSINHILHPGAGVAAGPATGW/REYLT
1	1	1	PVLKESKFKETGVITPEEFVAAGDHLVHHCPTWQWATGEELKVK
1	1		AYLPTGKQFLVTKNVPCYKRCKQMEYSDELEAIIEEDDGDGGWV
	1		DTYHNTGITGITEAVKEITLENKONIRLODCSALCEEEEDEDEG
1	1		
	1	I	EAADMEEYEESGLLETDEATLDTRKIVEACKAKTDAGGEDAILQ
1			TRTYDLYITYDKYYQTPRLWLFGYDEQRQPLTVEHMYEDISQDH
1	1		VKKTVTIENHPHLPPPPMCSVHPCRHAEVMKKIIETVAEGGGEL
		<u> </u>	GVHMYLLIFLKFVQAVIPTIEYDYTRHFTM
5978	160	3213	RDGARRWGGCQSPLTWAPGFYRRFDLATSGRRLRGQTAEPAGRQ
1		1	RPRREPEAMDEOSVESIABVFRCFICMEKLRDARLCPHCSKLCC
l		ļ	FSCIRRWLTEORAQCPHCRAPLQLRELVNCRWAEEVTQQLDTLQ
1		1	
ł	1	1	LCSLTKHEENEKDKCENHHEKLSVFCWTCKKCICHQCALWGGMH
1		1	GGHTFKPLAEIYEQHVTKVNEEVAKLRRRLMELISLVQEVERNV
l		1	EAVRNAKDERVRBIRNAVEMMIARLDTQLKNKLITLMGQKTSLT
1	1		
1			QETELLESLLQEVEHQLRSCSKSELISKSSEILMMFQQVHRKPM
ì			ASFVTTPVPPDFTSELVPSYDSATFVLENFSTLRQRADPVYSPP
]	1	1	LQVSGLCWRLKVYPDGNGVVRGYYLSVFLELSAGLPETSKYEYR
Į.			VEMVHOSCNDPTKNIIREFASDFEVGECWGYNRFFRLDLLANEG
ł			1 "
1			YLNĘQNDTVILRFQVRSPTFFQKSRDQHWYITQLEAAQTSYIQQ
ŀ		1	INNLKERLTIELSRTQKSRDLSPPDNHLSPQNDDALETRAKKSA

Degianing location corresponding cotion corresponding cotion corresponding cotion corresponding cotion corresponding cotion corresponding cotion corresponding cotion corresponding cotion corresponding cotion corresponding cotion	Deginning location corresponding cotion corresponding cofirst amino acid residue of amino acid sequence sequen	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Corresponding	Sociation Corresponding				(A=Alanine, C=Cvsteine, D=Aspartic Acid E
Cortesponding Coffee Contemporating Coffee Coff	Corresponding	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine G=Glycine
to first amino acid residue of amino acid residue of amino acid sequence se	Leleucine, M-Methicoine, N-Asparagine, seriade of amino acid sequence seque			corresponding	H=Histidine, I=Isoleucine, K=Lysine.
amino acid residue of amino acid sequence seq	amino acid residue of amino acid sequence e, Y-Unknown, *-Stop Codon, *possible nucleotide deletion, '*possible nucleotide deletion, '*possible nucleotide besettion by the sequence' sequence S-S-B-IR nucleotide insertion) SCDMLERE(GYPSAS (VERKAREDEDEDEERIONED/HHELSIGGL DLDLVYEDEVNOLDOSSSSASSTASNTSNTERNI DEETMSGENIUS APSSLADDEDLIHILDLAIDASSISIENIMGLOPREPASLLOPTA SYSKAKOROKOQAMPYSBLIKHIKKURMABEWARTIVAN TISSIKSSAASGOMYTSLESALOQALAACGTENSGELDLOME LLAKSSVANCYIRSYTHKSNBEPKARSENGSLECTHENE SORGKURMAN SERVENGER SERV	İ		1	L=Leucine, M=Methionine, N=Asparagine
S-Serine, T-Threonine, V-valine, sequence	### sequence Festidue of ### sequence ### seq			l .	P=Proline, Q=Glutamine, R=Arginine.
amino acid sequence Codon, /-possible mucleotide deletion, Codon, /-possible mucleotide deletion, CSDMLLER/GSYSER/VERAKEDE/DELEK/GNEYVHERLEDGDL CSDMLLER/GSYSER/VERAKEDE/DELEK/GNEYVHERLEDGDL DLDLVYEDSYNQLMOSSSSSSSTATSNTERNIDERTMSGENDY BYXMMELEGGLMERGAAAGGROSSYSVOSSSNISSRTHLGSA AFSSLUDIDFILLIHLIDLKDRSSIENLMGLOPRPPASLLOPTA SYSKKKONGKROAMWEVESLOKMEKKINONADVEKKTUVEN TISSIESSSAASGONG/TSIFSENDAALAAGGTENSGRLOLGME LLAKSSYNNCY! ENGASAAAGGROSSYSSVOSSSIERRAUPGE NSESKGDCGTLSESSPGSSQSGRISSFRALHGSIGDLDKYEE ENGCKLDSDAVVAVYSGLFAVEKRATVORAMSGHEGL QMTDLENNSTGELQPVLPSGASAAPEGMSSDDIECDTENSEE GRENTSVAGFHDSTWAVYSGLFAVEKRATVIANAKGHLEGL QMTDLENNSTGELQPVLPSGASAAPEGMSSDDIECDTENSEE GRENTSVAGFHDSTWAVYSGLFAVEKRATVIANAKGHLEGL QMTDLENNSTGELQPVLPSGASAAPEGMSSDDIECDTENSEE TTILSJSGSSAVISTTILATTSKYTCDEKVANITUVYLYNKETK LITAKLANNENNEGGNICTSINSTRAITECKRASVISHINSTRA FILSTSSSAVISTITLATTSKYTCDEKVANITUVYLYNKETK LITAKLANNENNEGGNICTSINSTRAITECKRASVISHINSTRA FILSTSSSAVISTITLATTSKYTCDEKVANITUVYLYNKETK FINASKIIKTDFGSFGEPGIIFCRSEAAHGGVITWAPFORSPHN FILSTYLKTERGCLINDRHILKTUDAINTECKRASVISHINSTRA FILSTYLKTERGCLINDRHILKTUDAINTECKRASVISHINSTRA FILSTYLKTERGCLINDRHILKTUDAINTECKRASVISHINSTRA FILSTYLKTERGCLINDRHILKTUDAINTECKRASVISHINSTRA FILSTYLKTERGCLINDRHILKTUDAINTECKRASVISHINSTRA FILSTYLKTERGCLINDRHILKTUDAINTECKRASVISHINSTRA FILSTYLKTERGCHINDRHILKTUDAINTECKRASVISHINSTRA FILSTYLKTERGCHINDRHILKTUDAINTECKRASVISHINSTRA FILSTYLKTERGCHINDRHILKTUDAINTECKRASVISHINSTRAIT RYNGNISHAMATATA KVORNOSAAMCHTTIKSAPPSOVWANITUSHTINDRHILKTUDAINTECKRASVISHINTI FILSTYLKTERGCHINDRHILKTUDAINTECKRASVISHINTI FILSTYLKTERGCHINTORA FILSTYLKTERGCHINTORA FILSTYLKTERGCHINTORA FILSTYLKTERGCHINTORA FILSTYLKTERGCHINTORA FILSTYLKTERGCHINTORA FILSTYLKTERGCHINTORA FILSTYLKTERGCHINTORA FILSTYLKTERGCHINTORA FILSTYLKTERGCHINTORA FILSTYLKTERGCHINTORA FILSTYLKTERGCHINTORA FILSTYLT FILSTYSSARTORA FILSTYLT FILSTYLT FILSTYSSARTORA FILSTYLT FILSTYSSARTORA FILSTYLT FILSTYLT FILSTYLT FILSTYLT FILSTY FILSTYLT FILSTY FILSTYLT FILSTY FILSTY FILSTY FILSTY	amino acid sequence			l .	S=Serine, T=Threonine, V=Valine.
Sequence Sequence	Sequence Appossible nucleotide insertion			1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
CSDMLLER\UPSYEAR\UPSAR\UPSAR\Upsar\Upsar\uppar\u	CSDMLERYGYSEAS VYREAGEDERIC GROUPHRELSDGDL DILLVENDEWGLOSS SIAS TATSTYLERO DECTHOSEROUY EVENMELREGISMEDALAD PAT STOTERO DECTHOSEROUY EVENMELREGISMEDALAD PAT STOTERO DECTHOSEROUY EVENMELREGISMEDALAD PAT STOTERO DECTHOSEROUY EVENMELREGISMEDALAD PAT STOTERO DECTHOSEROUY ATS SLALD IDPLIT HILLDLOKOR SI BRIMGLOPAP PASLLOPTA SYSKOKORKOAMMEN PSICHEK KYNGARVAKOKTUVAN TLISISISSAAS GENEROUTSERS DESCRICER KYNGARVAKOKTUVAN TLISISISSAAS GENEROUTSERS DESCRICER KYNGARVAKOKTUVAN TLISISISSAAS GENEROUTSERS DESCRICER STOTERISCH COLLEGE NE SKORCOLLERS DESCRICER STOTER FOR COLLEGE SERVENDE STALLINGS LICETURE BROCKALDSDAVVAY PSICHARVAY STOTER FOR COLLEGE SERVENDE STALLINGS CHECK THE STOTER CHECK THE STALL THE STOTER CHECK THE STALL THE STOTER CHECK THE STALL THE STALL THE STOTER CHECK THE STALL THE STALL THE STOTER CHECK THE STALL THE STA			sequence	Codon, /=possible nucleotide deletion,
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APSSLLIDPLILIHLLDIKORSSIENLINGLOPREPASALIJOH SYSKRODCORNOMENTSEDLINKIRKIKTUMANKUCKETTUVAN TASEIKSSSAASGOMOTSEDSADOALAACOTENSGELODLOME LLAKSSVANCTURSTNEKSINGSPERABSSVAGSIERPADPDGE NSRSKGDCOTLSGESGSGSGRISSPERALIHGSIGDLINGE DEROCKALDSBAVVAVFSGIPAVERERWYTLANAKOGHLEGL OMTDLENNSETGELOPUPBGASAPEEGHSSDDIECDTENEE GEEHTSVGGFIDSFWMTOPPDEDTHSSFPDGECIGFEDLSENT DENSGE 1 LPDMYNLALLLAFGFAPLDTEVFVTGGSPFPSFTDAVINASGE TITLSPSGSAVISTITIATTPSKFTCDEKYANITUVLYNKETK LPTAKLNVNERVSCONNTCTNBEWHILTECKNASVSISHINSTCA PDEKTLILDVPROEWEVPHICSCOVEROPSTIHLKIKKNIETSTC DTONITYRPCGRMIFDNKSIKLBRIEPEHFYKCDSEILVNSHK FINASKIIKTDFSGFGPGIIGESCHANGEVTHWKKIISTSTC DTONITYRPCGRMIFDNKSIKLBRIEPEHFYKCDSEILVNSHK FINASKIIKTDFSGFGPGIIGESCHANGEVTHWKCEPPR DRNOPHERYHLEVERGNTLURBESHKNCOPFVKDLOYSTDYTFK AVFANGDVEGEPFIHMSTYNSKALIAFALPHITSILLVV LYKIYDLAKKRSCNLDERGGELVERDEKGLANVETHADLILY KVORNGSAMMETTYKSAPPSGVANMTVSMTSNSHWKCEPPR DRNOPHERYHLEVERGNTLURBESHKNCOPFVKDLOYSTDYTFK AVFANGDVEGEPFIHMSTYNSKALIAFALPHITSILLVV LYKIYDLAKKRSCNLDERGGELVERDEKGLANVETHADLICKSTELVY LYKIYDLAKKRSCNLDERGGELVERDEKGLANVETHADLICKSTELVY VKRKIADEGRIFLAFGSIFFVKALIAFALPHITSILLVV LYKIYDLAKKRSCNLDERGGELVERDEKGLANVETHADLICKSTELVY LYKIYDLAKKRSCNLDERGGELVERDEKGLANVETHADLICKSTELVY LIPPDFWRMINGRAVTIVMTGECERONKKCAREVTBINDER PENDERGENCCKOLTHRICCI-DYILOKALIANASYN DEGENERY TARTIGIDALBELBERNINDOYSTVVKLERGRCIMVQVEAQYI LLHGALVENOPGETFUNLSEHPYLLBMKKCOPPSESFSLER PENDLAVENSGEGFTUNLSEHPYLLBMKKCOPPSESFSLER PENDLAVENSGEGFTUNLSEHPYLLBMKKCOPPSESFSLER PENDLAVENSGEGFTUNLSEHPYLLBMKKCOPPSESFSLER PENDLAVENSGEGFTUNLSEHPYLLBMKKCOPPSESFSLER PENDLAVENSGEGFTUNLSERSTRUSSENFSFSCTGGBEISVNING AAGGELKSTIGPBWIFFTUNLSKERSTRUSSPTTOTYRVELKER LEMSKESENDSDESDDDDSBEBESTYINASFINGSINGHKGENGT PENDLAVENSGEGFTUNLSERSTRUSSPTTOTTGBEISVNG GEGROTGIEVDLUNDTKSSTTTLRVFELRISKRKDSRTIVVYQ YTMINSTRUSPAPLEVDLASTTARVFELRISKRKDSRTIVVYQ YTMINSTRUSPAPLEVDLASTAVARAMINGPHOVATALITANAGONERY PTVDVLIGDLINDFLAVENSGERSTRUSSPTROTTGGPEISVNG ASPALNOGS DAMGCKLERRFYTYOTOTTWELLDONTMIHLINDROKAVENLYSSESVIT MLMGGINOTTHANASPLATERELPTHALLDINGVANA LLVHICHDIFINGAPMAPLDLATERELPTHALLDINGV	APSSLADIDPILILIHLIDLKORSITENIMGLOPPEPASLLOPTA SYSKKKOOKORGOMEVPSICHKIKKTOVABVAKMETOVKO TLSIIKSSAANGIONTSIJFSADQAALAACGTENGRLOLLOME LLAKSSVANCYTIROTKIKKSNOP KARRAVDOGE NSSKGDOCTIJEGS POSSOSGSIGSBERALIHGSIGDILBKTE DROCKALDSDAVVAVYSGLPAVEKRAVITGONANGGHEGI ONTDLENNSTGELOPVLERGASAAPEGKNSSGDITECTTENEE GEETIS VAGGFIGDFWATOOPPDEDTHSSFPDOEGJOFPEDISPNT DENGGR 5979 212 3665 LIDDFWYLHILLLAFGFAFLDTEVFVTGGSPTFSPTDAYLNASE TITLSPGSAVISTITIATTENSPTODEKVANITVYLYLYNETK LIFTAKLINVINSIVECGINTCTINBRVINLTECKNASVISIEHINGTA DENTILLDVPGVEKVEVVICCS OVEGEDSTIMLKWIN ETSTC UTONITYRFGCOMMIPINNEEL KLEHLEPEHEKKOBELLINGHK FIRASKILKTORSSFEPOILFGGSEAHAGVITVMPFORSFIN FILCYIKSTEROCLINDKHLIKYDLQNIKYTKYVLSLHAYILI KVORNSAANCHTETKASPSOVAMINVSHSINSHVHCKPPR DRNOPHERYHLBVERGENTILVENSSKKROOFRIKULQYSTDYTFK AYFANDOYFGOPFILHISTSYNSKALIFAFAILITYSLALIVV LYKIYDLHKKRSCNLDEQGELVERDDRKQLMVEPIHADILLET YKRRIJADGAGINTUN EVERCENNIKCAE PHYSKORNIKYVD LILYDDINKVELGEINGDAGSHYINASYIDOFKEPRYTIAAQGFR DETVODPFRMHIEGRAFOS IPPUSEFFY ICKARKPFONOKRYVD ILLYDDINKVELGEINGDAGSHYINASYIDOFKEPRYTIAAQGFR TOTYIGIDANLEGLEERIKVUVYGVVVLIRRORCIMVOVEADYI LIHADILVEYNOOFETSULLIKRRVANDENPSSEDTIT RAPGECCKOLITKHKRCP UPUI IOKLAIVIKKKRATGEEVTHILO FISHPHOVEEPHILLKIKRRVANDENPSSEDTITHONSGAWA TOTYIGIDANLEGLEERIKVUVYGVVVLIRRORCIMVOVEADYI LIHADILVEYNOOFETSULLSHIPPYLIHAMKKUDPSEPSPIPAA FORLBYSKSTODILGNONG BENKSKRRINNVIPYOYMARVELGHE LEMSKESHIDSDESSEDDDSDSEPSKYTIABFJIMSYMCP LEWIN AAQCPLKSTIOPPQMIPQRKVRIVILELHIPQUITELANGKUDPSEPSPIPAA FORLBYSKSTODILGNONG KNINGROKITE CONYMG ESKQTYGDISTOLDOTORSTITURVEERISKRKDSRTVYOYO YTMMSVRQLEARPEREISINSIONIVOKOKNINGROKITE ELONOOM ESKQTYGDISTOLDOTORSTITURVEERISKRKDSRTVYOYO YTMMSVRQLEARPEREISINSIONIVOKOKNINGROKITELSIAN AAQCPLKSTITUDPQMIPQRKVETVUVAKNINGROKITELSIAN AAQCPLKSTITUDPQMIPQRKVETVUVAKNINGROKITELSIAN LIKRGBSOOTORICALINLILBSATTEVVOITOVAKARKARD GMUSTEREGOVETVITASTATARVEELDAALANA LIVINGICGITERIONIVAKUNINGRINGRATATUTENSIANUNINGRINGRATUTENSIANUNINGRINGRATATUTENSIANUNINGRINGRATUTENSIANUNINGRATURENSIANUNINGRANINGRATURENSIANUNINGRANITELTISTIANUNINGRANITELTISTIANUNINGRANITELTISTIANU				DLDLVYEDEVNQLDGSSSSASSTATSNTEENDIDEETMSGENDV
SYSKNDORKQOAMREVESILANLERLKTUMAEVECHETUVER TISSIKSSSASSOMSTISIFISONQALAACTISSICADICAL LLAKSSVANCYIRISTINKKSNSPRPARSSVAGSLSLRARADPGE NSRSKGOCTIJSEGSPGSSGSGSGRSHSSPALIGSIGDILPKTE DRQCKALDSDAVVAVPSGLEAVEKREWTILGAVAKGGHLEGI OMTDLENNSETBELGPUPLEGGAAAPEEMSSDGDICTVERE GEETTSVGGFHDSFMWTQPPDEDTHSSFPDGGGGEDLSFNT DENSGR 1PDMTHYLMLKLLAFGFAFLDTEVFVTGQSPTFSPTDAVINASE TITISSPGSAVISTITIATTSSFPDGEVAGATITUVLYNKETK LLTAKLNIVERVEGGNITCTINREVNILTECKNASVSISHNGCTA PDKYLLLDVPROVEKVPVICCS\QVOPQPSTIMLKWRITESTC DTQNITYRPGCGNNIPDMKEK IKEMILEPEINGSILIVNSHK FINASKIIKTDFGSFGPQIIFCRSEAAHGQVITMNPFORSHN FILCYIKETEKDCLINLDNILKVDLQNLKYTYVLSLAHYIIA KVQRNGSAMCHFTTKSAPSQOWANTVSMTSDNSMMVKCRPPR DROMPERFYLLEVEANTULVUNGSIKNDCPHYTYVLSLAHYIIA KVQRNGSAMCHFTTKSAPSQOWANTVSMTSDNSMMVKCRPPR DROMPERFYLLEVEANTULVUNGSKHUCDFWFPHADILLIVT LLYVYNHEKSCNLDEQOLUVRSDLEVERDDEVQIAWVEPHADILLIVT LLYVYNHEKSCNLDEQOLUVRSCHEROBLOVANNVEYHIOD TILPTDYNRVELSEINGDAGNYINASYIDGFREPRKYLAAGGBR DETVDDFPRRMIMGCATTIVUNTCREGENORMCAEYMPOMERGY RAFGECCCKDLTHIKKCP\DYIIQKLUTVRCEGENORMCAEYMPOMERGY RAFGECCCKDLTHIKKCP\DYIIQKLUTVRCEGENORMCAEYWPOMERGY TGTYIGIDAMLEGLBERKVDVYGVVVKLRRGRCLMVQUQYY LLHQALVERNOFGETEVALSELEHTYLHIMKRENGAPTVYQVG TTYNSVEGLIPBERKGLISHIQVVKGKVVLRRGRCLMVQUQYY LLHQALVERNOFGETEVALSELEHTYLHIMKRENGETYVYQV TYNNSVEGLIPBERKGLISHIQVVKGKVVLLTELHGDGDEICAYMG GSKQTTGDIEVDLKDTIKSSTYTLAVFERSHKENGTYVYQV TYNNSVEGLIPBERKGLISHIQVVKGKVLYVALIFELHGDGDEICAYMG GSKQTTGDIEVDLKDTIKSSTYTLAVFERSHKENGTYVYQV TYNNSVEGLIPBERKGLISHIQVVKGKVLYVALIFELHGDGDEICAYMG GSKQTTGDIEVDLKADTIKSSTYTLAVFERSHKENGTYVYQV TYNNSVEGLIPBERKGLISHIQVVKGKVLYVALIFELHGGDEICAYMG GSKGTGGIEVDLKADTIKSSTYTLAVFERSHKENGTYVYQV TYNNSVEGLIPBERKGLISHIQVVKGKVVLYVALIFELHGGDEICAYMG GSKGTGGIEVDLKADTIKSSTYTLAVFERSHKENGTYVYQV TYNNSVEGLIPBERKGLISHIGVVKGKVLYVALIFELHGGBIGGENGTGTGFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	SYSKRONDORKOOAMMANTSDIKMIKALKITOMAGUNCHKTDVKON TISSIKISSSAASGONGTIESPAOAALAACTERIOLIGME LLAKSSUANCYIENSTNIKSINSERPAARSSVAGSISIRPAALIGOLIGME LLAKSSUANCYIENSTNIKSINSERPAARSSVAGSISIRPAALIGOLIGME BASRAKOCOTISEGS GSSGSSOSRISPAALIGISGOILIPATE DROCKALDSDAVVAVPSGLPAVEKRERWYTIGANAKOGHLEGIL OMTOLENNSETGELOPUVBEGSAAPEEMASSICCIPTEMEE GEBHTSVOGFRIDSFMMTOPPDEDTHSSFPDGGOPDLISFNT DENSGR 5979 212 3665 LDDMIWILLELLIAFCERFLDTEVEVTCGSFPTSPTDAVIJAGE TITLSSOSGAVISTTILATTPEKEYCOCHEYMITTOVILYINSET LLYTAKLINVERVECOMNITCHNEWHILTECKNASVSISINSCTA PDKYLLLOUP GEVEKYPHICOS VOR OPDSTIMLKOKNITSTIC DONITYRPOCOMHIPDIKEK LISHLEFSHEN KORSISINSCTA PDKYLLLOUP GEVEKYPHICOS VOR OPDSTIMLKOKNITSTIC PDKYLLLOUP GEVEKYPHICOS VOR OPDSTIMLKOKNITSTNIN FILCYIKETEKOCLALDIANLINYOLONIKEYTETYVISIHAYIIA KVORNOSAAMCHETTIKSAPPSQVWANTVSWITSINSMHVKCHPS DRAMOPHERYHLIKVERGOTILVINESHEKOCHEVALOUTSTYTYK AYFINOOTPOSPFILIHISTSYNSKALIAFLAFLITVISIHAYIIA KVORNOSAAMCHETTIKSAPPSQVWANTVSWITSINSMHVKCHPSTYPK AYFINOOTPOSPFILIHISTSYNSKALIAFAFLITVISIALIVV LYKIYDLAKRISELBINDAGSNITAASYILOFKERPYNONKKAYVY LIVITUALKIKISELBINDAGSNITAASYILOFKERPYNONKKAYVY LIVITUALKIKISELBINDAGSNITAASYILOFKERPYNONKKAYVY LIVITUALKIKISELBINDAGSNITAASYILOFKERPYNONKKAYVY LIVITUALKIKISELBINDAGSNITAASYILOFKERPYNONKKAYVY LIVITUALKIKISELBINDAGSNITAASYILOFKERPYNONKAYVY LIVITUALKIKISELBINDAGSNITAASYILOFKERPYNONKAYVY LIVITUALKIKISELBINDAGSNITAASYILOFKERPYNONKAYVY LIVITUALKIKISELBINDAGSNITAASYILOFKERPYNONKAYVY LIVITUALKIKISELBINDAGSNITAASYILOFKERPYNONKAYVY LIVITUALKIKISELBINDAGSNITAASYILOFKERPYNONKAYVY TINNYAYOLOFABPOMATAYILOFKERPYNONKAYVY LIVITUALKIKISELBINDAGSNITAASYILOFKERPYNONKAYVY LIVITUALKIKISELBARNONUTYVYVILTELKIROOPESCHITAA PARADOLOFKERPYNONKAYVYVILTELKIROOPESCHITAA LIHOLAVANCOLOFKERPYNONKAYVYVILTELKIROOPESCHITAA AAQOPLKATTIOPHOMIPORATYVILTIAKKERPOTYTIVARVELBE FORLPSYSSWITOHIGONE LIKKKERPONYVILTIALIKOOPESCHITAASHA AAQOPLKATTIOPHOMIPORATYVILTIAHKOELISELBINGANAY AAQOPLKATTIOPHOMIPORATYVILTIAHKOELISELBINGANAY AAQOPLKATTIOPHOMIPORATYVILTIAHKOELISELPINEVUTAAAANA AAQOPLKATAATAY AAQOPLKATAATAY AAQOPLKATAATAYAANAANAANAANA		[BYNNMELEEGELMEDAAAAGPAGSSHGYVGSSSRISRRTHLCSA
TISELENSSAASGEMOTISLFSADQAALACCTENSGELOLOME LLAKSSVANCTINSTINKSNSPYARSSVARSLSLERRAUDDEE NSEKGECGTLSEGSPGSSGSGSHSSPRALINGSIGDLENTE DROCKALDEBADVVANFSGLAPVERKERWITTLGAVAKGGHLEGL OMTDLENNSETOELOPVLFEGASAAPERGMSSDSDIECDTENEE GEENTSVOGFHDSFMWTOPPDEDTHSSFPDGEQIGEPDLSENT DENSGR 5979 212 3665 LPDMYHLUKLLLAFGFAFLDTEVFVTGQSPTFSFTDAYLNASE TITLSPSGSSAVISTITIATTESKPTORKYANITUTULYNKETK LFTAKLNAVSENVECGNNTCTNNEVHILTECKNASVISINSCTA PEKKILLDAVPEVEKVPVHCCS, OVEOPETHLKWINITESTC OTONITYRPGGGNNITOFRSEAHAGUITTENSPORSFINGTA PEKKILLDAVPEVEKVPVHCCS, OVEOPETHLKWINITESTC OTONITYRPGGSNITOTROSPHENDITERSEAHAGUITTSHAVEN FILCYI KFTEKDCLINLDKHLIKYDLGUNKPYTKYVLSLHAYI I A KVORNGSAMGHETYTKSAP PSOWNMTVSMTSDNSWKCRPPR DENGHERVHLEVEAGNTLVRNESKHNCDERVEKURPDEN AYFANSKI IKTORGSPÖEPOLI FKGSBAHAGUITTSHAPPORS SYM AYFANGDYPGDEPILHHTSYNSKALIAFLAULI IVTSIALIVV LYXIYDLHKRSCNLDEGGGLEVERDBERQLMAVEPIHADILLET YKRILABGGRIFLARFGGI PRVESKFPI KEARKPPHONKRYVD LLYDYNRVELSSINDDAGSNYINASYI DOFFWEFI HAGALERVEN DETVDDPMRMIMBORATVI WVYRCEGENENKCASVAPSHEGT RAPGECCKDLIYKHRCP, DYI JOKALI VYKRITAGVETPHADILLET TSKPPDHGYPEDPHLLILLRRRVNAFSNFFSGPI VVUCSAGVGR RAPGECCKDLIYKHKRCP, DYI JOKALI VYKRITAGVETYLAGGGR RAPGECCKDLIYKHKRCP, DYI JOKALI VYKRITAGVETYLAGGGR TGYTI GIDAMLEGILBARHKVONGVOVALVELMOWODAGYI LIHGALVENOFGETEVALLSELHPYLLHMKKDDPPSEPSPLEAE FORLPSYRSHENFOLINONG, BINKKNINNSNI YIPDINNYHKINE LEMSKESEHDDBSSDDDSBEEFSKI INASPINSYHKYN SWINFLEN AAGGFLKETIODPWOMI FORKVOKU VULHTELKHGDGDIGOYWG REKOTTGOILEVOLKOTIKKSTITLAVETELKHGDGDIGOYWG REKOTTGOILEVOLKOTIKKSTITLAVETELRHERRDSKRTVYOYO YTNASVEGLIPABPKELISMI QOVKKNINGKDKI EPDWEVD KVKQDANCVURGI FCALINLLISBATTEVVURYALLISBATTEV LLIHGRAGSGOTG FCALINLLISBATTEVVURYALLISBATHW AAGGFLKETIODPWOMI FORKVOKU VULHTELKHGDGDICOYWG REKOTTGOILEVOLKANING SWINFSFFOY VYFKVPLLASE I IDSSTRMBSERSE LIVGULYONAL COGGR GWUSTEGOYOPULTOVIASTYPADAGOVKNINGKDKI EPDWEVD KVKQDANCVURGI FCALINLISBATEVENOVYONALGRIKEFP VFFKVPLLASE I IDSSTRMBSERSE LIVGULYONAL COGGR FTVOLVOLLODI FINADADWAGNILIBERHADLYTULAGRITESSHAN LLVICHILDI FINADADWAGNILIBERHABLYTOLLOGNITESSHAN LLVICHILDI FINADAP	TISSIKSSSAASGOMOTILEFSADOAALAACOTENSGRIQDLOME LLAKSSUANCY INSTNEKSHSPEKPASSVAGSIKRADPGE NSRSKODCOTLSGGSGSGSGSRISSPRALHGSIGDILEFTE DROCKALDSDAVVAVFGGLPAVERRAWTIGANAKGHLEGL OMTDLENNSETGELOPVLPEGASAAPEENASUSDIECDTENEE GEBHTSVGGFTGDSFMTTOPPDEDTHSSFPDGBOLGPEDLSFNE GEBHTSVGGFTGDSFMTTOPPDEDTHSSFPDGBOLGPEDLSFNE DENSGR 1 DEDWINGLILLARGFAFLDFUTVGGSFPSFPTDAVILNASE LTTILSPGGSAVISTTIATTPSKPTCDEKVANITUDYLYNKETK LFTAKLNNSENVECNINTCTNNEWHILTECKNASVSISHNSCTST POKTLILLAVPROVENVENCHINTCTNNEWHOLITECKNASVSISHNSCTST DTONITYRGGGMIFDNKEIKLENLEPERFYKOSEILVNSH FILGYIKSTERDCLALDRALIKYDLONLEYTTYVISHAYIIA KVORNOSAMGHTTKSAPPSGVONMIVOMINTSMSTANKYLETGE DTONITYRGGGMIFDNKEIKLENLEPERFYKOSEILVNSH FILGYIKSTERDCLALDRALIKYDLONLEYTTYVISHAYIIA KVORNOSAMGHTTKSAPPSGVONMIVOMINTSMSTANKYLEDGE DROMPHERYHLEVEAGNTLURNESHKNCOFRVEDLOYSTTYTY AYFRINDDVGGEPP FILHISTYSNSKALIAFLAPILTYSIALLVV LYKIYDLHKKRSCNLDBOGGLVERDDEKQIMNVEPIHADILLYT ILFYDTNSVELSEINGDAGSNYINASYLIOGFKEPRKYLAAGGGF DETVODFFRMINGSRAVILVNTKESKAPLOGENOMICAPETYYL ILFYDTNSVELSEINGDAGSNYINASYLIOGFKEPRKYLAAGGGF BAPGECCCKOLTKHRCCP, DYIIGKEN TVINKEKATGREVTHI FISHPHGVVEDEPHLLIKLRRENVADVYGVVKLRGGCLMVGVEAGGGF RAPGECCCKOLTKHRCCP, DYIIGKEN TVINKEKATGREVTHI FISHPHGVVEDEPHLLIKLRRENVADVYGVVKLRGGCLMVGVEAGGGF RAPGECCCKOLTKHRCCP, DYIIGKEN TVINKEKATGREVTHI LEMBASSHADGSTETEVALSEH PLILAKRRENVADVYGVVKLRGGCLMVGVEAGGGF RAPGECCKOLTHRRCCP, DYIIGKEN TVINKEKATGREVTHI LEMBASSHADGSESDDDSDSBERSFYTINASTIBAPINCS ICAGVWG RAGGELKSTHOPPROMI PORKVKVIVMLITELKRIGGGI CAGVWG RAGGELKSTHOPPROMI PORKVKVIVMLITELKRIGGGI CAGVWG RAGGELKSTHOPPROMI PORKVKVIVMLITELKRIGGGI CAGVWG RAGGELKSTHOPPROMI PORKVKVIVMLITELKRIGGEI CAGVWG RAGGELKSTHOPPROMI PORKVKVIVMLITELKRIGGEI CAGVWG RAGGELKSTHOPPROMI PORKVKVIVMLTELKRIGGEI CAGVWG VYNNSVEQLERAPPKELISNIOVVKOLPONNSSGENHHISTSPIL LIIRCROBGGOTGI POALLBHLESAETEVVUDIFQVVKALRKANG RAGGELKGTT RAGGER GWUSTFERUTGULTUVALSTYTHANGELGLADAVANCH SSENGH RAGGELGKARDWYGUNGANANLISSUVALDESPOVOL VEGEBERGVANGHTON TVANKERARDERPERVENDE GROOT TVANGSGENGHT RAGGER TVANGSGUNG VYDRYGGGSSIAVLENSHARANTIKGER PLAYDERGENOM VARGELARGEN TVANGSGEN TVAN	1			ALSSELDIDELLI HELDEKERSSIENLWGLOPRPPASLLOPTA
LLAKSSVANCTIRNSTINKESNEYRARSSVAGSLSLERADDOE NSRSKGCOTISEGSCHSSESGRISHSFRALHGSIGDILPREE DROCKALDSDAVVAVPSGLEAVEKREWTILGAVAKGGHLEGL OMTDLENNESFEDELGPVLPEGASAAPERGMSSDDSICTPEREE GEHTSVOGFHDSFMMTGPPDEDTHSSFPDGEGIGFEDLSFNT DENSGR 1 DENSGR 1 DENSGR DENSTRATIATTESKPTCDEKVANITUTULYNKSTK LETTALSYSGSAVISTTITATTESKPTCDEKVANITUTULYNKSTK LETTALLNYSENVECGNNITCHNESVALIGEKUSISINSCTA POKILLIDVPROVEKVPVICCS\OVERPETTMIKKNITETSTC DRONITYRFOCGNNIPDINKEIKLENLEPEISKSISINSTINSTSTA POKILLIDVPROVEKVPVICCS\OVERPETTMIKKNITETSTC DRONITYRFOCGNNIPDINKEIKLENLEPEISKSISINSTYTKYNSK FILAYIKTETEKOLLINDINIIKTDLQNIKFYTKYJLSLHAYIIA KVORNSGAAMCHETTKSAPPSOVWMNITVSHISHSTITYRY RYPRINGSYLOEPILHHISTSVIKALIAFLAFILIVTSTALLIVV LYXIYDLHKKRSCNLDEQGELVERDDEKJUMVEPHIADILLET YKRKIADBEGIFLAFFOSIPNVSKYLIAFALFILIVTSTALLIVV LYXIYDLHKKRSCNLDEQGELVERDDEKJUMVEPHIADILLET YKRKIADBEGIFLAFFOSIPNVSKYPIKSKALIAFLAFILIVTSTALLIVV LYXIYDLHKKRSCNLDEQGELVERDDEKJUMVEPHIADILLET YKRKIADBEGIFLAFFOSIPNVSKYPIKSKALIAFLAGOPR DETTOPFRINKINGCRATIVUMVTGCEGDENKEVETWOSKPYBEGET RAPGECCCKDLTHKRCP\DYSKYPIKSKALIAFLAGOPR DETTOPFRINKINGCRATIVUMVTGCEGDENKEVTWSHEGET RAPGECCCKDLTHKRCP\DYSKYPIKSKALIAFISHTVNFVSKYPIKSKALIAFLAGOPR DETTOPFRINKINGCATATUWVTGCEGDENKEVTWSHEGET RAPGECCCKDLTHKRCP\DYSVIKSHINNKKRDPPSESPPLEAE FORLPSYKSHINGCHATUWGTGCEGDENKOTPHYNVELAKER THINGALDELERAKVOVYGVVKKARGRCLMVOVEAQYI LIHGALVENOFGETEVALSELHPYLLINMKKRDPPSESPPLEAE FORLPSYSSHINGTHONINGKKATORVVIVINTELLEHKKRDSFLTVYQY YTNINSVGLLABERKELISHJOVKVALVALTELLEHKKRDSFLTVYQY YTNINSVGLLABERKELISHJOVKVALVALTELLEHKKRDSFLTVYQY YTNINSVGLLABERKELSHVALVALUMARALING ESKOTTGOIEVMANTATATALLORVVALVALRARR GMVSTFEYYSPLIDVIASTTYLRVELEHKKRDSFLTVYQY YTNINSVGLABERKELSHVALUMARALINGENET PEBBLEVQENNEBAADLTELEVTMHARALLORVVALRARR GMVSTFEYYSPLIDVIASTTYLRVELEKKRAGEGEFENDEVO KVKQDANCVHPLAAPELLIPEKAPEDLAGESELIFKTLORM CGARPODTKAGALVERALEKTPINDAVANKLISSTGTGGEBISVNGP VGTREIKCTIGGELIISHKANDAVANKLISSTGTGGGERSVAL DHAGCKLERKERTYSTATINSHEARAASLROLEAGHSGLEKTEDLUFUKNA DHAGCKLERKERTONAVANKLISSTORGOVOVVVLCON GGHEFCALKSVVPDEKHMINDLALERFRIN	LLAKSSUNNCYIENSTNIKKSNEPRARSSYAGSILSURANDOPE BRSKACDCOTLSEGS GSSGSSERSPERALIES GODILPKTE DROCKALDSDAVVAVFSGLPAVEKRERWYTIGANAKGGHLEGIL OMTOLENNSETGELDVUP, DEGASAPEGMASSDE COPTENSE GEBITSVGGFIDSFWMTQPPDEDTHSSFPDGRQIGPEDLSTNT DENSGR 1. LPDMYWLUHLKLIAFGFAPIDTEVFVTQSPFPSPTDAYLNASE TTTILSPSGAVISTTI LATTPSKFTCDEKYANITUVNIKYMASE LFTAKLINVBENWSCQNNTCTNBEWHILTECKNASSI ISHSCTA PDKTLILDVPPGVEKVPVHCCS\QVEQPDSTIVLKWKNI ETSTGC DTQNITYRPGCGMTFONKE ILKBNLEPSHEYRGDELIVSHK FTNASKI IKTDFGSSGEPGI IFCRSEAAHQGVITWNPFQGSFLVSHK FTNASKI IKTDFGSSGEPGI IFCRSEAAHQGVITWNPFQGSFLVSHK FTNASKI IKTDFGSSGEPGI IFCRSEAAHQGVITWNPFQGSFLVSHK FTNASKI IKTDFGSSGEPGI IFCRSEAAHQGVITWNPFQGSFLVSHK FTNASKI IKTDFGSSGEPGI IFCRSEAAHQGVITWNPFQGSFLVSHK FTNASKI IKTDFGSSGEPGI IFCRSEAAHQGVITWNPFQGSFLVSHK FTNASKI IKTDFGSSGEPGI IFCRSEAAHQGVITWNPFQGSFTDYFK AVFRINGDVFGEPPILHISTSYNSKALIAFLAPILITVTS IALIV LVKIVPLIKKRSCHIDEQGSLUEDGDORGLWWEYDSTYPFK AYFRINGDVFGEPPILHISTSYNSKALIAFLAPILITVTS IALIV LIVENTPLIKAFGGST FRUFSKYPI IKGEREKPPRONMSEVYU LIVENTPLIKAFGGST FRUFSKYPI IKGEREKPPRONMSEVYU LIVENTPLIKAFGGST FRUFSKYPI IKGEREKPPRONMSEVYU LIVENTPLIKAFGGST FRUFSKYPI IKGEREKPPRONMSEVYU LIVENTPLIKAFGGST FRUFSKYPI IKGEREKPPRONMSEVYU LIVENTPLIKAFGGST FRUFSKYPI IKGEREKPPRONMSEVYU LIVENTPLIKAFGGST FRUFSKYPI IKGEREKPPRONMSEVYU LIVENTPLIKAFGGST FRUFSKYPI IKGEREKPRONMSEVI PRODECCCKOLDIKHKRCP Į VYVIKKEKATGREVTHI LIPENDROMSESSEDDDSSGESEPSKYPI INTOKAPISAFGGSEPI INTOKAPISAFGER FQLIPSYRSWRTOHIGNOC IKKKKRNISNYI PYDYNRVELIKHE LEMSKASBHODSESDDDSSGESEPSKY INASIF NASKORGENICH INTOKAPISAFGER FQLIPSYRSWRTOHIGNOC IKKKKRNISNYI PYDYNRVELIKHE LEMSKASBHODSESDDDSSGESEPSKY INASIF NASKORGENICH INTOXAPICA BAQGPI KASTIGOPPOMI FQRKKVI VIMITELKKGOGDI ICAVYESP FUNDALORUMAND INTOXAPISAFGEREVU IG POKAPICA INTOXAPICA BAQGPI KASTIGOPOMI FQRKKVI VIMITELKKGOGDI ICAVYESP LIKHGRASGOTOTI FALIALILISSFATEVU IG POKAPIC POMI AAQGPI KASTIGOPPOMI FQRKKVI VIMITELKKGOGDI ICAVICAVOY VYTNASVGOLPABPAKELTSHIOVANAKI ISSPUTALIONAMI ISSPUTA LIKHGRASGOTOTI FARAFGRAFTA FOR TOTA TARAFGRAFTA FOR TOTA TARA	1			TI.SFIKSSSAACCOMOTEL BEADOAN AN COMPINED AND
NSRSKGPCGTLSEGSFOSSGSGSRISPRALINGSIGDILPTE DRQCKALDSDAVVAVPSGLPAVEKRRWITJGANKAGGHLEGI OMTDLENNSETGELQPVLPEGASAAPEGMSSDSDIECPENEE QEEHTSWGGTHSFMWTQPPDEDTHSSFPDGGGPDLSFNT DRNSGR LPDMTHYLMLKLLAFGFAPLDTEVFVTQSFPFSPTDAYLNASE TITLSPSGSAVISTITIATTESKPTCDEKYANITJDYLYNKSEK LFTAKLNIVSENVEGGNTCTRNBVNNLTECKNASVISIHNSCTA PPKKLILDYPGVEKVPVHCCS, VOVEQPSTILLKWKNIETSTC DTQNITYRPQCGMNIFDNKEKLENLEPSHEYKCDSELLYNSHK FENASKIIKTDFGSFOEPGIIFCRSEAAAGGVILLKWKNIETSTC DTQNITYRPQCGMNIFDNKEKLENLEPSHEYKCDSELLYNSHK FENASKIIKTDFGSFOEPGIIFCRSEAAAGGVILLKWKNIETSTC DTQNITYRPQCGMNIFDNKEKLENLEPSHEYKCDSELLYNSHK FENASKIIKTDFGSFOEPGIIFCRSEAAAGGNAWTVCSPDRF PFLCYLKETEKDCLNLDKNLIKYDLQNLKPYTKYLSLHAYIIA KVORNGSAMGLETTKSAPPGOWANTVSNIMMYCKEDPSH DENGPHERYHLEVSAONTLVENSSHINDDFYKKLLQSTDYTFK AYFRINGDYGGPFILHSTSYNSKALIAFLAFLITVISIALLVV LYKIYDLHKKRSCNLDEQQELVERDDEQLMWRYPSHADILLET YKRILABGGLFLABFGSIFRVEKFFIKEAKKPPNNNKRYND LYKIYDLHKKRSCNLDEQGELVERDDEQLMWFFIHADILLET YKRILABGGLFLABFGSIFRVEKFFIKEAKKPPNNKRYND LIPDTNRVELSSHINDAGGSNINASYIDGFKPRKYIAAGGFR PETDDPRMMINEGLABAKTVIWVYRCEBENNENGSTAKTGREVTHIQ PETSMPDHGYPEBDHLLLKLRRRWAFSNFFSGPIVVICSAUGG RAPGGCCCKDLTKHKRCP, DYIJCKLILLKRRRAFTPLYDLG FORLPSYRSMRTOHIONG, BURSKINNENSYNTYDYVROVPLKHE LEMSKESENDEDSSDDSDBESEPSKYINASFINSTYNKYC LEMSKESENDEDSSDDSDBESEPSKYINASFINSTYNKYC AAQGPLKETIGDFWMIFQRKVKUTVLHTELKHGDGDIGAGYMG EGKQTYGDIEVDLKDTIKSSTYTLKVEELRISKRKDSRTVYOYG YTMSSUGLFABPKELISMIQVYKKULPGNNSSGSMKHKSTPL LIHGLIGSGGGTFGCALINLISBATEEVUTDFGVVKALRFARP GMNSTEGOYGPLDDVLASTYPAGNGGKSERSPTSGTGGBEISVNG KVKQDANCVHRGLASPETLAFTHYOTGTVSLALEGGYBLWTLVALRGGNBET PEEDLBVQENNEDAAHDLTSLEVTMHHALLQSVDVVVAPCQGLR PTUDVLGDLVADPLPVITYALIKGELLBARTERVTHGGESSWYR KVKQDANCVHRGLASPETLAFTHYTOTTRVSLALERBERSELLTVALAGGGREGGYGVVYVLCON MCGHFGTALKSSENDAMAKHLISTSGOVLGTHAVERSCHARS LVHCHCLDIFTNOAPDMGRIDGITTSKLEYTRKELSLASSKLAK SICSOPRTRINSSHAFAASLQQLBGRGGGYGVVYLCON MCGHFFCALKSVVPPDEKHWINDLAKGRANGLISHTELGSKYK DHAPRABALLSLESSELODVHADIKKUNDLJKORASCLASSKLAK SICSOPRTRINSSHAFAASLQQLBGAGGLEKTEDLULLVICON MCGHFFCALKSVUPPDEKHWINDLAKGRASGLEKTED	NSRSKGPCQTLSEGSPGSSGRISSPRALHGSIGDILPTU BROCKALDSBAVVAYFGGLPAVLPERRAWATGANAGGHEGL QMTDLENNSETGBLQPVLPEGASAAPEGANSDSDIECTENBE GEBHTSVGGFIDSFWMTQPPDEDTHSSFPDGRQIGPEDLSFTI DENSGR 1 EPDTYMYLHKILAFGFAFLDTEVFVTGGSPTSSFTDAYLMASE TTTLSPSGSAVISTTIATTPSKFTCDEKYANITVDYLYNKETK LFTAKLNVNENVSCQNNTCTNBEVHNLTECKNASVSISHNSCTA PDKKLLLDVPPGVKVPVHCGS, VORGPOSTIGLKKNISTSTC DTQNITYRPQCGMMIPDNKSILBRLEPFBFYKCDSEILWRSHK FINASKILKTDFSGPGPQIIFCKSPAAPGVTVHYLSHAYILA KVQNGSAAMGHTTKSAPPSQVMNTVSMTSDNHVCRPBR DRNGPHERYHLEVERQNTLVRNEGHKNCDFVKULQVSTDYTFK AVFRINDVGCBP FILHISTSYNSKALIAFLAPLIIVTSIALLVV LYKIYDLHKKRSCNLDEQGSLVERDDEKQLMVPETHADILLET YKRKIADBGREFILHASTSYNSKALIAFLAPLIIVTSIALLVV LYKIYDLHKKRSCNLDEQGSLVERDDEKQLMVPETHADILLET YKRKIADBGREFILHASTSYNSKALIAFLAPLIIVTSIALLVV LYKIYDLHKKRSCNLDEQGSLVERDDEKQLMVPETHADILLET YKRKIADBGREFILHASTSYNSKALIAFLAPLIIVTSIALLVV LYKIYDLHKKRSCNLDEQGSLVERDDEKQLMVPETHADILLET YKRKIADBGREFILHASTSYNSKALIAFLAPLIIVTSIALLVV LYKIYDLHKKRSCNLDEQGSLVERDDEKQLMVVPETHADILLET TSRPHOVEDPHLLLKLRRVVARSINFPSGFIVVICKSARGVF DETVDDFRRMIMEGRATVI VMYTECEENRIKCABYMFONSKRYVL TSRPHOVEDPHLLLKLRRRVARSINFPSGFIVVICKSARGVF TSTYIGIDAMLEGLEABRINGVVYVVVLKRGCKLMVQVEAQYI LIHQALVSYNOPGETEVNLSEHPYLHMMKKRDPPSSFEPLEAE FORLPSYNSNSTOHIGNGE LENKSKRYNSNYITPYNRVPLEHE LEMSKESENSDESSDDDSBSEBSYINAFIKSTYNYVY AAQGPLKSTTIGDPMOMT FORKVVLVILNTELKRIGDGRIVYVYOY YNNSVEQLPAPPKELISHOVYKOLLOKNSSEGNHCHKSTYD LIHCRDSGOTGIFCALLALLESSATEEVVDIFGVVALRKARAP GMYSTERVQPLYDVIASTYPAQNGQVKKNNIGGBKIEPTWED KNXQDANCVBPLGAPEKLELSKARGSESTYSTORGRRYVYOYO YNNSVEQLPAPPKELISHOVYKOLLOKNSKEGNHCHKSTYD KNXQDANCVBPLGAPEKLELSKEGABGSESTYSTORGERINGRY VYOYO KNXQDANCVBPLGAPEKLELSKEGABGSESTYSTORGERINGRY KNXQDANCVBPLGAPEKLELSKEGABGSESTYSTORGERINGRY VYOYO KNXQDANCVBPLGAPEKLELSKEGABGSESTYSTORGERINGRY VYOYO KNXQDANCVBPLGABEKLESKORGESTYNOPTORGERINGRY LUCHCLDIFTNAFFICHTYTOTTVSLALLGEQUELVTTLVAHQONNETI PEBDLEVQENBDAAHDLTELEVTHMHALLGEVDVVALCKARAP GMYSTERVQPLYDVALGNAMLTISSVYLYRESPVOTL ERCLSSLEKSQDVSVHITSNYLLQGLKGRCGLEKTGDHISCHUNG VGTRRYLGGGLIGGLTGLTGLANGLTUNGRYNICH LUCHCLDIFTNAFFICHTUNGRYNDAAPHEVELSTENDLYCHUNG VGTRRYLG	}		Ì	LLAKSSVANCYIPNSTNKKSNSDKDARSSVACSI SI DRAWDOG
DRQCKALDSDAVVAVPSGLPAVERREKMYTLGANAKGGHLEGIL QNTDLENNSGTORLOPULPGGASAAPERSBSDIECTCHEME QEBHTSVOGFHDSFMVMTQPPDEDTHSSFPDGQIGFEDLSFNT DENSGR 1 LPDMTWYLWLKLLAFGFAFLDTEVFVTGQSPTPSPTDAYLNASE TTTLSPSGSAVISTITIATTPSKSPTCDEXYANITYDYLNKSTK LFTAKLAVVRENVECQNTTCNBVWNLTGKASVSISINSCTA PDKTLLLDVPGVVEKVPVLCCS\QVEQPDSTTWLXWKNLETSTC DTQNITYMFQCGNNIFDNEKILKINLEPKSCASSISINSCTA PDKTLLLDVPGVVEKVPVLCCS\QVEQPDSTTWLXWKNLETSTC DTQNITYMFQCGNNIFDNEKILKINLEPKSCASSISINSCHA FFINASKIIKTDFGSFGEPQIIFCRSEAAHGGVITWNPPORSFNN FFILCYIKETERDCLINLDRILIKYLDQLKYKVLSVLSHAYIIA KVORNGSAMCLFTTKSAPPSQVMNMTVSMTSINSMHVKCRPPR DRNGPHERYHLEVFACNTLVRNESHKNCDFRVKDLQYSTDYTFK AYFRINGTYFGEPFILHATSYNSKALLAFLITVTSTALLVV LYXIYDLHKKRSCHLDEQQELVERDDEKQLMNVEPHABILLET YKRRIADBGGFLFLAEFGSIFVNSKALLAFRLITVTSTALLVV LYXIYDLHKKRSCHLDEQQELVERDDEKQLMNVEPHABILLET YKRRIADBGGFLFLAEFGSIFVNSKALLAFRLITVTSTALLVV LYXIYDLHKKRSCHLDEQQELVERDDEKQLMNVEPHABILLET YKRRIADBGMFLFLEFGSIFVNSKALLAFRLITVTSTALLVV LYXIYDLHKKRSCHLDEQQELVERDDEKQLMNVEPHABILLET YKRRIADBGMFLFLEFGSIFVNSKALLAFRLITVTSTALLVV LYXIYDLHKKRSCHLDEQQELVERDDEKQLMNVEPHABILLET YKRRIADBGMFLFLEFFSTAVSTALLAFRLITVTSTALLVV LYXIYDLHKKRSCHLDEQQELVERDDEKQLMNVEPHABILLET TSHPDHGYVEDEPHLLLKLKRRYNAFSNFFSGPIVVHCSAGVGR RAFGECCKDLTRKKRCP\DYIIOKLMIVNKKRDPSFBFDFLABA FQRLPSYRSWRIGHCINGS\ENKSKNENNSNVIPYDNNVPLKHE LEMSKESENDSDESSDDDSDEBESKYINASFINSVMKF\ENVI TATYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEQQYI LIHQALVERNOFGSTEVNLSLHBYLHNNKKRDPSFBPPLEAB FQRLPSYRSWRITGHGNGG\ENKSKNENNSNVIPYDNNRVPLKHE LEMSKESENDSDESDDDSBESKYINASFINSVMKF\ENVI AAQCPLKETIGDFMQNIFGRVKVIVINAHKKRDDGPLGAYWS BGKGTYGDLEVDLKDTDKSSTYTLRVFELRISKRDSRTVYQYQ YTNNSVGLPAPEKELISHOVAVOKLLPGAYBGDGVVVALARARP GMVSTFEGYDPLAPDKELISHOVAVOKLLPGAYBGDGVVVALARARP GMVSTFEGYDPLAPDKELISHOVAVOKLLPGAYBCGGGFLKYSSP VFFKVPKLGSEIIDSSTRRMESERSPLYRGLDLDAYJCSSHNN CGAPGDTTAHAHDELSTGAYDAVALLLOPUTVLAHACALLD LVHCLLDIFINQAFDMQRDQUTTKRLEYTRKNELYESIMN LANKQEEMUMIVTETLATMKEELLDDATMMEKDLIDDATKSSMN CGAPGDTTALAHKEELDDATMMEELDDATMMEKDLIDLEVKX DHAPRLARLSESSGJOVALHHKPKHLGGGGGGEKTETLULKURK DHAPRLARLSESSGJOVALHHKPKHLGGGGGGGGGEKTERLQLIGG SVIDNYG	DRQCKALDSDAVVANYEGLEAVERREMTIGANAKGGILGIL OMTDLENNSETBELGPUYLEGGASAAPEGMSSDSIECOTEMEE GEBITSVGGFHDSFMWITOPPDEDTHSSFPDGEQIGPEDLSFNT DENSGR 5979 212 3665 LPDMWINLHLILLAFGFAFLITEVFUTOGSFTSFTDAYLNASE TTTLSPSGSAVISTTILATPSKYCCEKYANITUVIKKETK LFTAKLNUNENVECQNNITCTNIREVRILIECKNASVISIHSCTA PDKILLIDVPRGVEKVPVICCS\QVEQPDSTINLKWRITISTC DTQNITYRRQCGMNITDKKEK KLENLEPEIECKNASVISIHSCTA PDKILLIDVPRGVEKVPVICCS\QVEQPDSTINLKWRITISTC DTQNITYRRQCGMNITDKKEK KLENLEPEIECKNASVISIHSCTA PDKILLIDVPRGVEKVPVICCS\QVEQPDSTINLKWRITISTC DTQNITYRRQCGMNITDKKEK KLENLEPEIECKSSILVNSHK FTNASKIKTDFOSGPRQUITCRSEAAHGQVITMPPGRSHN FTLCYIKETERDCLINDKNILKTDQNIKKTYLSHAYIIA KVQRNGSAAMCHTTKSAPPSQVWNNTUSHTSDNSMHVKCRPPR DRNOPHERYHLEVEANTILVURDSKIKCDRYVLSHAYIIA KVQRNGSAAMCHTTKSAPPSQVWNNTUSHTSDNSMHVKCRPPR DRNOPHERYHLEVEANTILVURDSKIKCDRYVLSHAYIIA KVQRNGSAAMCHTTKSAPPSQVWNNTUSHTSDNSMHVKCRPPR DRNOPHERYHLEVEANTILVURDSKIKCDRYVLSHAYIIA KVQRNGSAAMCHTTKSAPPSQVWNNTUSHTSDNSMHVKCRPPR DRNOPHERYHLEVEANTILVURDSKIKCDRYVLSHAYIIA KVQRNGSAAMCHTTKSAPPSQVWNNTUSHTANILITUTSIALLIV LYKIYDLHKKSCNLDQUERDREGOSTRAVILAGUTSHAYIIA VKRKIADGGUFFLALESSINDAGURSTUNASYIDGFHIADILLUT LYKRIADGGAPTAGUTSHAYAWATATAYIIAVTRCCEGONONKCABYWPSMEGOT RAPGECCKDLITHKRSCP\DYLINGKINGAPYVLARRQCLMVQUAQYI LINQALVEXNIQOFETVANLSSLINDYKARRQCLMVQUAQYI LINQALVEXNIQOFETVANLSSLINDYKARRQCLMVQUAQYI LINQALVEXNIQOFETVANLSSLINDYKARRQCLMVQUAQYI LINQALVEXNIQOFETVANLSSLIPVILINMKREKATGREVHIQ PTSKPPHSPBSDSSDDDSDSESBESSEPSKYINASINSTYYPOYNYPLKHE LEMSKSSENDSDSSDDDDSBESBFSKYINASINSTYYPOYNYPLKHE LEMSKSSENDSDSSDDDDSBESPSKYINASINSTYYPOYNYPLKHE LEMSKSSENDSDSSDDDDSBESPSKYINASINSTYYPOYNYPLKHE LEMSKSSENDSSSDDDDSBESPSKYINASINSTYYPOYNYPLKHE LEMSKSSENDSSSDDDDSBESPSKYINASINSTYNYWYAKRAY AAGGPLKTICOPPWOHIQRKVKUIVALITELKHODGEICAYWG GRWSTEGYQFULDVINASITHAYPEKKSPRTYOYQY YTRNSYGQLFACHAYONGCONGTYNACHAYNY GRWSTEGYQFULDVINASITHAYPEKKRYDGYTOYVACARRARP GWSTEGYQFULDVINASITHAYPEKKYDGYTOYVACARRARP AAGGPLKTICOPPWOHIGATAKLEYTILAVERKYBGTYVYAP CARACARRACAACAACAAAAAAAAAAAAAAAAAAAAA	Ì			NSRSKGDCOTLSEGSPGSSOSGSRHSSDRALTUGSTGDTLDVTD
OMTOLENNSTGELGPVLPEGASAAPEEMASSIBISICOTEMEE CREHTSVOGFHDSFWATQPPDEDTHSSFPDGEQIGPEDLSFNT DENSGR 1 LPDMTWLWLKLLAFGFAFLDTEVFVTGGSPTFSFTDAYLNASE TTILSPSGSAVISTITIATTPSKPTCDEKYAMITVDYLVIKSTK LFTAKLMVNENVECGNNTCTNNBUWNLTECKMASVSISINSCTA PEPKTLLILDVPEVEKVEVYHCCS\OVCEPTIKLWKMISTESTC DTONITYRFQCGNNIFDNKSIKLINLEPHEVKCDSSILYNSHK FFILCYIKETEKDCLINLDKNLIKYDLQNLKPYTKYVLSLHAYIIA KVORNGSAMCHFTKSAPPSQUVMMTVSMTSINSMHVKCRPPR DRNGPHERYHLEVBAGNILVRNESHKNCFPKKLOLYSTDYTFK AVFRINGSYBGEPFILHHSTSYNSKALDFLARLIIVTSIALLVV LYXYDLHKKRSCKLIDEQGLUVERDDEKQLMVPPHADILLET YKRKIADEGREFLEHEFOSTPRVFSKFPIKEARKPFNONINRYVU LIPVDYNYRUSBEINDGASVYINASYICKPRYLYIAQQPR DETVDDFWRMIWEGKAFVI VMVTRCEEGNRNKCAEYWFSMEGGT RAPGECCKDLTKHKRCP LDYIJCKLNIVNKEKBARGFRVTHIG FTSMPDHGVPEDPHLLIKLRRWAMFSNFSGPIVVHCSAGGYR TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLAVQUAQYI LIHQALVENVOFGSTEVNISSHHYLINKHKRAPPSEPEPLEAE FORLPSYRSWRTORIGNGE\ENKKRNSNNIPPDYNWPLKHE LEMSKSSEIGEDSESDIDDSDEBERSYINKFRYDYMPVLKHE LEMSKSSEIGEDSESDIDDSDEBERSYINKFRYWHYRPLKHE LEMSKSSEIGEDSESDIDDSDEBERSYINKFRYWHYRPLKHE LEMSKSSEIGEDSESDIDDSDEBERSYINKFRYWHYRPLKHE LEMSKSSEIGEDSESDIDDSDEBERSYINKFRYWHYRPLKHE LEMSKSSEIGEDSESDIDDSBEBERSYINKRRORPRYPLKHE LEMSKSSEIGEDSESDIDDSBEBERSYINKRRORPRYPLKHE LEMSKSSEIGDSSGNOBESEBERSYINKKRROPPSEPEPLEAE FORLPSYRSWRTORIGNGE\ERKSKRNSNNIPPDYNRYPLKHE LEMSKSSEIGDSSGNOBESEBERSYINKKRROPPSEPEPLEAE FORLPSYRSWRTORIGNGE\ERKSKRNSNNIPPDYNRYPLKHE LEMSKSSEIGDSSGNOBESEBERSYINKKRROPPSEPEPLEAE FORLPSYRSWRTORIGNGE\ERKSTRUSHSTWYNKYR\ERKTYDY YTWKSVEGLPABEFRELISNIOVYKGLLPOKRSSEGRKHHKSTPL LIHCRDSGOTGIFCALINLLESAETEEVVDIFQVVKALRARRY GMVSTFEGVOYLIVDIASTTARVFERSKRNBSRTVYOY YTWRSVEGLPABEFRELISNIOVYKGLLPOKRSSEGRKHHKSTPL LIHCRDSGOTGIFCALINLLESAETEEVDIFGROWATCHCAGNIE GWVSTFEGVOYLIVDIASTTARVFERSKRNBGENETISSENDING KYKGDANCVNPLGAPBKLPETATARVBELLTARVBELDGETOKYRSTORY GROWSTFEGVOYLIVUTATARTHALLESEVOYLICHONAKALN CGAPGOTTAAHNOSITARVBELOTARVBEVOYLENGE PTVDVLGGIVADELPVITYAHKSELLDAATNMEPKVIVPENGEP VFFKVPKLGGEILDSGNACHKETHERSINGSSVTR MLEGIKGITGRTWSPPATITEMERKYAQAANLLISSSHAN SICSOFRTRINSSHRSMATARVBEVTTHRESSVTR MLEGIKGITGRTWSTORTHARPELFTG	OMTDLENNSETGELGPUPERGASAAPEGMSSISSIEUTEUTENEE GEERTSWGGFHDSFMMTOPPDEDTHSSFPDGGGPDEDSFNT DENSGR 1 DENSGREVITIATFDSKPTGGBTFSFTDAYLNASE 1 LIPTAKLNVNENVECONNTCTNREVNLIECKAASVISINGCTA 2 DENTLILLDVPSGVEKVPVICCS\QVEQPGDTILHKEWNIETSTC DTQNITYRPQGGMIEDBKEIKLERLEPEIKKCDSRIVISHKT FINASIIKINFDGSGREPGITGKSBAARGQUTWNPPGRSFHN FILCYIKETERDCLNLDRNLIKYDLQNLKPYTKYLSLHAYIIA KVQKNGSAAMCHTTKSAPPGWWNNTVSHSWHYKCRPPR DRNOPHERVHLEVBAONTLVRNESIKHODRRVEDLGVSTDYPFK AYFRIGDYSGPFILHHSTSYNSKALIAFLAITUTSIALLUV LYKIYDLHKKRSCNLDEQGELVERDDEKQIMNVEPIHADILLET YKRKIADBGEILFLAEPGGSIPRVSKALIAFLAFRERVHIQ DETVDDPWRPINRVELSEINGDAGGNYINASYIDGFERRKYIAAQGPR RAPGECCKDLITHKRCP\DYIGKNINKKAPPSKEPRKYIAAQGPR RAPGECCKDLITHKRCP\DYIGKNINKKAPPSKEPSPLAVE FORLPSYRSWRTORIGHGEGERENKVOVGGVVLKARGREGHT RAPGECCKDLITHKRCP\DYIGKNINKKAPPSPSSPLADE FORLPSYRSWRTORIGHGGELERENKVOVGGVVLVALTAKTREBVHIQ FTSKPPHGVFEDDHLULLLIKRRVNAFSINFSGPIVVUCSAUGGR RGGTYGIGDEVDLKDTIKSSTYTLRVFERRKKRDSRTVYQYQ YTNKSVGLLPBAPKELISMIQVVKKVIVLTHLEKKRFDPLOYDARVEL LEMSKRSSHIDSDESSEDFSKYINASFINSYNKP\PWI AAQGPLKSTIGDFWOMI-PGRKVKVIVVLTLEKHOOPSICAQMW EGKQTYGDIEVDLKDTIKSSTYTLRVFERRKKRDSRTVYQYQ YTNKSVGLLPBAPKELISMIQVVKKNINGBDKIEFDENVO KVKQDANCVNBERERPKYGLTORIGVENVIVLTURLINGKKRDDRIETDENVO KVKQDANCVNBERERPKYGLTORIGVENVIVLTURLINGKKRTPL LIHCRDSQQTGIF-CALINLISSAETTEVUPI-GVVKALRARR GMUSTFEQYOPLUDVIASTYPAQMQCKKNNNGBDKIEFDENVO KVKQDANCVNBERERPFYGTOTRVSLALEGGYELVRUTUVAHQGNNETI PEBBLBVQSNNEDAAHDLTELSVTMHRALLORVDVVARGGER FVTUPI-GGRANDHIVENTURTURDELPTITYALHKENELDEGGEGERITSTEDENVO GGRAPGTKAGAGNUNGSSENKHENLENSTFIGOPLORVIARANI LVHCHCLDIFINOAPDWRDLQTTPRRIETTKRENELYBERGGVVVYLCO MGCHFFCALKSVVPPDEKHMNDLALEFHMISCHERLUDLIG SVLDNYAGGGSSTAVLLIMBERLUNDVTLAGRAGENERRSVTR MLMCGIKGITGRITATVSPPATILERENKTVAGGEATELSASALAK SICSOPRIRINSSHAPAGLGGLAHAROLGENGLIETTGLURFYTCGSVK DHAPGAGGSTAVLLIMBERLEHDLYTTLLAHLLTPRLQIAL DVWEGIRFLUSGCUHUDIKARDRUTARGRUFU				DROCKALDSDAVVVAVFSGLPAVEKRRKMVTLGANAKGGULFGI
S979 212 3665 LPDMTWLLARGRAPLOTEVEVTOGSPTSSTDAYLNASE TTTLS PSGSAVISTITIATTPSKPTCDEKYANITVDYLINKETK LPTAKLINVENVECONTICTNIEVHNITEKASVISISINSCTA PDKTLILDVPGVSKVEVICCS\QVEQPDSTTWLKWKINLETSTC DTQNITYRFQCONNIFDNISKILKINLEPHSCKOSBILLYNSHK FINASKIIKTDFGSPGSPQTIFCRSEAAHGGVITWNPPORSFIN FILCYIKETEKDCLINLDKILIKYDLQNLKPYTKYJSLHAYIIA KVORNGSAAMCHFTIKSAPPSQVANMTVSMTSDNSMHVKCRPPR DRNGPHERYHLEVSEAGNTLVRNESHKNCDFRVKDLQYSTDYTFK AYFINGSYJSGEPFILHAFSTYNSKALIAFALIVISTALLIVV LYKIYDLHKKRSCHIDEQGELVERDDEKQLMNVEPHADILLET YKRKIADEGEFFILHAFSTYNSKALIAFALIVISTALLIVV LLYKIYDLHKKRSCHIDEQGELVERDDEKQLMNVEPHADILLET YKRKIADEGERFLALEFGS PRVPKEPF JENFUKSPHYLARGGPR DETVDDFWRMIWRQKATVIVMYTKCEGGNRNKCAEVWPSMEGGT RAPGECCCKDLTKHKRCP QNTICKLINLERGRCLMQVQCAQYI LLHQALVENOPGSTEVNLSSHPYLHINKKRDDPSEPSPLEAE FORLPSYSKRTQHICNQE\ENKSKNRNSNVIPYDYNRKPLKAL LEMSKESEHDSDESSDIDSDBESEPSKYINASFINSVKR\EVMI AAGGPLKETIGDFWQMIFGRKVKIVINLTELKHGDQEICAQYWG ESGKOTTGDIEDDLKDTDKSSTYTLRVFERKRNDSRTVYQYQ YTNNSVEQLPABPKELISNIQVVKQKLPCNSSSERMKNSSNVIPYOYV YTNNSVEQLPABPKELISNIQVVKQKLPCNSSSERMKHKSTPL LLHCRIGSGOTGTCALLALLESAFTEEVDFOVWALRKRARG GMVSTFEQYQPLYDVIASTYPANGQVKKNNHGENKIEFONEVD KVKQDANCVNPICAPFKLIESAFTEXPLLLEBSTETEVDFOVWALRKRAR GMVSTFEQYQPLYDVIASTYPANGQVKKNHGENKIEFONEVD KVKQDANCVNPICAPFKLIESAFTEXPLLLEBSTTERVERKOPITYVOY YTNNSVEQLPABPKELISNIGVVKSLPCHANGARGLISSSHINN CGAPGQDTYAQSNIEVDSGEKHRHISTFEHOVLYTVALVAGNNETI PETDLIQUGUNDPLPYTYALHKDELSERDEGELQEIRKYTSPF VFFFKVPKLGSEIIDSTRRRESERSPLYRQLLIDLIYLISSHINN CGAPGQDTYAQSNIEVDSGEKKRHISTSTENFOLYLJSSHINN CGAPGGDTYAQSNIEVDSGEKKRIHISTSTENFOLYLJSSHINN LAVRKGEEKMEMTVETLINTKREELLDATURVAGARALL LVHCHCLDIFTNQSPMCROLLINRAFKKUPIGSSVTR MLMEGIKGIIQRITHWSPPANTLEKKRNVAQEAIESLSASKLAK SICSGFRTRLNSSHREMPASLROLLERGHSCRIEKTUFSISHASKLAK SICSGFRTRLNSSHREMPASLROLLERGHSCRIEKTUFGSSVTR MLMEGIKGIIQRITHWSPPATTLEMKRKVAQEAIESLSASKLAK SICSGFRTRLNSSHREMPASLROLLERGHSCRIEKTUFLUGGSVK DHAPRIAARLSESRSLOVLHHRKYKLOGELGRGGYGVVVILCON WGGHFFCALKSVVPPDEHMNDLALEFFYWRSLDPHERGDVILCONFOR	DENSIGN 5979 212 3665 DENSIGN LIPDMYMILMILKILAFGFAPLUTEVPTYGGSPTSSTEDAYIANSE TITLSPGSSAVISTITIATPISKYTCEKYANITYDLYNKETK LIPTAKLNVMENVECGNITCTNNEVNILITECKYASVISINSCTA PDKTLLILDVPRGVEKVPVICCS\QVEQPGSTIMLKKMILITETGC DTQNITYRPGCGMNIPDKKEK LKEMLEPEIEVKCKSILITSTAC PDKTLLILDVPRGVEKVPVICCS\QVEQPGSTIMLKKMILITSTC DTQNITYRPGCGMNIPDKKEK LKEMLEPEIEVKCKSILITSTC DTQNITYRPGCGMNIPDKKEK LKEMLEPEIEVKCKSILITSTC DTQNITYRPGCGMNIPDKKEK LKEMLEPEIEVKCKSILITSTC DTQNITYRPGCGMNIPDKKEK LKEMLEPEIEVKCKSILITSTC DTQNITYRPGCGMNIPDKKEK LKEMLEPEIEVKCKSILITSTC FINASKIIKTDFGSPGPQIIFCRSEAHGGVITMNPPGRSHN FILCYIKTEKECHOLINDKNIK KYDQUNLKYPUKSLHAYILA KVQRNGSAAMCHTTKSAPPGOWNMTVSHTSINSMHVKCRPPR DRNGPHERYHLEVEANTLUKNESIKHODEVKLJANITUTSIALIVV LYKIYDLHKKSKCNILDQUGEVERDDEKQLMNVEPIHADILLET YKRKIADEGRIFILAFGSI PRVESKFPIKERKPNONKRRVO LYKIYDLHKKSKCNILDQUGEVDEKQLMNVEPIHADILLET YKRKIADEGRIFILAFGSI PRVESKFPIKERKPNONKRRVO LIPYDTNRVELSSIINGDAGSNYINASY IDOFKEPRKYIAAQGPR DETVDDFFRMI WEQKATIVUMVTGCECCENNEAVPROMEGET RAPGECCCKDLTHKKCP\DYIJQKLIVVKERQRCIMVQVEAQYI LIHQALVEKNOPGETEVALLSELHPYLINMKERGATGREVTHIQ FTSWPHGVERDFHILLLIKERVAFAFFSENYBMEKPONTYVOY YTWASYBCLPBEPHLLILLIKERVAFAFFSIKSKNDSRYVYOY YTWASYBCLPBEPKELISMIQVWKKLPQNNSSSGNNHKSTPL LIHCRDGSQOTGIFCALINILISBATEEVVDIFGVWAKAKRAP GMVSTEGYQPULDVIATSTYPAQNOVKKNHQEDKIEPDKEVD KVKQDANCVMPLGAPEKLLEHVPLANKRORGEK EPDKEVD KVKQDANCVMPLGAPEKLLEHVPLANKRORGEK EPDKEVD KVKQDANCVMPLGAPEKLLEHVPLANKRORGEK EPDKEVD KVKQDANCVMPLGAPEKLLEHVTHHKARLOGDKICHVDAKAKAR GMVSTEGYQPULDVIATSTYPAQNOVKKNHQEDKIEPDKEVD VFFKKVPKLGSEI IDSSTRMMSSRSBYRGULTQLIVLSISSHNN CGAPGODTXAGGMIVEDSEKHKHELISTSSIGVULTVDAAKAM LVHCHCLDIFINQAFDMGRDLGITPKKLEYTHKKRKELYEBLIND TANRKGEMKDMIVETITNIKKELLESERDEGEGGIFVYDAAKAM CGAPGODTXAGGMIVEDSEKHKHELISTSSIGVULTVDAAKAM LVHCHCLDIFINQAFDMGRDLGITPKKLESTSFVOUTVDAAKAM CANROGEMBFOALSSIAVLIIMEREKLEDATINGEGGGGGVGVVVICON MGGHFFCALKSVVPPDEKHNDALIEFTMGRAGGGGGGVGVVVICON MGGHFFCALKSVVPPDEKHNNUKRARPEELEVTURGAGGVGVVVICON MGGHFFCALKSVVPPDEKHNNUKRGARPEELEVTDEGGGVGVVICON MGGGFFCALKSVVPPDEKHNNUKRGARSELEKTIDLUKRVK DHAPALARILISERSIADULLIKRRKLYGGGGGGGVGFCGSVK	}			QMTDLENNSETGELOPVLPEGASAAPEEGMSSDSDIECDTENEE
DENSGR 1 DEDMINULMIKALIAFGFAFLDTEVPVTQSPTPSPTDAVINASE 1 TTLSPSGSAVI SITTIATTPSKPTQLEKYANITVDYLYNKETK LFTAKLNVNENVECONNTCTNNEVHILIBCKNASVISINGCTA PORTLILDVPPEVEKYPVICCS\QVEOPDSTIMLKMENIETSTC DTQNITYRPQCONNIFDNKEI KLENLEPEHEVKCDSEI LYNSHK FFINASKI IKTDFGSGEPGDI IFCRSEANGTVTMPEPORSFHN FFILCYIKETEKDCLINLDKNILKYDLONLKPYTKYVLJSHAYI IA KVQNRGSAMCHFTIKSP PSQVMNTWYSMTDNSMHVKCRPPR DENGGHERYHLEVERGNTLURNESHKNCDFRVKDLQYSTDYTFK AYFHNGDY PGEP FILHHSTSINKSCLAMINDSHHVKCRPPR DRNGGHERYHLEVERGNTLURNESHKNCDFRVKDLQYSTDYTFK AYFHNGDY PGEP FILHHSTSINKSCLAMINDSHIMLLET YKRKIADEGREFLEFGS TRWFSKFF IKEARKPPNONENNYVU LIPUTNYRVELSEINENGASYVINASY IECHARVPPNONENNYVU LIPUTNYRVELSEINENGASYVINASY IECHARVPRONENNYVU LIPUTNYRVELSEINENGASYVINASY IECHARVPSMONENNYVU LIPUTNYRVELSEINENGASYVINASY IECHARVPSMONENNYVU LIPUTNYRVELSEINENGASYVINASY IECHARVPSMONENNYVU LIPUTNYRVELSEINENGASYVINASY IECHARVPSMONENNYVU LIPUTNYRVELSEINENGASYVINASY IECHARVPSMONENNYVU LIPUTNYRVELSEINENGASYVINASY IECHARVPSMONENGYVI LIHQALVENGFGETEVILASHENSHYVYOXIVALRRQRICHWOPEQYI LIHQALVENGFGETEVILASHINSHHYLINASFINSYWK PEWII AAQGPLKETIGDFWOMI FORNYKVIVALITELKHODGELGAYWG EGKOTYGOLETULLEDSTSTYLVFELHSKKKDSRTVYOYG YTNNSVEQLPABPKELISMIQVVKQKLEPORSSEGKKHHKSTPL LIHCRDSSCOTGIFCALINLLESAETEEVUDI FOUVALRRAPE GWUSTEGYOZILIVULASTYPAONGOVKANHORDKI EFDNEVU KVKQDANCUNPLGAPEKLPTYGOTRVSLALPGQVELVHTLVAHGGNWETI PEEDLEVQENNEDAAHOLTELEVTYHALLGEDOVLACGGER GWUSTEGYOZILIVULASTYPAONGOVKANHORDKI EFDNEVU KVKQDANCUNPLGAPEKLPTYGTOTRVSLALPGQVELVHTLVAHGGNWETI PEEDLEVQENNEDAAHOLTELEVTYHKINDELLYSSHNN CGAPGOTTAGSMILVOGSEKKHINISTSFENOUTHULDBANALNA LVHHCLIDIFINQAFMORDLOTTPKRLEYTRKKNELYSSHN TANKKGEEMKOMI VETLINTRKELLDDATNAVALNISSSHUHK MLWEGI KQI IQRITHWSPHATLLEKKRVAJCELIESLSASKLAK SICSGPRTRINSSHERSERSJLVALLERELVOLHG SVLDYNYGGGSI AVLLIHKERLHDALYTALKAJCELIESLSASKLAK SICSGPRTRINSSHERSERSPRONGARAPRELVEROULTULDINGVK DHAPRIARLISERSSI,OUCHHRINGLARPREVU IUPENGES VGTREI KCCIRCIGGEGGYGVVVLLON WGGHFFCALKSVVPPDEHHMDLALEPTYMBSLPRHEBUVLUCH SVLDYNYGGGSSI AVLLIHKERLHDALYTGLKGLORGGOTGOVVLLON WGGH	DENSGR DENSGR DENSGR TTILSPGGSAVISITIIATTSKPTODEKVANITUDLINKETK LETAKLNUKENVECGNNITUDRUN WENTEKVESTENSTENSTENSTENSTENSTENSTENSTENSTENSTE	ł		1	QEEHTSVGGFHDSFMVMTOPPDEDTHSSFPDGEOIGPEDISENT
TTTLSPSGSAVISTITIATTPSKPTODEKYANTTUDYLYNKETK LFTAKLAVNENNECONTICTNENHHLITECKNASVSISHINSCTA PPKTLILLDVPPGVEKVYVHCCS\QVSPSTIMLKWANLETSTC DTQNITTRFQCQMMIPONKEIKLENLEPEHSYKCDSEILYNSHK FTNASKIIKTDFGSPGEPQIIFCKSEAHQQVITWHPPGRSFHIM FTLCYIKETEKDCLILDKNIIKKTDUNKEYTKYUSLHAYIIA KVQRNGSAMCHFTKSAPPSQVWMNTVSMTSNINSHVVKCRPPR DRNGHFRYTLSVERGNTUVRNESKHADLAFLAFLIUTSIALLVV LVKYDLHKKRSCNLDEQGELVERDDEKQLMVVEPIHADILLET YKRKIADEGRIFIAEFGSIPRVSKYPIKCHAVVEPIHADILLET YKRKIADEGRIFIAEFGSIPRVSKYPIKCHAVVEPIHADILLET YKRKIADEGRIFIAEFGSIPRVSKYPIKCHAVVEPIHADILLET YKRKIADEGRIFIAEFGSIPRVSKYPIKCHAVVEPIHADILLET YKRKIADEGRIFIAEFGSIPRVSKYPIKCHAVVEPIHADILLET YKRKIADEGRIFIAEFGSIPRVSKYPIKCHAVVEPIHADILLET YKRKIADEGRIFIAEFGSIPRVSKYPIKCHAVVEPIHADILLET YKRKIADEGRIFIAEFGSIPRVSKYPIKCHAVVEPIHADILLET YKRKIADEGRIFIAEFGSIPRVSKYPIKCHAVVERVOKNOKNYVU LIKYDVAKKEKADEGRIFIAEFGSIPRVSKYPIKCHAVVERVOKNOKNYVV LILYDVARVELEEINGDAGSNYINASYIDGFKEPRKYIAAGGFR PSTSPDBIRGHTENNINGERENKALTENNIKCAEKWPSMEGGT RAFGECCCKOLIKHKRCP\DYIJOKALTUNKKERAFGREVTHIO FTSSPDBIRGVEPROMPANAFSNFSGFIVVANKERGREWHIH FTSSPDBIRGVEPROMPANAFSNFSGFIVIVANKERGREWHIH ARAGGELKETIODFWOMITOREVKVAVIVAVERRQRCLMVOVERQVY LIHQALVENNOFGTEVULSEHPYLHMKKRDPPSEPSPLEAE FORLPSYRWRTQHIKGRE KNOKSTVITEVYLERHSKRIDSTVYQTQ YTMRSVEQLPAEPKELISMIQVVKKULPQINSSENKHHKSTPIL LIHCHGSGOTGIFCALIMLLESAETEVVDIFQVVKAKLRARR GMUSTFEQVQPIYDVIASTYPAQNQVKKNINGERKIEFDNEVU KVKQDANCVPIGASPEKLINLISSAETEVVDIFQVKKAKRARR GMUSTFEQVQPIYDVIASTYPAQNQVKKNINGERKIEFDNEVU KVKQDANCVPIGASPEKLINLISSAETEVVDIFQVKAKRARR GMUSTFEQVQPIYDVIASTYPAQNQVKKNINGERKIEFDNEVUN ASPALNQGS ASPALNQGS DAMGCKLRRIPTYGTOTRVSLAIPGYSLVITLVALAGGNWETI PEEBLEVQENNEDAAHDLTELEVTMHALLQEVDVVVAPCOGGR PTVUVIGOLVNDFLPVITTVALHKDELLDAIMFKVILDRGNESTIM CGAPGQDTKAQSMIVEQSEKRHISTSTSHUVLQTTALVDAAKALN LVHCHCLDIFINGAFDMQRDLQITTKRLESTRENGLYESIAM CGAPGQDTKAQSMIVEQSEKRHISTSTSHUVLQTRLIVDAAKALN LVHCHCLDIFINGAFDMADALTHRINKECHLDAIMFKWILDENGEP VGTREIKCCIRGIGELISKYPSDYVTACHOLDARGRACYGGGYGYGVYVLCON MGGHFCALKSVVPPDEKWMOLALEFHYMRSLERKELLYESIAM ANAKGEERMEMINDELSESSERDEGRGGYGYGVYVLCON MGGHFCALKSVVPPDEKWMOLALEFHYMRSLERKELLUDLIG S	TITLS PSGSAVISTITIATTERSKYTCEKYANITYDYLINKETK LPTAKLMVNENVECQNITCTNNEWNILTECKHASUSISINSCTA PDKTLLLDVPEVEKVEVYEVICCS\OVERPOSTIWLKWENTETSTC DTONITTRFQCGNNIFDNKEIKLENLEPBHEVKCSSINSCTA PDKTLLLDVPEVEKVEVYEVICCS\OVERPOSTIWLKWENTETSTC DTONITTRFQCGNNIFDNKEIKLENLEPBHEVKCSSILVNSHK FTNASKIIKTDFGSGEPGOLIFCRSEARDVITMNPORSHN FTLCYIKFTEKDCLINLDKHLIKYDLONLKPYTKYVLSLHAYIIA KVORNGSAMACHFTIKSAPPSQVMNMTVSMTSINSHHVKCRPPR DRNGPHERYHLEVSAGNTLVRNSEHKNCDFRYKLLOYSTDYTFK AYFRINGIYGGEPFILHHSTSYNSKALIALARLIVISTALLVY LYKIYDLHKKRSCNLLDSQGLIVERDDEKOLFOKYDKLOYSTDYTFK AYFRINGIYGGEPFILHHSTSYNSKALIALARLIVISTALLVY LYKIYDLHKKRSCNLLDSQGLIVERDDEKOLFOKYDKLOYSTDYTFK AYFRINGIYGGEPFILHHSTSYNSKALIALARLIVISTALLVY LYKIYDLHKKRSCNLLDSQGLIVERDDEKOLFOKYDKHOKYPVU LYKIYDLHKKRSCNLLDSQGLIVERDDEKOLFOKYPKILAJOPR AYFRINGIYGGEPFILHHSTSYNSKALIALARLIVISTALLVY LIPADYNRVUSEBINGDAGNYINASY ICKPERYYIAAQOPR DETVDDFWRMIWEKSATVIVMTCEGGNRIKCAEYYPGMEGT RAPGECCCKOLDTHKKRCP JVYIIOKUNIVNKKRAPGMEPSHEGT RAPGECCKOLDTHKKRCP JVYIIOKUNIVNKKRAPGREPHETH FTSWPDHGVPEDPHLLLLKRRVMAFSFFSGFIVVHCSAGVGR RAPGECCKOLDTHKKRCP JVYIIOKUNIVNKRAPGREVTHIO LIHQALVERVORGTETVINISHHPYLHMKKRDPPSEPSPILEA FORLPSYRSWRTORIGNOS\ENKRYNNNIPPDWRPUKHE LEMSKSSENDSSSDDDSDESEPSKYINASFINSYWKK\EVMI AAQGPLKSTIGDPWONIFORNVENTUNITHELKHGDQBICAQYWG EGKOTYGDIEDDLKDTURSSTYTLRVEBLHSKKNDSRTVYQYQ YTMWSVEQLPABPKELISMIOWVKOKLPQNRSSEGNKHHKSTPL LIHCRDGSOCTIGIFOLINLLESAETEEVVDIFQVVKALRARAR GMVSTFEGYQPLVDVIASTYTARVEBLHSKKNDSRTVYQYQ YTMWSVEQLPABPKELISMIOWVKOKLPQNRSSEGNKHHKSTPL LIHCRDGSOCTIGIFOALINLLESAETEEVVDIFQVVKALRARAR GMVSTFEGYQPLVDVIASTYTARVEBLHSKKNDSKIFENDEVUK KVKQDANCUNDLGAPSKLPEARQAGSSPTSGTEGPBEISVNG ASPALNQGS SAPALNQGS DAMGCKLRRLEFTYGTORVSLALPGQVELVHTLVAARALN CGAPGODTKAQSNLVEGSEKKHHSTSFEHOVLYTRUVDAARALN LVICHCLDIFTNQAFPMQRDLQITHRALLCGOVUTVAPACOGLR PTUVLUGDLUMDPLPVITYALHKDELLSGROUTHCUNDARALN LAVRKGEEMKHMITTELLNTKKEELLDDATWEKVUTVAPAGAAAA CGAPGODTKAQSNLVEGEKHALSTSFEHOVLTRUVDAARALN LAVRKGEEMKHMITTARVELLDAANAKITDLOPCKPEA MLMEGIVOTIHAPBLEJTVINVLOVINARVELDEKONTENDUTUCHUK DAMGGIVOTIHAPBLEJTRIKANDLAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA			į	DENSGR
TTTLSPSGSAVISTTILATPSKYTDEKYANITVDYLVNKSTK LETAKLAWNENNECGNOTTCTNREWHILTEKKASVSISHNSCTA PDKTLILDVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNISTA PDKTLILDVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNISTSTC DTQNITYRPGCGMMIFDNKSIKLBRLEPEHSYKCDSEILYNSHK FINASKIKTDGSSGSPGQIIFCRSEMQVITMSPFGRSFHN FILCYIKETERDCLMLDENLIKYDLQNLKPYTKYVLSLHAYIIA KVORNGSAANCHETTKASPPSQWANTASTDINSMHVKCRPPR DRNGPHERYHLEVEAGNTLVRNESHKNCDFRVENDLQYSTDTTFK AYPRINGDYPGEPFILHHSTSYNSKALIAFLAFLITUTSIALLVV LYKIYDLHKKRSCNLDBGQSLVERDBCJMNVEPIHADILLET YKRKIADEGRLFLAFFGSIPRVSKFPIKEARKPFMONKNYVVD LLFYDYNRVELSEINGDGGSNYINASYIDGFKEPRKYIAAQGPR DETVDDFWRMIWEQKATVIVMTRCEPENRNKCAPYWSMEBGGT RAPGECCCKDLTKHRCP\DYIIQKLNITVNKKRATGREVTHIO FTSMPDDHEVPEDPHLLKLKLRRRVNAFSFFSGFIVVHCSAGVGR TGTYIGIDAMLBGLBERNKVDVYGYVVKLRRQRCLMVQVBAQYI LIHQALVENNQGGSTEVULSELHPYLHMKKRDPPSEPSPLEAE FQRLPSYRSWRTQHIGNQE\ENKSKNKSNVIPYDYNRVPLKHE LEMSKESEHDSDSSDDDSDSEEPSKYINASFIRMSYMF\EVMI AAQGPLKETTIGDFWGMTFQRKVKVIVMTELKHGDQBICAQYWG BGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNNSVBQLPAPPKELISMIQVVKQKLFPGNSSEGNKHHKSTPL LHCRDGSQQTGIFCALINLLESAETEEVVDIFQVVKALRRARP GMVSTFEQYQFLYDVIASTYPAQMQVKKNNHQBDKIEFDNEVD KVKQDANCVNPLGAPBELIPBAKQAGSGSFTGSTEGPBHSVNGP ASPALMQGS 5980 3 2363 DAWGCKLRRIFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEBDLBVQENNEDAAHDLFELBVTMHRALLQEVDVVVAPCOGGR PTVUVLGDLVNDFLPVITYALHKDELSERNDEGLEIRKYFSFP VFFFKVPKLGSEIIDSTRMSSERSPLYRQLIDLGYLSSSHNN CGARGQDTKAGSMLVEGSKLHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQTIPRRLEYTRKKRELYPSIMN GGARGQDTKAGSMLVEGSKLHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQTIPRRLEYTRKKRELYPSIMN NARKGEEMKOMIVETLNTMKEELLDDATMMEFKDVIVVPENGEP VGTREIKCCIRGIGELIIGRLMOAVANKLISSVDYLRSSFVGTI MLMEGIKQIIGRTWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSGPRTRLNSSHEAFAASKQLEAGHSGRLBKTEDLMURVEK DHAPRLARLSLESRSJQDVLHHRYRKERDLYRGSVTR MLMEGIKGGSIAVLHGRESHDAULHERFHYMSLPKHRLVDLHG SVUDNYNGGSSIAVLHGRENGDAUTHLFRINGGGERGCYGUVYLCDN WGGHFCALKSVVPPDEKWMNDLALEFHYMRSLPKHRLUDLHG SVUDNYNGGSSIAVLHGRENDFULLAGFTRUCIAL DVVEGIRFLHSGESVTRWMSUDVVAFGGIERGCYGUVYLCDN WGGGSTAVTLINAFRGSSPTGTLHADELFFYTYDEECMOLMEACONG LPAPHERGASKDHLMWNARGARPEELBLFYGT	TTTLSPSGSAVISTITIATTDSKYPTCDEKYANITYDYLINKETIK LPTAKLINVENIVECONITOTNNEWNLITEKANSVSISINSCTA PDKTLILDVEPGVEKVPVHCCS\QVEQPDSTIWLKWKNIETSTC DTONITYRPCCONNIPDNKEIKLENLEPBHEYKCDSEILYNSHK FTNASKIIKTDTGSPGEPQTIFCKSEAAMCGVITWNPPORSFHN FTLCYIKETEKDCLINLDKHLIKYPLONLKYTKYVLSHAYIIA KVORNGSAMCHETTKASPPSQVNMTVSMSDMHVKCRPPR DRNOPHERYHLEVSEAONTLUVNESHKNCDFRVKDLQYSTDYTFK AYFINGSVEGPEP FILHETSYNSKALLIFLIIVTSIALLIVV LYKIYDLHKKRSCHLDEQOELVERDDEKQLMNVEPIHADILLET YKRKLADEGRLFLAEFGSIPRVFSKFPIKEARKPFNONNKYVD ILPYDTNRVELSEINGDAGSNYTNASYIDGFRKYLIAGOFR DETVDDFWRMIWRGKATVIVMTRECEGNRNKCAEWPSMEGST RAFGECCCEULTHKRECP DYTIQKLINLERGRCLMVQUSAQYI LIHQALVENOPGETEVNLSIHPYLHNMKKRDPPSEPSPLEAE FORLPSYRSWRTQHIGNQE\ENKSKARNSNNIPYDVARVPLKHE LEMSKSSEMBSDESSDDDSDESERSKYINAFINSVKRLSVEYNI AAGGPLKSTIGDFWQMIFGRKVKIVINLTELKHGDQEICAGYWG EGKQTYGDIEDDLKDTDKSSTYTLRVFEKRKDSRTVYQYQ YTNNSVEQLPABPKELISNIQVVKQVLVKLRRCRLDAWQUSAQYI LIHGRIGSGONGIFCALLINLESAETEEVVDIFQVVKALRKAR GMUSTFEQYQPLYDVLASTYSTYTLRVELKKRNDSRTVYQYQ YTNNSVEQLPABPKELISNIQVVKQLPCKSSESGRHKKSTPL LIHCRIGSGONGIFCALLINLESAETEEVVDIFQVVKALRKAR GMUSTFEQYQPLYDVLASTYPAQNGQVKKNNHQBKIEFDDEVD KVKQDANCVNPLGAPEKLPEAKCQAEGSEPTSCTEGPBEISVNGP ASPALNQGS 3 2363 DAMGCKLRRLEFTYGTORVSLALPGQVELVHTLVAHGGNNETI LYCHCLDIFTNQAFDMGROLQITFRRESTRRESKRPLYRQVILGNNETI AGREGLIKGLEFTYGTORVSLALPGQVELVHTLVAHGGNNETI LYCHCLDIFTNQAFDMGROLQITFRRESTYRKRENDERVVILGENGRE FYTUVLIGDLVNDELBVTTYALHKORLSERDEGOLOZIRKYFSFP VFFFKVPKLGSEILDSGEILBSTRHESERSPLYRQLILGYLLSSHM CGAPGQDTKAQSMLVEQSEKLRRLESTFSHQVTLTVAHGRONETI LYCHCLDIFTNQAFDMGROLQITFRRESTYRKKRUSPFYOTU- BERCLSCLEKSQUSVHITISNIKAVILLGEVONAVNKLISSVDYLKSSHM CGAPGGOTKAQSMLVEQSEKLRRLESTFSHQVTLYTHGSSVX MLMEGIKGITGRITHWSPPAITLEKKRVAQEBIESLSASKLAK SICSQFFTRIKSGELBGRSCQVGVVVLCN WGGHFFCALKSVVPPDEHMNDLALEFFTYMSLIPKHERLUDLEG SVUDNYNGGGSSIAVLLIRERKRENGGLIGKGCYGVVVLCN WGGHFFCALKSVVPPDEHMNDLALEFFTYMSLIPKHERLUDLED DVEGIRPLASGLIVHRDIKTKNINDVLDKONRAXTIDLOFCKPEA MMGGSIVOTIPHAPBLEJTKRYNDSVDYLAGLIFTRICJILL DVVEGIRPLASGLIVHRONLKNINGLNINGLIFTRICJILL DVVEGIRPLASGLIVHRONLKNINGLNINGLNIN	5979	212	3665	LPDMTMYLWLKLLAFGFAFLDTEVFVTGQSPTPSPTDAYLNASE
LETAKLAWNENUECONTICTINEVHALITECKNASVSISINSCTA PPKTLILUPPEGUEKVPUNCCS_QUEETINLKWAN_ETSTC DTONITYREPCCOMMIPDINGEIKLENLEPEHEYKCDSEILYNSHK FTNASKIIKTDFGSPGEPQIIFCRSEAHQOVITKWPTGRSEILYNSHK FTNASKIIKTDFGSPGEPQIIFCRSEAHQOVITKWPTGRSEILYNSHK FTNASKIIKTDFGSPGEPQIIFCRSEAHQOVITKWPTGRSEILYNSHK KVORNGSAMCHFTTKSAPPSQWMNTVSMTSINSHVKCRPPR DRINGHFRYHLSVERGINTURNESKHALIAFLAFLIUTSIALLVV LYKIYDLHKKRS.CNILDEQQELVERDDEKQLMVVEPITADILLET YKRKIADEGRLFLAEFGSIPRVSKFPIKEARKPPRONENRYVU LYKIYDLHKKRS.CNILDEQQELVERDDEKQLMVVEPIHADILLET YKRKIADEGRLFLAEFGSIPRVSKFPIKEARKPPRONENRYVU LYKYDLHKKRS.CNILDEQQELVERDDEKQLMVVEPIHADILLET YKRKIADEGRLFLAEFGSIPRVSKFPIKEARKPPRONENRYVU LIHYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAGGPR DETTUDPBWRINHQKARVIVWYNCKLERRKCAFWPSMEGGT RAFGECCCKDLIKHKRCP_DYLIQKLMIVWKKRAFGREWVHIO FTSMPDBHGVEEPHALLLKRRVNAFSNFFSGPIVVHCSAGVGR TGTYIGIDAMLEGLEAENKUDVGYVVVALRRQRCLMVQVEAQVI LIHQALVENOPGETEVALSELHPYLHMMKKRDPPSEPSPLEAE FORLPSYRSWRTOHIRGNE VENKYMAFSNFFSGPIVVHCSAGVGR TGTYIGIDAMLEGLEAENKUDVGYVVVALRRQRCLMVQVEAQVI LIHQALVENOPGETEVALSELHPYLHMMKKRDPPSEPSPLEAE FORLPSYRSWRTOHIRGNE VENKYMAFSNFFSGPILVACQVWG EGKQTYGDIEVALKATURPGEVKUYIVLTEKWGDPLICAQVWG EGKQTYGDIEVALKATURPGEVKUYIVLTEKWGDPLICAQVWG EGKQTYGDIEVALKATURPGEVKUYIVLTEKWGROPEICAQVWG GEGKQTYGDIEVALKATURPGEVKUYIVULFGWWGKLFFONWO YTWNSVEQLIPAEPKELISMIQVVKKKLPQNNSSEGNKHHKSTPIL LIHCHGSGOTGIFCALIANLLSSAFEVQTEPHSVNGP ASPALNQGS ASPALNQGS ASPALNQGS ASPALNQGS ASPALNQGS DAWGCKLRRLFTYGTOTRVSLALPGQYELVHTLVAHQGNWETI DEEDLEVGNENDAAHDLTELBVTMHHALLQSVDVVVAPCQGLR PTVUVLGDLVNDFLPVITYALHKDELLGROPGLIRKYFSFP VFFFKVWFLGSBIIDSTRMSSERSPLYNQLIDLGYLSSHMN CGAPGODTKAQSMIVEQSEKRHISTSTBIVULTALHQGNWETI EFECLSUSVENDAAHDLTELBVTMHHALLQSVDVVVAPCQGLR PTVUVLGDLVNDFLPVITYALHKDELLDAMREFNOTIVENGE VGTYRTURSSELBAFAASLRQLEAGHSGREKTEDLMLRVKK SICSGPRITALNSHEAFAASLRQLEAGHSGRERCTEDLMLRVKK SICSGPRITALNSHEAFAASLRQLEAGHGGGTGGYGYVYLCON WGGHFCALKSVVPPDEKWMUNDALLEFHYMICSGSVK MMSGSIVOTPIHAPBLEFTGKYDNSVDVVAFGILFRYICGSGVK LPRAFFERGASKDHLMWNVRGARPEREJDEGECO	LPTAKINVENVECQNITCTNINEVHITECKNASVISINNSCTA PDEKTILIDVPEVEKEVYPUKCS\QVEQPDSTIWLKMENIETSTC DTONITTREQCOMMIPONKEIKLISHLEPSHEVKCDSEILYNSHK FTNASKIIKTDFGSPGEPQIIFCRSEAARQQVITWHPORSTHIN FTLCYIKETEKDCLINDKHLIKYDLQNIKPTKKYUSLIHAYIIA KVORNGSAAMCHFTTKSAPPSQVWNMTVSMTSDNSHMEVKCRPPR DRNOPHERYHLEVSAGNTLURNESHKNDEVKDLQVSTDYTFK AVFRINGDYFGEPFILHISTSYNSKALIAFLARLITUTSIALLVV LYKYDLHKKRSCALDSQGSLVERDDEKQLMWREPIHADILLET YKRKIADEGRLFLAFFQSIPRVFKKFPIKEARKPFNONNRKYVD LYKYYDLHKKRSCALDSQGSLVERDDEKQLMWREPIHADILLET YKRKIADEGRLFLAFFQSIPRVFKKFPIKEARKPFNONNRKYVD ILEYDTNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPR DETVDDFWRMWEKGATUTVWTTCECEGREPTVYHCSAGREF TRAPBGCCCKDLTKKKRCP\DYIIQKLNIVNKKERATGREVTHIQ FTSMPDHGYVEBPHILLKLKRRRWAPSIPSTVWHCSAGREFYTHIQ FTSMPDHGYVEBPHILLKLKRRRWAPSIPSTVWHCSAGREFYTHIQ FTSMPDHGYVEBPHILLKLKRRRWAPSIPSTVWHCSAGREFYTHIQ FTSMPDHGYVEBPHILLKLKRRRWAPSIPSTVWHCSAGREFYTHIQ FTSMPDHGYVEBPHILLKLKRRRWAPSIPSTVWHCSAGREFYTHIQ FTSMPDHGYVEBPHILLKLKRRRWAPSIPSTVWHCSAGREFYTHIQ FTSMPDHGYVEBPHILLKLKRRRWAPSITSTVWFLKRRRFYPGYO YTMSVEQLPABPKELISHIQVVKOKLPQKNSSEGNKHKFSTPI LHQALVEYNQFGETEVNLSSTYTLRVFELRISKKNDSRTVYQYO YTMSVEQLPABPKELISHIQVVKOKLPQKNSSEGNKHKKSTPI LHCRDGSQOTGIFCALINLLESAETEEVVDIFQVVKALRRARR GMVSTFEQYQFLYDVIASTTYPAQNGQVKKNHHQEDKIEFDNEVD KVXQDANCMNPLGAPPKLGPAKCGAGSEPTSGTEGPBEISVNGP KVXQDANCMNPLGAPPKLGPAKCGAGSEPTSGTEGPBEISVNGP ASPALNQGS ASPALNAGGS ASPALNQGS ASPALNQGGAPTAGAHUNGGAPRTRKKRNELYESLMN LVHCHCLDIFTNAGAFTGARGERSPTYRQLIDLYTLSSHMN CGAPGGDTKAGSHUNGGERKRRENDENTYGLUTHARKERIDLYTIKARRENDLYTHABFYGTUL ARROGERMOMIVETLINTMKERLLDDATMMPEKVUTVPENGGB VGTTRIKCCIRQIQELITSRINGANANAURLITSSVDTIMARFYGT MLMEGIKOITQITTMVSPPAITLEMKRVAQEAITSLASSKLAR AMGGSIVOTPHAGGSISAVLUKRNYLLDKQNRAKITDLOPCKPEA MMGGSIVOTPHAPBELSTKRNSNBAFARSLRCHEMGREKETLDWICKGSVK LPBAFRCASKOHLUNNVRRGAPPRIJEUFUTWISLDKIRKUDLILLYTLGGGV				TTTLSPSGSAVISTTTIATTPSKPTCDEKYANITVDYLYNKETK
PEKTLILDVPGVEKVPVICCS\QVEQPESTIALKMKNIETSTC DTONITYRPQCGMIPEDHEINKLEPEHEYKCDSEILYNSHK FTNASKIIKTDFGSPGEPQIIFCRSEAAHQGVITMNPPQRSFHN FTLCYIKETEKDCLNLDKNLIKYDLQNLKPYTKYVLSLHAYIIA KVQRNGSAAMCHSTTKSAPPSQVWNMTVSHTSNNSHMYVCRPPB DRNGPHERYHLEVEAGNTLVRNESHKNCDPRVKDLQYSTDYTFK AYFNNGDYPGEPPILHSTSYNSKALIAFLAPLIIVTSIALLVV LYKIYDLHKKRSCNLDEQQELVERDDEKQLMAVPEIHADILLET YKRKIADEGRIFLAEFQSIPRVFKFFFIKEARKPPNQNKNRYVD ILPYDYNRVELSEIRODAGSNYINASYIDDFEPRKYIAAGGPB DETVDDFWRNIWBOKATVIVMTRCEEGNENKCAEYWPSMEEGT RAPGECCKDLTKHKRCP\DYIIQKLNIVNKKEKATGREVTHIQ FTSWPDHGVPEPPHLLLKLRRNWAFSNFFSGPIVHCSAGVGR TGTTIGIDANLESLEAENKUDVGYVVVKLRGRCLMVQVEAQVI LIHQALVENYQFGETEVAVLSLHPYLHNMKKDPPSEPSPLEAE FORLDSYRSWRTGHIGNGD\ENKSKNENSNYIPYDYNRVPLKHE LEMSKESEHDSDESDDDSDEEPSKYINASFIMSYNKP\EVMI AAQOPLKETIGDFWOMIFQRVKVIVMLTELHHGDGELCAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYOYQ YTNNSVEQLPABPKELISMIQVVKLQNONSSEGNHHKSTPL LIHCRDGSQOTGIFCALLINLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHGBKLEFDNEVD KVKQDANCVNPIGAPEKLPEAKEAGSFPTGGTEGPHSVNGGI ASPALNGGS 5980 3 2363 DAWGCKLRRIRFFYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHALLGEVDVVVAPCQGIR PTVUVLGDLVNDFLEVTTYALHKDELSEEDEGLGETRKYFSPP VFFKKVRLGSSI IDSSTRRMESERPLYGQLIDGYLSSSHMN CGAPGQOTKAGSMLVEGSEKLRHLSTFSHQVLQTRLUDAAKALN LVHCHCLDIFINGAPTQRDQLITPKLEYTKKENELYESSMN CGAPGQOTKAGSMLVEGSEKLRHLSTFSHQVLQTRLUDAAKALN LVHCHCLDIFINGAPTQRDQLITPKLEYTKKENELYESSMN CGAPGQOTKAGSMLVEGSEKLRHLSTFSHQVLQTRLUDAAKALN LVHCHCLDIFINGAPTQRDQLITPKLEYTKKENELYESGSVTR MLWEGIKOTHINSHEADALRAVHEVTPHSGSSVTR MLWEGIKGLERSGDVSVHTSNYKAGILNAAYHVEVTPHSGSSVTR MLWEGIKGLERSGDVSVHTSNYKAGILNAAYHVEVTPHSGSSVTR MLWEGIKGLERSGLOVSVHTSNYKAGILNAAYHVEVTPHSGSSVTR MLWEGIKGLERSGLOVSVHTSNYKAGILNAAYHVEVTRHSGSSVTR MLWEGIKGLERSGLOVSVHTSNYKAGLIKRTEDLMLRVKK DHAPRLARLSLESRSLQDVLLHRKRKVAQEAIESLSASKLAK SICSOPTRINSSHEAFAASLRQLEAGGIGGGGCQVVVVLCDN WGGHFFCALKSVUPPDEKHMNDLALEFFYMBSLEKRERLUDLHG SVLDWYNGGGSSIAULLIMBERHERDYLKARGLOFERGA	DENTILLIDVPROVEKVPVHCCS\QVEQPDSTIMLXMKNIETSTC DTQNITYRPCQCAMIPEDNEK ILKENLEPKCKOSELLYNSHK FTNASKIIKTDFGSFGEPQITFCRSEAHQGVITMPPPQRS*HN FTLCYIKETEKDCLNLDKNLIKYDLQNLCYTKVVLSHAYIIA KVQRNGSAAMCHFTTKSAPPGQVMNMTVZMTSDNSMHVKCRPR DRNOPHERYHLEVPSACNTLVRNESHKNCDFRVKDLQYSTDYTFK AYFINGSTYGEPFILHATSYNSKALIAFLIIVTSTALLVV LYKIYDLHKKSCGLDEQQELVERDDEKQLMNVEPIHADILLET YKRKIADEGRIPLAFEGSI PRVFKEPPI EARLIVTSTALLVV LYKIYDLHKKSCGLDEQQELVERDDEKQLMNVEPIHADILLET YKRKIADEGRIPLAFEGSI PRVFKEPPI EARLIVTSTALLVV LYKIYDLHKKSCGLDEQGELVERDDEKQLMNVEPHADILLET YKRKIADEGRIPLAFEGSI PRVFKEPPI EARLIVTSTALLVV LYKIYDLHKKSCGLDEQGELVERDDEKQLMNVEPHADILLET YKRRIADEGRIPLAFEGSI PRVFKEPPI EARLIVTSTALLVV LYKIYDLHKKSCGLDEQGELVERDDEKQLMNVEPHADILLET YKRRIADEGRIPLAFEGSI PRVFKEPPI EARLIVTSTALLVV LYKIYDLHKKRSCRIDEQGELVERDDEKGLMNVEPHADILLET YKRRIADEGRIPMENEVDYGYVVKLNKRAPPOMEGSI RAFGECCCKDLTHKKRCP DYTIQKLNIVNKKERADGREVPHOE FTSMPDHGYPEDPHLLLLKRRRVARSFNSFGSDIVVLGSAGVGR TGTYIGIDAMLEGGLEBRIKVDVVGYVVKLRRQRCLMVQVEAQYI LIHQALVENOFGETEVNLSELHPYLHNNKKRDPDSEPPILEAE FORLB-YSFRENTORIGNOE, ENKINKKRNDSNVIPPDYNRVPLKHE LEMSKESENDSDESSDDDSDSEEPSKYINASFIMSWRPLVEND AAGGPLKETIGDFWQNIFQRRVKKIVMLTELKKHDQBICAQYME EGKQTTGDIEDTUNLDTIKSSTYTLRVFELKRKDSRTVYQYQ YTMWSVEQLPABPKELISNIQVVKQKLPQNSSEGRHKKRSTPLYQYQ YTMWSVEQLPABPKELISNIQVVKQKLPQNSSEGRHKKRSTPL LIHCRDSGOGTGTCALLINLLESAFTEEVVDIFQVVKALRRARP GMVSTFEQYQPLIVVLASTYPAOMGQVKKNNHGBDKIEDMEVD KVKQDANCNPLJGAPEKLPEAKQQGVKKNNHGBDKIEDMEVD KVKQDANCNPLJGAPEKLPEAKQQGVKKNHGBDKIEDMEVD KVKQDANCNPLJGAPEKLPEAVQQVELVHTLVAHQGNMETI LHCRDSGOGTGTGTCALLNILESAFTEEVTHSKNENDRAVQYQ KVKQDANCNPLJGAPEKLPEVTTYALHKDELLDDATMRTKR GMVSTFEQYQPLIVVTLASTYPAOMGQVKKNHGBDKIEDMEVD KVKQDANCNPLJGAPEKLPEVTTYALHKLELLDDATMRTKR CGARGQDTKAGSALVVEQSEKKRHLSTFSHQVLQTRLVDARACNN CGARGQDTKAGSALVVEQSEKKRHLSTFSHQVLQTRLVDARACNN CGARGQDTKAGSALVVEQSEKKRHLSTFSHQVLQTRLVDARACNN CGARGQDTKAGSALVVEQSEKKRHLSTFSHQVLQTRLVDARACNN CGARGQDTKAGSALVVEQSEKKRHLSTFSHQVLQTRLVDARACNN CGARGQDTKAGSALVVEQSEKKRHLSTFSHQVLQTRLVDARACNN CGARGQDTKAGSALVVEQSEKKRHLSTFSHQVILVENTKANNEVTHFBGSSVTR MLMEQIKOTINGTKAGKAGANAKATATURLTPTKAGATANAV				LFTAKLNVNENVECGNNTCTNNEVHNLTECKNASVSISHNSCTA
FTNASKIIKTDFGSPGEPQITCRSEAAHGGVITMNPPORSFHN FTLCY!KETERCLALDKMIIKYDLGMLKPYTKYVISLHAYIIA KVORNGSAAMCHFTTKSAPPSQVMMMTVSMTSDNSMHVKCRPPE DRNGPHBRYHLEVEAGNTI.VRNESHKNCDFYKDLQYSTDYTFK AYFINIGNYPGEPPIILHFSTYNISKALIAFIAPI.IVTSIALLVV LYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLET YKRKIADEGRIFLAEPGSI PRVFSKFPIKEARKPPNQNKNRYVD LYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLET YKRKIADEGRIFLAEPGSI PRVFSKFPIKEARKPPNQNKNRYVD LILPYDYNRVELSEINGDAGSNYINAKSKATGEVYHIQ FTSMPDHGVPEDHLLLKLRRVWAFSNFFSGFIVVHCSAGVGR RAFGECCCKDLTMKRCP\DYILQKLMIVNKKEKATGEVYHIQ FTSMPDHGVPEDHLLLKLRRRVWAFSNFFSGFIVVHCSAGVGR TGTYIGIDAMLEGLEAENKVDVGYVVKHRGRGCLMVQVEAQYI LIHQALVEYNQRGETEVNLSELHFYLHINMKKRDPPSESPLEAE FQRLPSYRSWRTQHIGNGE\SENKKNRNSNYINYPDYNRVPLKHE LEMSKESHENDSDSSDSDSDSSESPSYSTNAFINSTWENP\SWMI AAQGPLKETIGDFWOMIFQRKVKVIVMLTELKHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRCDSRTVYQYQ YTNNSVBQLPABPKELISMIQVVKGQNNSSEGNKHKKSTFL LIHCRDGSQOTGIFCALLINLESAETEEVVDIFQVVKALKRARP GMVSTFEQYQFLYDVLASTYPAQNGQVKNNHGDKIEFDNEVD KVKQDANCVNPLGAPEKLDEAKCQABGSEPTSGTEGBEHSVNGP ASPALNQGS 5980 3 2363 DAMGCKLRFLRFTYGTGTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHALLQBVDVVVAPCQGLR PTVDVLGGLVRHOFLDFLYTYLHKDELSERBGELQEIRKYFSSP VFFFKVPKLGSEIIDSSTRIMESERSPLYRQLIDLGYLSSSHINN CGAPGQDTRAGSMLVEGSBKLRHLSTFSIGVLTGTLSSSHINN CGAPGGOTKAGSMLVEGSBKLRHLSTFSIGVLTGTLSSSHINN LJANKQEEMKDMIVETLNTMKEELLDDATNMEPTDVIVPENGEP VGTREIKCCIRQIGELIISRINQAVANKLISSUVYLRESSFVGTL ERCLGSLESSQDVSVHTSNNIKQILNAAYHVEVTPHSGSSVTR MLMGOIKGIIGRITMVSPPAITLEWKRKVAQGAIESLSABKLAK SICSQPTRINSSHEAPAASLRQLEAGHGSGRLBKTEDLBURNEK DHAPRLARLSLESSLGDVLLHHKPKLGGELGGRGQVGVVVLCDN WGGHFPCALKSVVPPDEKHMNDLALEFFYMSGSVTR MLMGOIKGIIGRITMVSPPAITLEWKRKVAGGAIESLSABKLAK SICSQPTRINSSHEAPAASLRQLEAGHGRGRLBKTEDLBURNEK DHAPRLARLSLESSLGDVLLHKPKLGGELGGRGQVGVVVLCDN WGGHFPCALKSVVPPDBSKHMNDLALEFFYMSGSVTR MLMGOIKOTHMAPBELFTCKYDNASODVYARGILFFYICSGSVK LPBAFFRCASKOHLMINNVRGABRIPELPVPTEECWQLIKRACOMG	FTNASKIIKTDGGSPGEQIIFCRSEAAHQGVITWNFPGRSTHN FILCYIKETEKDCINLINKINLINGYDIKYYTKYVISHLAYIIA KVQRGSAAMCHFTKSAPPSQVWNMTVSMTSDNSMHVKCRPPR DRNGPHERYHLEVERGNTLVRBSHKNCDFRVUKLQYSTDTYTH AYFINGDYBGEPFILHHISTSYNSKLIAFLAPLIIVTSIALIVV LYKIYDLHKKRSCNIDEQGLVERDDEKQLMNVEPHADILLET YKRIKADEGRIFLAFGS I FRVESKFY LERARKPFNONKNRYVD ILPYDYMRVELSEINGDAGSNYINASYIDGFKEPRKYITAAGGPR DETVDDFWRMIHEGKATVI YMVTRCESENRNKCABEWPSMEEGT RAFGECCCKDLTKHRECP NYIIGKHUKKRKATGREVHOOR FTSWPDHGVPEDPHILLKLERRVNAFSNFFSGFIVVHCSAGVGR TGTYIGIDAMLGGLEBERKVUVYGYVUKKRKATGREVHOVAQVIA LIHQALVEYNGFGETEVNLSELHPYLHNMKKRDPSPERSPLEAE FQRLPSYRSWRTQHIGNGE LENKSKNINSNYIPYDYNRVPLKHE LEMSKESEHDSDESSDDDSDSEESKYNINASFIMSTWHYNPKVPLKHE LEMSKESEHDSDESSDDDSDSEESKYNINASFIMSTWHYNPKVPLKHE LEMSKESEHDSDESSDDDSDSEESKYNINASFIMSTWHYNFKVPLKHE GROTTGOLIEVDLKDTUKSTYTLRVFELRSKRKDSRTVYQYQ YTNKSVEQLPABPKELISMIQVVKQKLPQNNSSEGNKHKKSTPL LIHCRDGSQOTGIFCALLMILESABTEEVVDIFGVVKALRRARP GWYSTTEGVQFLYDVIASTTPAQNGOVKNNHGENKIEPDDEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALMQS 5980 3 2363 DAWGCKLRFLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEBLEVQENNEDAAHDLTELEVTMHHALLGSVDVVAPCOGUR PTVDVLGDLVNDFLPYTTALHKOLEDGEGLGEIKYKFSPP VFFFKVPKLGSEIIDSSTRRMSSRSSPLYRQLIDLGYLSSSHMN CGAPGQDTKAQSMLVEQSEKLRHLSTFSIQVIQVTATLVDAAKALN LVICHCLDIFINQAFDMQRDLQITPKRLEETRKKRNELYSSLNN LANKKGEEMKMIVETLNTMKEELLDDATMBEFKVUTVPENGEP VGTREIKCCTRQIGELIISRINDAVANKLISSVDVLRSSFVOTIL ERCLOSLEKSGOVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWGQIKQIIQRITWVSPPAITLEWKRKVAQSATESLSASKLAK SICSGFRTRLMSSHEAFAASIRQLEAGHGSGEEKTEDLINGRVK DHAPRIABLISLESRSIQDVLLHRKERKVAGGGELGRGQYGVVVLCDN WGGHFFCALKSVVPPDEKKWNDLALEFTGLOTHL DVVEGIRFLHSQGLVRICHKKNLDKRNKKLDLHURVK DHAPRIABLISLESRSIQDVLLHRRELHDLYTGLKAGLTLEFTLQUTAL DVVEGIRFLHSQGLVRIPHAPAFLFGRYDNSVCHOFGILFWITCGGSVK LPBAFFRCASKOHLMINVRRGARPERLPVPDECMILMEACNDG DPLKRPULGIVOPHILGRINGNICKS,NSGDPNRGLDDSTT DAPPPAAAPLERNSGGIGVSMGLLAAAAGGGFPERGGRWERSAP GEDEECKROWEDVAALAANTHORVEDGESVISKWONDESTIYV				PDKTLILDVPPGVEKVPVHCCS\QVEQPDSTIWLKWKNIETSTC
FILCYIKETEROCLINLDRINIKYDLONLEPYTKYLSLHAYIIA KVORGSAAMCHFTTKSAPPSOWINTUSMTDOSIMHVKCRPPR DRINGPHERYHLEVEAGNTLVRNESHKNCDFWKDLQYSTDYTFK AYFINGDYPGEPFILHHISTSYNSKALIAFLAPRIITVTSIALLVV LYKIYDLHKKRSCNIDEQQELVERDDEKQLMVVEPHADILLET YKRKIADBGRLFLAEFGSIPRVESKPPIKEARKPPNQNKNRYVD ILPYDYNRVELSEINGDAGSNYINASYIDGKEPKRYVIAAQGPR DETVDDTWRNIWEQKATVIVMVYTRCEEGONRINKCAEYWPSMEEGT RAFGECCKDLTKHKRCP\DYJIOKLINIVNKEKATGREVTHIQ FTSWPDHGVVEPDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR RAFGECCKDLTKHKRCP\DYJIOKLINIVNKEKATGREVTHIQ FTSWPDHGVVEPDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR TGTYIGIDAMLEGLEAENKUDVGVVVLVINKRRCLMVQVEAQYI LIHQALVEXYQFGETEVNLSELHPYLHMKKRDPPSEPSPLEAE FORLDSYNSWRTORDIONGP\EMSKSNRNSNNIPDYDYNRVPLKHE LEMSKESEHDSDESSDDDSDSEPSKYINASFIMSYWKP\EVMI AAQGPLKETIGPFWOMIFQRKVKVIVMITELKHGDQSICAQYMG EGKQTYGDIEVDLWDTDKSTITTLEVHFLIKHGRDGSICAQYMG EGKQTYGDIEVDLWDTDKSTITTLEVHFLIKHGRDSRICAQYMG WANTFEQYGPLYDULADTDKSTITLFURFLRISKREDSRIVYOYO YTNNSVRQLPABPKELISMIQVVKQKLPOXNSSEGNRHHKSTPL LIHCRDGSQOTGIFCALINLLESAETEEVVDIFQVVKALRKARP GMYSTFEQYGPLYDULATATYPAQMGQVKKNHNGRDKIEFDNEVD KVKQDANCVMPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQBVDVVVAPCOGGR PTUDVLGDLVNDPLPVITTVAHKDELSERDEGGLGIRTKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGGDTKAQSMLVEQEEKKHHLSTTSHOVLQTRLVDAAKALN LVHCHCLDIFINQAFPMRGRDGJTFKKLETYRKKRELVESIMN IANRKQEEMKDMIVETLINTMKEELLDDATMMEKRDUIVPENGEP VGTREI KCCTRQIOELIISRLNQAVANKLISSVDYLRESFVOTL ERCLQSLEKSQDVSVHITSNIVLKQILKAAYHVEVTFHSGSSVTR MLMEQIKQIIQRITWSPPATTLEWKRVAQEAIESLSASKLAK SICSGFTRILNSSHEAFAASLGBEHGSGREKTEDLWIRKKA SICSGFTRILNSSHEAFAASLGBEHGSGREKTEDLWIRKKA SICSGFTRILNSSHEAFAASLGBEHGSGREKTEDLWIRVK DHAPRLARLSLESRSLQDVLHRKPKLGGELGRGCGVGVVYLCDN WGGHFFCALKSVVPPDEKHWNDLALEFHYMRSLPKKEDLUESGSVK DHAPRLARLSLESRSLQDVLHRKPKLGGELGRGCTGVTVYLCDN WGGHFFCALKSVVPPDEKHWNDLALEFHYMRSLPKKEDLUELGGGEVA SVIDVNYGGGGSSIAVLLIMERHDLYTGLKAGATLDETLGCGSVK LPBAFFERCASKOHLBWNVYRGARPERLPVFDEECWQLMBACNDG	FTLCYIKETERDCLMLDRNIIKYDTKYVISLHAYILA KVQRNGSAMCHETTKAE, PSGOWMYMSINSMNHVKCRPR DRNGPHERYHLE VERGYDTLVRNESHKNCDFRVKDLQYSTDYTFK AYFHNGDYPGEPPILHISTSYNSKALIAFLAFILIVTSIALIVV LYKIYDLHKKRSCNLDEQGELVERDDEQMNVEPIHADILLET YKRKIADEGGLELAEFGSIPRVEKFPIKEARKPPRONNNRVVD ILEPDYNRVELSEINGDGGSNYINASYDEKARKPPRONNNRVVD ILEPDYNRVELSEINGDGGSNYINASYDEKARKPPRONNNRVVD DETVDDFWRNIWGKAZVIVWTRCEEGNRNKCAEYWPSMEEGT RAPGECCKDLTKHKRCP/DYIIQKAIVIVKKAATGKEVTHIO FTSWPDHGVPEDPHLLLKLRRRVNAFSFFSGIVWHCSAGVGR TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQKCLMVQVEAQYI LIHQALVENNOFGETEVULSEHPYLHKKRCPPSEPSPEPLAE FORLPSYRSWRTOHLGNGCNLSKIKNRNSNVIPYDYNRVPLKWI AAQGPLKETIGDFWMFGRKVKVIVMLTELKHGDQELCAQYWG EGKQTTGDIEVDLKOTTKSSTYTLRVFELEHSKRKDSRTVYOYQ YTNNSVGLPAPBKELISHIOVVKQKUNSSENNSHKKSTPL LIHGRDGSOOTSIFCALLAILISABTEEVVDIFQVVKALRKARG GWUSTEGVQFLYDVLASTYPAQNGQVKKNNQEDKIEFDNEVD KVKQDANCVNPLGAPEKLEISHIOVVKGKUNSSENNSHKKSTPL LIHGRDGSOOTSIFCALLAILISABTEEVVDIFQVVKALRKARG GWUSTEGVQFLYDVLASTYPAQNGQVKKNNQEDKIEFDNEVD KVKQDANCVNPLGAPEKLEISHIOVVKGKUNSSENNSHKKSTPL LIHGRDGSOOTSIFCALLAILISABTEEVVDIFQVVKALRKARG GWUSTEGVQFLYDVLASTYPAQNGQVKKNNQEDKIEFDNEVD KVKQDANCVNPLGAPEKLEPTAGCAEGSETTSGTBGPBHSVNGP ASPALNQGS JAMGCKLRRLRFTYGTOTRVSLALEGGYELVHTLVAHGGNWETI PEBDLEVGENNEDAAHDLTELEVTMHALLGEVDVVVAPCQGLR PTVOVLGIDLVNDFLPVITYALHKDELSERDGELGEIRKYFFSN VFFFKVPKLGSEIIDSSTRRMSERSPLYKQLIDLGYLSSSHNN CGAPGQDTKAQSMLVEQSEKLEHLSTTSHOVLOTTALVDAARALN LVHCHCLDIFTNQAFMQRDLQITFRKLEVTRKKENELYSSLNN IANKGEEMKDMIVETLNTMKEELLDDATMMERKUVI VPENGEP VGTREIKCCIRQIGELIISIRLNQAVANKLISVDYDLRESFVOTL ERCLQSLEKSQDVSVHITSNYLKQLINAAYHVEVTFHSGSSVTR MLMEQIKQIIQTRTWSSPATTLEWKRKVAQGBAIESLSASKLAK SICSOFRTRLNSSHERFAASIRQLEAGREEKTEDIMLRVK DHAPRIARLSLEERSLQDVLLHRRPKLGGELGRCQYGVVVLCON WGGHFFCALKSVVPPDEKHMDLALEFTYMKSLPKHERLVDLIG SVIDYNYGGSSIAVLLIMERLHRDLYTGLKGGTLEKTETGUIAL DVVEGIRELBGGORTPHAPABLETGRYNDKYOTAGLEFWITCSGSVK LPEAFFCCASKDHMINNVRGGAPERLPVPDECMLMEACNDG DVLKRPLIGIVOPMLGHRINLCKS\NSGQPRGLUDGTC DVLKRPLIGIVOPMLGHRINLCKS\NSGQPRGLUDGTC JORDEGGRUNGLCKSVLOWYGDSTIY GERBSAAMERFWGAADGGSRAAAAAGGGFPERGGRWERSAP GLEDEGGRUNGDTGVSGGLEAAAAAGGGFPERGGRW				DTQNITYRPQCGNMIFDNKEIKLENLEPEHEYKCDSEILYNSHK
XVQRNGSAMCHFTKSAPPSQVWMTVYSMTSDMSMHVKCRPPPD DRNGPHERYHLEVPRGMTLVRNESHKNCDFRVKDLQYSTDYTFK AYFHNGDYPGEPPILHHSTSYNSKALIAFLAPLIIVTSIALIVV LYKIYDLHKKRSCNLDEQGELVERDDEKQLMNVEPIHADILLET YKRKIADBGRIFLAFGGSIPFVFSKPPIKEARKPPNQNKNRYVD ILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPR DETVDDFWRMIWEQKATVIVMVTRCEEGNRNKCAEYWFSMEGT RAPGGCCKDLTHKRCP(DYLKINIVNKKRERMSMEGT TGTYIGIDANLEGLEAENKUDVYGYVVKLRGRCLMYQVBAQVI LIHQALVEYNOFGGTETVNLSEIHPYLHMNKKRDPSEPSILEAE FORLDSYNSWRTQHIGNGE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHDSDESSDDDSDSEEPSKYINAFINSYMKP\EVMI AAQGPLKETIGDFWQMIFQRKVKJVMLTELKHGDSICAQYWG EGKQTYGDIEVDLKDTDKSSTYTILRYFELRISKREDGSTVQYQ YTNWSVEQLPAEPKELISMIQVVKQKLPQXNSSEGNKHHKSTFL LIHCRDGSQOTGIFCALINLLESAETEEVVDIFQVVKALRKARP GMVSTFRQYQFLVDVIASTYPAQNQQVKKNHQBKLEFDNEVD KVKQDANCVMPLGAPEKLPAEKQAEGSEPTSGTEGPEHSVNGP KVKQDANCVMPLGAPEKLPAEKQAEGSEPTSGTEGPEHSVNGP ASPALNQGS 5980 3 2363 DAWGCKLRREFTYGTOTRVSLALFGQYELVHTLVAHQGNWETI PEBGLEVQENNEDAAJDLTELEVTMHHALLQEVDVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEGELQEIRYYFSSP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHM CGAFGGOTKAGSMLVEQSEKLREFTSHQVLOTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKRELYESIMN IANRKGEBMOMIVETLNTMKEELLDDATKMEKPDVIVEBNGEP VGTREILKCITRGIGELITSRINGAHKRISTSHQVJUTRESFVGTL ERCLGSLEXSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIQRITMVSPAITLEWKRKVAQEAIESLSASKLAK SICSGPRTRINSSHEAPAASUGBEHGSHGSKETEDLBLRVRK DHAPRLARLSLESRSLQDVLHRRKPKLGGELGRGQYGVVVLCDN WGGHFPCALKSVVPPDEKHMNDLALEFTHYRSLPKHEDLUTLHG SVIDYNYGGGSSIAVLLIMBELHBOLTTGLKARTIDLERGRYVDLHG SVIDYNYGGGSSIAVLLIMBELHBOLTTGLKARTIDLERGRYVLCTOL DVVEGIRFLHSGCLVHRDIKLKNVLLDKQNRAXITDLGPCKPEA MMSGSIVGTPIHMAPELFTGKYDTSVAFGILKWITCSGSVK MMSGSIVGTPIHMAPELFTGKYDNYDFGGLEWGLOFGG	KVQRNGSAMCHETTIKSAPPSGVWNMTUSHTSINSMHVKCRPPR DRNGPHERYHLEVERGANTILVINERGOPRVEDLOYSTDYTFK AYFINGDYPGEPPILHHSTSYNSKALIAFLAFLITVTSIALLUV LYKIYDLHKKRSCNLDEQGELVERDDEKQLMWTEPIHADILLET YKRKIADEGRLFILABFGSIPRVFSH IKEARKPINGNKNFYUP ILEYDYMRVELSEINDAGSYNTASYIDGFKEPRKYIAAGGPR DETVDDPWRMIWEGKATVIVWMTGEGENRNKCAEYWPSMEEGT RAPGECCKCLTKHKRCP\DYIIQKLMIVNKKEKATGKEVTHIQ FTSMPDHGYVPEDPHLLLLKIRRWAFSNFFSGPIVVHCSAGVGR TGTYIGIDAMLGELBEARKVDVYGYVVKLRGRCLUMVQVBAQYI LIHQALVENOFGETEVALISLHBYLHIMKKRDPPSEPSDLEAE FORLPSYRSWRTQHIGNOE\ENKSKNRSNVIPYDYNRVPLKHE LEMSKESEHDSDESSDDDSDSEEFSKYINASFINSYMKP\EVWI AAQCPLKETIGDFWOMIFQRKVKVIVMLTELKHGDQBICAQYMG ESKQTYTQDIEVDLKDYDKSSTYTHVELRHGRKDSRTYVQVG YTNNSVEQLPABPKELISMIQVVKQKLPQKNSSBGNKHKKSTPL LIHCRDGSQOTGIFCALLNLLESAETEEVVOUTFQVVKALRKARP GMVSTFEQVQFLYDVIASTYPAGNGVKKNNNQBRKLFEDNEVD KVXQDANCVNPIGAPEKELJSMIQVKKQNLPQKNSSBGNKHKKSTPL LIHCRDGSQOTGIFCALLNLLESAETEEVVOUTFQVVKALRKARP GMVSTFEQVQFLYDVIASTYPAGNGVKKNNNQBRKLFEDNEVD KVXQDANCVNPIGAPEKELDERAFGEVGETERKYFSPP VFFKVPKLGSSIDSTRRMESERSPLYRQLIDLGYLSSSHNN CGAPGGOTTAGSMLVJCSEKLRHLSTFSHQVLQTTLVAHQGNWETI PEBDLEVGENNEDAAHDLTELEVTMHHALLGEVDVVVAPCOGLR PTVDUJGDLVNDFIJVYLTYALHKDEERBOEGTGETRKYFSPP VFFKVPKLGSSIDSTRRMESERSPLYRQLIDLGYLSSSHNN CGAPGGOTTAGSMLVJCSEKLRHLSTFSHQVLQTTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQTTFKREYTRKKRNELYESIMN CGAPGGOTTAGSMLVJCSEKLRHLSTFSHQVLQTTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQTTFKREYTRKKRNELYESIMN CAGAPGDTAGASMLVJCSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQTTFKREYTRKKRNELYESSWTR MLWEQIKQIIQRITWSPPAITLEWKRVAQEAIESLSASKLAK SICSGPRTRLNSSHEAFAASLRQLEGHIGSGLEKELDHLRVUK DHAPRLARLSLESSSLQDVLHHRKFRLGGEGGGGYGVVYLCON WGGHFFCALKSVVVPDBEKHNDILLAGEFHYMSLGVEKERLVDLHG SVIDYNYGGGSSIAVLLHKERKLRQLGFGGGGGYGVVYLCON WGGHFFCALKSVVVPDBEKHNDILLAGEFHYMSLDFWITGGSSVK LPBAFERCASKOHLWNNVRGARPERLPVTPBECMQLMBACNDG DPLKRPLEDFTNYKTNOVAYAGGLERSLTGREMGERAD DDLKRPLEDFTNYKTNOVAYAGGLERSLTGROTGUTSACNG DPLKRPLEDFTNYKTNOVAYAGGLERSLTGREMGRAPA ORDERFERDERFTNYKTNOVAYAGGLERSLTGROTGUTSGRC LPBAFERCASKOHLWNNVRGARPERLPVTPGEGGONGACNGG DPLKRPLOGIMBACKSAKANTGGAPRGGARRGSAPA	1			FTNASKIIKTDFGSPGEPQIIFCRSEAAHQGVITWNPPQRSFHN
DRNGPHERYHLEVEAGNTLVRNESHKNCDFRVKULQYSTDYTFK AYFHRGDYPGEPFILHHSTSYNSKALIAFLAFLIIVTSIALLVV LYKIYDHKKRSCNLDEQQELVERDDEXQLMWVEPIHADILLET YKRKIADBGRIFLAEFGSIFRVESKFPIKGARKPPNOMKRYVD LLPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPR BAPGECCKDLTKHKRCP\DYIIQKLMIVMKERKATGERVTHIQ FTSMPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR RAPGECCKDLTKHKRCP\DYIIQKLMIVMKERKATGERVTHIQ FTSMPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR TGTYIGIDANLEGLEAENKUDVYGYVVKLRRQRCLMWQVEAQYI LIHQALVEYNQFGETEVNLSELHPYLHMKKRDPPSEPSPLEAE FORLDSYRSWRTOHIGNQE\ENKSKRNSNSVIPYDYNRVPLKHE LEMSKESEHBSDESSDDSDSEDSEPSKYINASFIMSYMKP\EVMI AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYMG EGKQTYGDIEVDLKDTDKSSTYTLKYFELRHSKRKDSRTVYQYQ YTNWSVEQLPABPKELISNIQVVKQKLPQKNSSEGNNHHSSTEL LHCRDGSQQTGIFCALIMILESABTEEVVDIFQVKALRKARP GMVSTFEQYQPLYDVIASTYPAQNGQVKKNHQEDKIEFDNEVD KVKQDANCVAPLGAPEKLPEAACQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDGELQEIRXYFSPP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLSYLSSSHM CGAPGGDTKAQGMILVEGESKIRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMGDLQITPKRLEYTRKKRNELVESLAM LANKQEEMKDMIVETLNTMKEELLDAATMMEPKDVIVPENGEP VGTREIKCCIRQIQELIISRINQAVANKLISSVDYLRESFVOTL ERCLGSLEKSQDVSVHITSNYLKQILMAAVHVEVTPHSGSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLGSSVTR MLWEQIKQIIQRITWSPPAITLEWKRKVAQEAIESLGSSVTR MLWEQIKQIIQRITWSPPAITLEWKRKVAQEAIESLGSSVTR MLWEQIKQIIQRITWSPPAITLEWRYRKAGELIGERGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALGEHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGKKAGLTLETTLQIAL DVVEGIRFLHSGCLVHRDIKLKNVLLDKQNRAXITDLGPCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVAPAGILFWYICSGSVK DVWEGIRFLHSGCLVHRDIKLKNVLDKQRAXITDLGPCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVAPAGILFWYICSGSVK LPEAFFERCASKOHLMNNVRGARPERLPVFDEECMQLMEACOPG	DRNGPHERYHLEVEAGNTLVRNESHKRCDFRVKDLQYSETDTFFK AYFINGDYPGOEP ILHHETSYNSKALIAFLAPLAPLIIVTSIALLVU LYKIYDLHKKRSCNLDEQGELVERDDEKQIMNVEPIHADILLET YKRKIADEGGLFLABEGGI PRUFSKFFFIKERKFPRONKNRYVD ILFYDTWRVELSEINDAGSNYITASYIDGFKEPRKYTAAGGPR DETVDDFWRMINEGKATTU VMYTRCEEGNRNKCAEYWPSMEEGT RAPGECCCKDLTKHKRCP\DYIIQKLMIVNKKRATGREVYHIQ FTSWPDHGVPEDPHLLLKLRRVAMFSNFFSGPIVVHCSAGVGR TGTTIGIDANLEGLEAENKUDVYGYVVKLRRQRCLMVQVEAQYI LIHQALVENYNGGETEVVNLSELHYMMKKRDPSEPPLEAE FQRLPSYRSWRTQHIGNQE\ENKSKRRNSNVIPTYNNVELKHE LEMSKESEHDSDESDDDSDEEPSKYINASFIMSYWKP\EVMI AAQGPLKETIGDFWOMIFORKVKUHTELHKHOGELCAQYWG EGKQTYGDIEVDLKUTUKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNMSVEQLPABPKELISMIQVVKQKLPQKNKSBGNKHHKSTPL LIHCRDGSQOTGIFCALLINLESSAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHOBEKIEFDNEVD KVKQDANCVNPIGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNOP ASPALNQGS 5980 3 2363 DAMGCKLRRLRFTYGTOTRVSLALPGQYELVHTLVAHQGNWETI PEEDLSVQSNNEDAAHDLTELETTMHHALLOBVDVVVAPCOGUR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFKVPKLGSEI IDSSTRMESERSPLYRQLDILGYLSSSHMN CGAPGQDTKAGSMLVEQSEKLRHLSFTSGVUQTRLUDAKALN LVHCHCLDIFINQAFDMGRDLGITPKRLEYTRKKENELYESLMN LANKGEEMKGMIVENSPENLTRHKEELLDDATMMEFKOVIVVPENGEP VGTREIKCCIRQIQELISRLNOAVAKLISSVDYJRESSVOTR MLMEQIKGIIQRITWSPPATILEWRKRVAQEAIESLSAKLAK SICSQPRTELNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSJQDVLHHKRKRLYGGERGGGYGVVYLCON WGGHFFCALKSVVPPDEKHMNULALEFFYMSLDSKHERLUDLHG SVIDYNYGGGSSIAVLLIMBREHERDLYTGLKAGLTLETRLQIAL DVVGGTEPHSGGLVHYDIKKRNLYLDGKORRAKTIDLGFCKEPEA MMSGSIVOTPHMAPELFTGKYDNSVDYYAFGLEFTRYICGGSVK LPBAFERCASKOHLWNNVRGARPERLPYTGECWQLMEACNDG DPLKRPPLIGJUOPHLOGIMNRLCKS\NSEOPRIGGLDDST 6RHSAAMERPWGAADGLSRWPHGLILLLQLLPFFTSLSOBRL DAPPPPAAPLPRMSGPIGSULLLAULLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL				KUOPNGSAAMCHETTIKSA DEGULINAMIKAMIKANTARIA
AYFHRGDYGEPFILHHSTSYNSKALIAFLAPLIIUTSIALLUV LYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLET YKRKIADEGRIFLAEFGSI PRVFSKFPIKEARKPFNONKWRYVD ILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPR DETVDDFWRWIMEQKATU VMYRCEEGNRNKCAEYWPSMEEGT RAPGECCKDLTRHRCP\DYIIQKLMIVNKKEKATGREVTHIQ FTSWPDHGVPEDPHLLKLRRRWAAFSNFFSGFIVVHCSAGVGR TGTTYIGIDAMLEGLEAENKVUNGVEVVKLRRQRCLMVQVEAQYI LIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE FQRLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESSHDSDESSDDDSDESPSKYINASFIMSYMKP\EVWI AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTYYQYQ YTNNSYRQLPBAPKELISHIQVVKQKLPQXNSSBGKMHKSTPL LIHCRDGSQQTGIFCALLNLLESAETEVVDIFQVVKALRKARP GMYSTFRQYGPLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD KVKQDANCVWPLGAPEKLPEAKEQAESPTSGTEGPEHSVNGP ASPALNQSS 3 2363 DAWGCKLRRLFFYGTCTRVSLALPGQYELVHTLVAHQGNWETI PEEBLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGGLVANDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQOTKAGSMIVEGSEKIRHLSTSHGVUTQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKBNELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCTRQIQELISERLNQAVANKLISSDVINESPVOTL ERCLGSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWSPPAITLEWKRVAQGAIESLSASKLAK SICSQFRTELNSSHEAFAASLRQLEAGHGGRIEKTEDLMLRVRK DHAPRLARLSLESRSLQDVLLHHKPKLQGLLGRQGYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLAKLGGLLGRQGYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLAKLGTLEFTHGKTDARLTURRK DHAPRLARLSLESRSLQDVLLHKKPRLDGELGRGGYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLAKGILFWTYLCSGSVK DVDYNYGGGSSIAVLLIMERHRDLYTLKAGILFWTYLCSGSVK LPRAFERCASKOHLWNNVRRGARPERLPVPDEECWQLMEACMDG	AYFRNGDYPGEPFILHHSTSYNSKALLAFLAPLITUTSIALLUV LYKIVDHKKRSCNLDEQQELVERDDEQLMENDVEPIHADILLET YKRKIADEGRLFLAEFGSI PRVFSKFFIKEAKRPPNOKKNEYVU ILPYDYNRVELSEINGDAGSNYINASYIODFKPPRKYIAAGGPR DETVDDPWRMINEGCKATVIVWMTGEGENRNKCAEYWPSMEEGT RAPGECCCKDLTKHKRCP\DYIIQKLNIVNKKEKATGREVTHIQ FTSMPDHGVFEDPHLLLLKLRRVMAFSNFFSGFIVVHCSAGVGR TGTTIGIDAMLGGLEAENKUVUYVALRGQCLUMCQVEAQYI LIHQALVEYNQFGETEVALLSLHPYLHIMKKRDPSEPSPLEAE FQRLPSYRSWRTQHIGNQE\ENKSKRRINNYPYDYNRVELKHE LEMSKESEHDSDESSDDDDSDESEFSYINASFINSYMEP\BVMI AAQGPLKETIGDFWOMIFORKVKVIVMLTELKHGDQBICAQYWG EGKQTYTODIEVDLKDTUKSSTYTLRVFELRHSKRKDSRTYYQYQ YTNWSVEQLPABPKELISMIQVVKQLPQXNSSEGNKHHKSTPL LIHCRDGSQOTGIFCALINLLESAETEEVVDIFQVVKALRRARP GMVSTFEQVQFLYDVLASTYPAGNGQVKNNHQRDKIEFDNEVD KVKQDANCVNPIGAPEKLISMIQVVKQLPQXNSSEGNKHHKSTPL LIHCRDGSQOTGIFCALINLLESAETEEVVDIFQVVKALRRARP GMVSTFEQVQFLYDVIASTYPAGNGQVKNNHQRDKIEFDNEVD KVKQDANCVNPIGAPEKLISMIQVVKNHQRDKIEFDNEVD KVKQDANCVNPIGAPEKLISMIQVKKNHQRDKIEFDNEVD KVKQDANCVNPIGAPEKLISMIQVEKNHQRDKIEFDNEVD KVKQDANCVNPIGAPEKLISMIQVEKNHQRDKIEFDNEVD KVKQDANCVNPIGAPEKLISMIQVEKNHQRDKIEFDNEVD KVKQDANCVNPIGAPEKLISMIQVEKNHQRJCKISSHINN CGARGQOTKAGJMLVEGSEKLRHLSTFSHQVLQTTLVDAQKALN CGARGQOTKAGJMLVEGSEKLRHLSTFSHQVLQTTLVDAAKALN LVHCHCLDIFINQAFDNQRLQITFKRENSTYRKENBLYESIMN CGARGQOTKAGJMLVEGSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDNQRLQITFKREFSTYTKKENBLYESIMN CGARGQOTKAGJMLVEGSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDNQRLQITFKRESSVITR MLWEQIKGIIQRITWVSPPAITLEWRKVAQBAIESLSASKLAK SICSQFRTELNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVEK DHAPRLARLSLESSRSLQDVLLHKRPKLQGELGRGYGVVVLCDN WGGHFPCALKSVVPPDEKWNDLALEFFYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMBERHRDLYTGLKAGITLETRLQIAL DVVEGIRFHLSGGLVHADIKLIKNYLDKQNRAKITDLGPCKPEA MMSGSIVGTPHMAPELPTGKYDDNVDVYAPGILFRYICSGSVK LPEAFERCASKUHLWINNVRRGARPERLEVTDECWQLMEACNGG DPLKRPPLIGJIVOPHLOGINMRLCKS\NSEGPNRGLDDST DPLKRPPLIGJIVOPHLOGINMRLCKS\NSEGPNRGLDDST GREHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPFSTLSQDRL DAPPPAAPLPRMSGFIGVGLARAAA\GGAFRGGARRASAAP G\EDECGCRAFGCGARRACANALNITHQHVFODLRGSSVLEWWODSTGV	1			DRUGDHERVUL EVENCHTELURNGERUNG DER WEDLEN GERAUSTE
LYKIYDLHKKRSCNLDEQQELVERDDEKQLMNVEPIHADILLET YKRKIADEGRIFLAEFQSIPRVFSKFPIKEARKPFNQNKRYYU ILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPR DETVDDFWRMIWEQKATVIVWYTRCEEGNRNKCAEYWPSMEEGT RAPGECCKDLTKHKRCP\DYIIQKLMIVNKKBRATGREVTHIQ FTSWPDHGVPEDPHLLKLRRRVMAFSNFFSEFIVVHCSAGVGR GRYTGTIGIOAMLEGLEAENKVDVYGYVVKLRRQRCLWYQVEAQYI LIHQALVEYNQFGETEVINLSELHPYLHNMKKRDPPSEPSPLEAE FQRLPSYRSWRTQHIGNGE\ENKSKNENSNYIPYDYNRVPLKHE LEMSKESHDJGESSDDDSDEEFSKYINASFIMSYWKP\EVMI AAQGPLKETIGDFWQMIFQRKVKVINATELKRGDQEICAQYWG EGKQTYGDIEVDLKDTKKSSTYTLRVFELRHSKRKDSRTYVQYQ YTNNSVEQLPABPKELISMIQVVKQKLPQKNSSEGNKHHKSTPL LIHCRDGSQTGIFGCALINLLESAETEVVDIFQVVKALRKARP GMVSTFRQYQPLYDVASTYPAQNGQVKKNHNGBDKIEFDNEVD KVKQDANCVNPLGAPEKLISMIQVVKQKLPQKNSSEGNKHKKSTPL LIHCRDGSQTGIFGCALINLLESAETEVVDIFQVVKALRKARP GMVSTFRQYQPLYDVIASTYPAQNGQVKKNHNGBDKIEFDNEVD KVKQDANCVNPLGAPEKLISMIQVVKQLPQKNSSEGNKHKSTPL LYTHCHGASQTGIFTYTTYALHKDELSERDEGLGEIRKYFSFP VFFFKVPKLGSEIIDSSTRMESERSPLVYGLUDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFPMQRDLQITPKRLEYTRKKRNELYESIMN TANRKQEEMKOMIVETTITNHEELDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVOTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEGIKOITQITTHWSPPAITEWKRKVAQEAIESLSASKLAK SICSQPRTRLNSSHEAFAASLRQLEEGRGGREKETEDULRVRVK DHAPRLARLSLESRSJQDVLLHHKKPKLGGELGRGGYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFFYWRSLPKHERIVDLHG SVLDYNYGGGSSIAVLLIHERLHRDLYTGLKGGLLERGLYGGVVVLCDN WGGHFPCALKSVVPPDEKHWNDLALEFFYHRRSLPKHERIVDLHG SVLDYNYGGGSSIAVLLIHERLHRDLYTGLKAGLTLETTLQTAL DVVEGIRFLHSQGLVKRDIKKLNNVLLDKGNRAKITDLGFCKPEA MMSGSIVOTPIHMAPBLFTGKYDNSVDVYAFGILFWYICSGSVK LPBAFERCASKOHLWNNVRGARPERLEVPDEECCMQLMEACMDG	LYXIYDLHKRSCNLDEQGELVERDDEXCLMNVEPIHADILLET YKRKLADEGELFLAEFGSI PRYSKFPIKEARKPFNONKNRYVD ILFYDYNRVELSEINGDAGSNYINASYILGFKEPRKYIAAQGPR DETUDDFWRNIWEQKATUY UNVTRCEEGNRNCCAEYWFSMEGET RAFGECCKULTHKRCP, DYILGKINI TUNKKERTGREVTHIO FTSWPDHGVFEDPHLLLKLRRVNAFSNFFSGPIVVHCSAGVGR TGTYIGIDANLEGLEAENKUDVYGYVVKLRQRCLMVQVEAQYI LIHQALVENYGFGETEVNISELHFYLHMKKRUPPSFSPFLEAE FQRLPSYRSWRTCHLIGNGE LEKKSKNRNSNVIPYDDYRRVPLKHE LEMSKESEHBSDESSDDDSDSEEPSKYINASFIMSYMKPLEVHE AAQGPLKETIGDFWOMIFQRKVKIVMITELKHDQDSICAQYMG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRISKRKDSRTVYOYO YTNNSYNQLPABFRELISNIQVKKQKLPONSSSEGNHHKKSTPL LIHCRDGSQOTGIFCALLNLLESAETBEVVDIFQVKALRKARP GMVSTFEQYQFLYDDVIASTYPAQNQVKKNHQRBKIEFDNEVD KVKQDANCVWPLJADFPKLPEAFGAEGSEPTSGTEGFBHSVNGP ASPALNGGS 3 2363 DAMGCKLRRLRFTYGTQTRVSLALFGQYELVHTLVAHQGNMETI PEBBLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCOGUR PTVDVLGDLVNDFLPVITYALHKDELSERBOGLQEIRXYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEGSEKLRHLSTFSHQVLQTRLVAHQAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELVESLMN IANRKGEEMGMIVTETLNTMKERKDVIVPBNGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVOTL ERCLOSLEKSQDVSVHITSNYLKQILADATMMEKVDIVPBCGSSVTR MLMEQIKQIIQRITHWSPPATICHKNYLADATHVEVTHSGSSVTR MLMEQIKQIIQRITHWSPPATICHKNRVAQEAELSLASKLAK SICSGPRTELNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLHRRPKKRVAQEAELSLSASKLAK SICSGPRTELNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLHRPKKRNVAGEAELSLSASKLAK SICSGPRTELNSSHEAFFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLHRPKKNVAGAELSLSASKLAK SICSGPRTELNSCHARHVEVVYPDECCMQLMREACHOG MMSGSIVOTPIHMAPELFTGKYDNSVDVYAFGILFMYICSGSVK LPEAFFRCASKOHLWNNVYRGARPERLPYVDEECCMCLMBACNOG DPLKRPLLGIVOPMLOGIMNELKSN\NSDPNREGDDST 5981 1 2519 GRRHSAAMERPWGADGLSRAPAANGAGFPROGSWRRSAP GEDEECGRVEDFYNGLENALANGAGFPROGSWRRSAP GEDEECGRVEDFYNALANNTHQOVFOLRGSVSLGWODSTGV				AYFHNGDYPGEPFILHHSTSVNSKALTAGLABITIUTGTALLARI
YKRKIADEGRIFLAEFOSI PRVESKPPIKEARRPFNONKRYVD ILPYDYNRVELSEINGDAGSNYINASY IDGKEPRKYIAAQGPR DETVDDFWRMIMEQKATVI VMVTRCEEGKRNKCAEWPSMEEGT RAFGECCKDLTKHRCP\DYIIQKLINIVNKKEKATGREVTHIQ FTSWPDHGVPEDPHLLLKLRRRVINAFSNFFSGPIVVHCSAGVGR TGTYTGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQVI LIHQALVEXNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE FQRLDSYRSWRIQHIGNOE\EMKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHDSDESSDDSSEPESKYINASFIMSYWKP\EVMI AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYMG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRDSRTVYQYQ YTNNSVEQLPABPKELISMIQVVKQKLPQKNSSEGNKHHKSTPL LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQRIYDVIASTYPAQNGQVKKNNHQBDKIEFDNEVD KVKQDANCVNPLGAPEKLEMPAGGVKKNNHQBDKIEFDNEVD KVKQDANCVNPLGAPEKLEMPAGGVKKNNHQBDKIEFDNEVD KVKQDANCVNPLGAPEKLPFYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEBDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGGLUNDFLPATYLHKDELSERDEGELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRCLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLOTILVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKEMELYESLMN IANKQEBMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCTRQIQGLIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVETYFHGSSSVTR MLMEDIAQIIQTTWVSPPAITLEWKRKVAQGATESLSASKLAK SICSQPRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVYUCDN WGGHFPCALKSVVPPDEKHLGQELGRGCYGVYVLCDN WGGHFPCALKSVVPPDEKHLGQELGRGCYGVYVLCDN WGGHFPCALKSVVPPDEKHLGQELGRGCYGVYVLCDN WGGHFPCALKSVVPPDEKHLGQELGRGCYGVYVLCDN SVIDYNYGGGSSIAVLLIMERLHRDLFTYMSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLFTYMSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLFTYMSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLFTYMSLPKHERLVDLHG MMSGSIVOTPIHMAPELFTGKYDNSVDVAFGILFWYICGSSVK LPBAFERCASKOHLWNNVRRGARPERLPVFDEECMQLMEACMDG	YKRKIADEGRIFLAEFOSI FRVESKFPIKERAKYPNONKNRYVD LLPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPR RAPGECCKDLTHKRKCP\DYIJQKILIVINKEKATGREVTHIQ FTSMPDHGVVEDPHLLLKLRRRVNAFSHFSGPIVVHCSAGVGR RAPGECCKDLTHKRKCP\DYIJQKILIVINKEKATGREVTHIQ FTSMPDHGVVEDPHLLLKLRRRVNAFSHFSGPIVVHCSAGVGR TGYYIGIDAMLEGLEAENKVDVYGVVKLRRQRCLMVQVEAQYI LIHQALVEYNQFGETEVNLSELHPYLHMKKRDPPSEPSPLEAE FQRLPSYRSWRTQHIGNQP\ LENKSNNRSNNIPYDYDYNRVPLKHE LEMSKESEHDSDESSDDDSDSEPSKYINASFIMSYMKP\EVMI AAQGPLKETIGDFWOMIPQRKVKVIVMITELKHGDQSICAQYMG GGKQTYGDIEVDLKDTDKSTTIRVFELRHSKRGSRTYVGYQ YTNNSVRQLPABPKELISMIQVVKQKLPQKNSSEGNKHHKSTPL LIHCRDGSQQTGIFCALLNLLESAETEEVDIFQVVKALKARAP GMYSTFEQYQPLYDVLASTYPAQNGQVKKNHQSDKIEFDNEVD KVKQDANCVMPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAMGCKLRRLRFTYGTOTRVSLALPGQYELVHTLVAHQGNWETI PEEDLBVQENNEDAAHDLTELSEVTMHHALLQEVDVVVAPQCQLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRYFFSP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCD1FIRQAFPMQRDLQITPKRLEYTRKKENELYESLMN CGAPGGDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVBSLAND LVHCHCD1FIRQAFPMQRDLQITARAYVEVTPHSGSSVTR MLWEQIKQIIQRITUSPPAITLEWKRKVAQEAIESLSSASKLAK SICSQFRTELNSCHSAFAASLRQLEACHSGRLEKTEDLURVRK SKICSQFRTELNSSHSAFAASLRQLEACHSGRLEKTEDLURURK DHAPFILARISLESSIJODVLLHRKPKLGGELGRGQTGVVYLCDN WGGHFFCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLUTLHG SVIDNYNGGGSSIAVLLIMERLHRDLYTGLKAGLTLETELQTAL MMGGSIVGTPIHMAPELFTGKYDNSVDVVAFGILFWYICSGSVK LPEAFERGASKDHLWNNVRRGARPERLPVDEECMQLMEACHDG DLKRPLLGIVQPHMGGIMNILKCK\NSEQPNRGLDDST DPLKRPLGIJUOPHMGGIMNILKCK\NSEQPNRGLDDST DPLKRPLGIJUOPHMGGIMNILKCK\NSEQPNRGLDDST DDLKRPLLGIVOPHMGGIMNILKCK\NSEQPNRGLDDST DAPPPPAAPLPRMSGPICUSWGLRAAAN\OGAFPROGRWRRSAP GEDEECGRVRDFVAKLANNTHQRVFDLRGSVLGWDJSTGV	1			LYKIYDLHKKRSCNI.DEOOELVERDDEKOLMMVEDTUADILLET
ILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAQGPR DETVDDFWRMIWEQKATVI WAVTRCEEGNRNKCAEYWPSMEEGT RAFGECCCKDLTKHRKCP DYIJOKLNI VNKKEKATGREVTHIQ FTSWPDHGVPEDPHILLKLRRRWAFSNFFSGPIVVHCSAGVGR TGTYIGIDAMLEGLEAENKUVTGVVKLRRGRCLMVQVEAQVI LIHQALVEYNOFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE FORLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHDSDESSDDDSDESEPSKYINASFIMSYWKP\EVWI AAQGPLKETIGDFWQMIFQRKVKIVTWHITELHHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNNSVEQLPAEPKELISMIQVVKQKLPQXNSSEGNKHHKSTFL LIHCRDGSGOTGIFCALINLLESSAFTEEVVDIFQVVKALRKARP GMVSTFEQYQPLYDVIASTYPAQNGQVKKNNHQBDKIEFDNEVD KVKQDANCVNPLGAPEKLISMIQVVKQKLPQXKNNHQBDKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS 3 2363 DAWGCKLRRLRFTYGTQTRVSLALPGQVELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTHHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDBEGELGEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGODTKAGSMLVEGSEKLRHLSTFFHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKNELEYESLMN 1ANRKQEEMKDMIVETINTMKEELLDDATMBFFKDVIVENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKGILKAAYHVEVTFHSGSSVTR MLMEGIKQIIQRITWVSPPATTLEWKRKVAQGATESLASKLAK SICSQPRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLMLRVRK DHAPRLARLSLESRSLQDVVLHRRPKLGQELGRGQYGVYVLCDN WGGHFCALKSVVPPDEKHMUDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLTTGLKAGITLETRLQIAL DVVEGIRFILKSQGLVHRDIKLKNYLLDKQNRAKTDLGFCREA MMSGSIVOTPIHMAPELFTGKYDNSVDVAAFGILFWYICSSVK LPBAFERCASKOHLWNNVRRGARPERLPVFDEECMQLMEACNDG	ILPYDYNRVELSEINGDAGSNYINASYIDGKEPRKYIAAGGPR DETVDDFWRMIWEQKATVI VMYTRCEGNRNKCAEYWPSMEGGT RAPGECCCKDLTKHRKCP\DYIIQKINIVNKKKEATGREVTHIQ FTSWPDHGVFEDHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQVI LIHQALVENQFGETEVNLSELHPYLHMKKRDPPSEPSPLEAE FQRLPSYRSWRTCHIGNGE\EMSKNRNSNVIPYDYNRVPLKHE LEMSKESEHBSDESSDDDSDSEPSKYINASFIMSYMKP\EVMI AAQGPLKETIGDFWQMIFQRKVKVIVMITELKHGDQBICAQYMG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRISKRKDGRTYQYQ YTNNSVRQLPABPKELISMIQVVKQKLPQKNSSEGNKHKKSTPL LIHCRDGSQQTGIFCALLMLESSAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNQVKKNHQBDKIEFDNEUD KVKQDANCVAPLGAPEKLPEAKCQAEGSEPTSGTEGPEHSVNGP ASPALNQGS 5980 3 2363 DAMGCKLRRIRFTYGTOTRVSLLALBGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHALLQVDVVVXAPCQGLR PTVDVLGDLVNDFLEVITYALHKDELSERDEQGLQEIRKYFSFP VFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVVAPCQGLR VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL LVHCHCLDIFINQAFPMGRDLQITPKRLEYTRKKRNELYESIMN IANRKQEEMKDMIVETLINTMKEELLDDATMMEKCDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLGSLEKSQDVSVHITSNYLKQILMAAYHVEVTFHSGSSVTR MLMEQIKGIIQRITMVSPPAITLEWKKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLIRVRK MLMEQIKGIIQRITMVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLIRVRK DHAPRLARLSLESRSLQDVLHRERKPKLGQELGRGQYGVYVLCDN WGGHFFCALKSVVPPDEEHMNDLALEFHYMRSLPKHERLUTLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLITLETRLQITAL DVVEGIRFLHSGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELETGKYDNSUDVXAFGILFWYICSGSVK LPEAFERCASKOHLWNNVRRGARPERLPVFDECCMLMEACNDG DPLKRPLLGIVOPMLQGIMNLCKS\NSEQNNGLDDST 5981 1 2519 GRRHSAMMERPFRGAADGLSRWHGLGLLLLLQLLPFSTLSQDRL DAPPPPAAPLPRMSGPICVSWGLRAAAA(GAFPREGRBRRSAP G\EDBECGRVRDFVAKLANNTVRGARFRGRERRSAP	1			YKRKIADEGRLFLAEFOSIPRVFSKFPIKEARKPFNONKNRVVD
DETVDDFWRMINEQKATVIVMVTRCEEGNRNKCAEYWPSMEEGT RAFGECCKDLTKKRCP, DYIIQKLNIVNKKEKATGREVTHIQ FTSWPDHGVPEDPHLLIKLRRRVMAFSNFFSGPIVVHCSAGVGR TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQYI LIHQALVEYNJGFGTTEVNLSELHFYLHMMKKRDPPSEPSPLEAE FQRIPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHDSDESSDDDSDSEEPSKYINASFIMSYWKP\EVMI AAQQPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQVWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNNSVEQLPABPKELISMIQVVKQKLPQKNSSSEGNKHHKSTPL LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNHQBDKIEFDNEVD KVKQDANCVNPLGAPEKELISMIQVVKQKHPQKNSSEGNKHHKSTPL LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNHQBDKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPBENSVGP ASPALNQGS 3 2363 DAWGCKLRRLRFTYGTOTRVSLALPGGYELVHTLVAHQGNWBTI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPGQLR PTVDVLGDLVNDFLEVITTALHKDELSERDEQEIQEIRKYFSFP VFFRVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLTTRLVDAAKALN LVHCHCLDIFINQAFFDMCRDLQITPKRLEYTRKKBRLLYESLMN LANRKQEEMKDMIVETLNTMKEELLDDATNMEPKDVIVPENCGP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLGSLEKSQDVSVHITSNYLKQILNAAYHVEVTPHSGSSVTR MLWEQIKQIIQRITHVSPPAITLEWKRKVAQEALESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHKKKKLQGELGRGQYGVYLCDN WGGHFPCALKSVVPPDEEHKWNLLALEFYMRSLGKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLRNVLLDKKQRLTEFLTPLLQIAL DVVEGIRFLHSQGLVHRDIKLRNVLLDKKQRLTEFLTPLQIAL DVVEGIRFLHSQGLVHRDIKLRNVLLDKKGNTAKITDLGFCKPEA MMSGSIVOTPIHMAPELFTGKYDNSVDVVAFGILFWYICSGSVK LPBAFERCASKDHLWMNVRGARPERLPVFDEECWQLMEACWDG	DETVDDFWRMIWEQKATVI WWTRCEESNRNKCAEYWPSMEEGT RAPGECCKULTKHRCP\DYIJQKLNIVNKKKATGREVTHIQ FTSWPDHGVPEDPHLLKKRRWAMFSNFFSGFIVHCSAGVGR TGTTIGIDAMLEGLEBENKUVVYGYVVKLRRQRCLWYQVEAQYI LIHQALVEYNQFGETEUNLSHPYVKLRWKRDPSSEPSPLEAE FQRLPSYRSWRTQHIGNQE\ENKSKNENSNVIPYDYNRVPLKHE LEMSKESEHDSDESSEDDSDSEDEFSYINASFIMSYWKP\EVMI AQQPLKETIGDFWQMIFGRKVKVIVMLTELKHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSTYTLRVFELRHSKRKDSRTVYQYQ YTMNSVBQLFABPKELISMIQVVVKQKLPQKNSSEGNKHHKSTFL LIHCRDGSQOTG FCALLINLSEAFTEEVVD1FQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD KVXQDANCVMPLGAPBEKLPBAKEQAEGSEPTSGTEGPBHSVNGP ASPALNQGS DAWGCKLRRIRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEBBLEVQENNEDAAHDLTELEVTHHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYAHKDELSERDEGLQSIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLDLGYLSSSIHN CGAPGGDTKAQSMLVEQSEKLRRLSTFSIQVLQTTRLVDAAKALN LVHCHCLDFIROAFFMQRDLQITPKRLEYTRKKNELVESLMN LANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRGIQELISRLNQAVANKLISSVDTVLRESFVGTL ERCLGSLEKSQDVSVHITSNYLKQILNAAYHEVTPHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFTRINSSHEAFAASLRQLEEGHGGRUEKTEDLWLRVRK DHAPRLARISLESRSLQDVJLHKKPKLGGELGRGGYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFFYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERRHRDLYTGLKAGLTLETRLQTAL DVVEGIRFHSQCLVHRDIKNYLLDKKORRAKITDLGFKEPEA MMSGSIVOTPIHMAPELFTGKYDNSVDVYAPGILFWYICSGSVK LPEAFERCASKHHLWNNVERGARPERLEVFDEECMQLMEACNDG DPLKRPLLGIVQPMLGGINNFLCKS\NSEQFRRGLDDST DPLKRPLLGIVQPMLGGINNFLCKS\NSEQFRRGLDDST DPLKRPLLGIVQPMLGGINNFLCKS\NSEQFRRGLDDST DPLKRPLLGIVQPMLGGINNFLCKS\NSEQFRRGLDDST DPLKRPLLGIVQPMLGGINNFLCKS\NSEQFRRGLDDST DAPPPPAAPLPRWSGFIGVSMLSKAGAA\GGAFPRGGWRRSAP G\EDEECGKORPHYAVALANNTHQHVFDDLRGSVELSWWGDSTGV				ILPYDYNRVELSEINGDAGSNYINASYIDGFKEPRKYIAAOGPR
RAFGECCCKDLTHHKRCP\DYITQKLNIVNKKEKATGREVTHIQ FTSWPDHGVPEDPHLLLKRRVNAFSNIFSGPIVVHCSAGVGR TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQYI LIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE FQRLDSYRSWRYQHIGNQE\ENKSKNRNSNIVPYDYNRVPLKHE LEMSKESEHDSDESSDDDSDESEPSKYINASFIMSYWKP\EVMI AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQVWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNWSVEQLPABPKELISMIQOVKQKLPQKNSSSGNKHHKSTPL LIHCRDGSQOTGIFCALLNLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNHQBKISEPDNEVD KVKQDANCUNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRUSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITTALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYKQLIDLGYLSSSHWN CGAPGODTKAGSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATMMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLMLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFFCALKSVVPPDEEKHWNDLALEFHYMRSLPKHERIVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLRNVLLDKQNRARITDLGFCKPEA MMSGSIVGTPHMAPELFTGKYDNSVDVVAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRGGAPPERLPYFDEECWQLMEACMDG	RAPGECCCKDLTKHKRCP\DYIIQKLMIVNKKRATGRETTHIQ FTSMPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR TGTYIGIDAMLEGLEABNKVDVYGYVVKLRRQRCLMYQVBAQVI LIHQALWEYNGFGETEVNLSELHPYLHMMKKRDPPSEPSPLEAE FQRLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHDSDESSDDDSDSEBESKYINASFIMSYWKP\EWNI AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKKKDSRTVYQYQ YTNNSVBQLPABPKELISMIQVVKQKLPQNNSSBGNKHHKSTPL LIHCRDGSQQTGIFCALINLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQBDKIEFDNEVD KVKQDANCVMPLGAPEKLPBAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRIPFYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEBBLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFKKYKLGSEIIDSSTRRMESERSPLVRQUIDLGYLSSSHWN CGAPGQDTKAQSMLVEGSEKLRHLSTSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKENELYESISMN IANRKGEMDMIVETLNTMKEELLDDAYNMEFKDVIVENGEP VGTREIKCCIRGIQELIISHLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWYSPPAITLEWKRKVAQEAIESLSASKLAK SICSGPRTRLINSHEAFAASLRQLEAGHSGRIEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHMKPKLGGELGRGQYGVVYLCDN WGGHFFCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFHSQGLVHRDIKLRNVLLDKQNRAKITDLGPCKPEA MMSGSIVGTPIHMAPBLFTGKYDNSVDYAPGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACMDG DPLKRRLLGIVOPMLQGINNRLCKS\NESQPNRGLDBST DPLKRPLLGIVOPMLQGINNRLCKS\NESQPNRGLDBST GRRHSAAMREPRGAADGLSRWPFGGLLLLLQLLPFSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGBWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWYGGBTGV	1 .			DETVDDFWRMIWEQKATVIVMVTRCEEGNRNKCAEYWPSMEEGT
FTSWPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVHCSAGVGR TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAGYI LIHQALVEXNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE FQRLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHDSDESSDDDSDESEPSKYINASFIMSYWKP\EVMI AAQGPLKETIGDPWQMIFQRKVKVIVWLTELKHGDQBICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDGRTVYQYQ YTNMSVEQLPABPKELISMIQVVKQKLPQKNSSEGNKHHKSTPL LIHCRDGSQOTGIFCALLNLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQBKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS ASPALNQGS DAWGCKLRRLRPTYGTGTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLGEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMSERSPLYRQLIDLGFLSSSHWN CGAPSQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKRNELYESLMN IANKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISNQAVANKLISSVDYLRESFYGTL ERCLQSLEKSQDVSVNITSNYLKQILNAAYHEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQVVLLHRKPKLGQELGRGQYGVVVLCDN WGGHFPCALKSVVPPDEKHNDLALEFFYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIBFLHSGGLVHRDIKLRNYLLDKQNRAKITDLGFCKPEA MMSGSIVOTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECMQLMEACWDG	FTSMPDHGVPEDPHILLKLIRRRVNAFSNFFSGPIVVHCSAGVGR TGTYIGIDAMLEGLEAENKUVYGYVVKLRRQRCLMVQVEAQYI LIHQALVEYNOFGETEVNLSELHPYLHNKKRDPPSEPSPLEAE FORLDSYRSWRTQHLGNQE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHDSDESSDDDSDSEEPSKYINASFINSYWKP\EVWI AAQGPLKETIGDFWGMIFQRKVKVIVMLTELHHGDQELCAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTMNSVRQLPABPKELISMIQOVKQKLPQXNSSEGNKHHKSTPL LIHCRDGSOGGIFCALINLLESABTEEVVDIFQVVKALRKARP GMVSTFEQYQPLYDVIASTYPAQNGQVKKNNHQBDKIEPDNEVD KVXQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRPTYGTQTRVSLALPGQVELVHTLVAHQGNWETI PEBDLEVQENNEDAAHDLTELEVTMHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVTTYALHKDELSRRDEGELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRMSESRSPLYRQLDILDGYLSSSHUN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKNELYESIMN TANRKQEEMKDMIVETINKEELDDATNMEPKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVOTL ERCLGSLEKSQDVSVHTTSNYLKGILNAAYHVEVTPHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHNDLALAHEPHYMKSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMREHHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHAAPSLFTCKYNNSVDVYARGLIFWYICSGSVK LPBAFBCRASKOHLHWNINGARPPELDFTCKYNNSVDVYARGLIFWYICSGSVK LPBAFBCRASKOHLHWNINGARPPELDFTCKYNNSVDVYARGLIFWYICSGSVK LPBAFBCRASKOHLHWNINGARPPELDFTCKYNNSVDVYARGLIFWYICSGSVK LPBAFBCRASKOHLHWNINGARPERLPVFDEECWQLMEACWDG DPLKRPLLGIVOPMLOGIMWRLCKS\NSEQPNRGLDDST 5981 1 2519 GRRHSAAMERPWGAADGLSRYPHGLGLLLLLLLDLDFTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRSSAP G\EDEECGRVRDFVAKLANNTHQBVFDDLRGSVPLSWVGDSTGV				RAPGECCCKDLTKHKRCP\DYIIQKLNIVNKKEKATGREVTHIO
LIHQALVEYNOFGETEVNLSELHPYLHMKKRDPPSEPSPLEAE FORLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHBSDESSDDDSBEBESKYINASFIMSYMKP\EVMI AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNWSVEQLPABPKELISMIQVVKQKLPQKNSSBGNKHHKSTPL LIHCRDGSQQTGIFCALLNILLESAETBEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVTTYALHKDELSERDEGELGEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKBENELYESLMN IANRKQEEMKDMIVETINTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHTTSNYLKQILNAAYNVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAABSURQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGGELGRGQYGVVVLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLEKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQCLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVOTPIHMAPELFTGKYDNSVDVVAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRGARPPERLPVVPDEECMQLMEACWDG	LIHQALVEYNOFGETEVNILSELHFYLHMMKKRDPPSEPSPLEAE FORLPSYRSWRTCHICNOE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESHDSDESSDDSDSEBESKYINASFIMSYWKF\EVMI AAQOPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNNSVEQLPABPKELISMIQVVKQKLPQKNSSBGNKHHKSTPL LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNHQEBKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS 5980 3 2363 DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEBDLEVQENNEDAADDLTELEVTMHHALLQEVDVVVAPCQCILR PTVDVLGDLVNDFLPUITVALHKDELSERDEQEIQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRKENELYESLMN IANKQEEMKDMIVETLNTMKEELLDDATMMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFFISGSSVTR MLWEQIKQIIQRITWSPPAITLEWKRKVAQEAIESLSASKLAK SICSQPRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGGELGRGQYGVYLCDN WGGHFPCALKSVVPPDEKHMDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGIVGTPIHMAPELETIGKYDNSVDVAFGILFWYICSGSVK LPBAFFERCASKDHLWNNVRGGAPPERLPVFDEECWQLMEACWDG DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST 5981 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPFTLSQDRL DAPPPPAAPLPRWSGPIGUSUGLRAAAA\GGAFPRCGWRRSAP G\EDEECGRVRDFVAKLANNTHQHYFDDLRGSVSLSWVGDSTGV	ľ		•	FTSWPDHGVPEDPHLLLKLRRRVNAFSNFFSGPIVVHCSAGVGR
FORLPSYRSWRTQHIGNQE\ENKSKNRNSNVIPYDYNRVPLKHE LEMSKESEHDSDESSDDDSDEEPSKYINASFIMSYWKP\EVMI AAQGPLKETIGDFWQMIFQRVVKVIVMLTELKHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNWSVEQLPABPKELISMIQVVKQKLPQKNSSEGNKHKKSTPL LIHCRDGSQQTGIFCALINLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQBKIEFDNEVD KVKQDANCVMPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAANDLTELEVTMHALLQEVDVVVAPCOGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMKDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKOMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWSPPAITLEWKRKVAQEATESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK SICSGFRTRLNSSLESRSLQDVLLHRKPKKLQGELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHHDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRARITDLGFCKPEA MMSGSIVOTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRGARPERLEVFDEECWQLMEACWDG	FORLPSYRSWRTOHIGNOE VENSKNRNSNUTPYDYNRVPLKHE LEMSKESEHDSDESEDSDEDSEEFSKYINASFIMSYMKYEVMI AAQQPLKETIGDFWOMFORKVKVIVMLTELKHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKKDSRTVYQYQ YTNWSVEQLPABPKELISHIQVVKQKLPQKNSSEGNKHHKSTPL LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP GMYSTFEQYQFLYDVIASTYPAQNGQVKKNHNGBKIEFDREVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEBBLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRMBSERSPLYRQLIDLGYLSSSHWN CGAPGODTKAQSMLVEQSSKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAPDMCRDLQITPKRLETTRKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFYGTL ERCLOSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEALESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGGELGRGQYGVVYLCDN WGGHFFCALKSVVPPDEEHHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRIQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFFERCASKDHLWNNVRRGRPERLPVFDEECWQLMEACWDG DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL DAPPPPAAPLPRWSGPIGVSULSWVGDSTGV	ł			TGTYIGIDAMLEGLEAENKVDVYGYVVKLRRQRCLMVQVEAQYI
LEMSKESEHDSDESSDDDSDEEPSKYINASFIMSYWKP\EVMI AAQGPLKETIGDFWOMIFQRRVKVIVMLTELKHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTYVQYQ YTNMSVEQLPABPKELISMIQVVKQKLPQKNSSEGNKHHKSTPL LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD KVKQDANCVAPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTOTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFKVPKLGSEIIDSTRRMESSERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVVENGGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSSAKLAK SICSQFRTELNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGITLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLDKQNRAKITDLGFCKPEA MMSGSIVOTPIHAAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG	LEMSKESEHDSDESSEDDSDESEEPSKYINASFIMSYWKP\EVMI AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHIGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKREDSRTVYQYQ YTNWSVEQLPABPKELISMIQVVKQKLPQKNSSEGNKHKSTPL LIHCRDGSQOTGIFCALLINLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD KVKQDANCUNPLGAPEKLPBAKEQAEGSEPTSGTEGPBHSVNGP ASPALNQGS DAWGCKLRRPTYGTGTRVSLALPGQYELVHTLVAHQGNWETI PEBDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEGELQEIRKYRSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFFHQVLQTRLUDDAKALIN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFYGTL ERCLOSLEKSQDVSVHITSNYLKQILNAAYHVEVTPHSGSSVTR MLWEQIKQIIQRITWSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLHKRPKLGQELGRGQYGVVVLCDN WGGHFPCALKSVVPPPEKHNDLALEFTYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHKDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKWYLLDKQNRRKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG DPLKRPLLGIVOPMLQGIMNRLCKS\NSEQPNRGLDDST 1 2519 GRRHSAAMERFWGAADGLSRWPGSGLGLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLLL	f			LIHQALVEYNQFGETEVNLSELHPYLHNMKKRDPPSEPSPLEAE
AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTYYQYQ YTNWSVEQLPABPKELISMIQVVKQKLPQXNSSEGNKHHKSTPL LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQBCKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQEIQEIRYYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLHHLSTFSHQVLQTTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTELNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVVLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG	AAQGPLKETIGDFWQMIFQRKVKVIVMLTELKHGDQEICAQYWG EGKQTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNMSVEQLPABPKELISMIQVVKQKLPQKMSSEGNKHHKSTPL LIHCRDGSQQTGIFCALINLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS 5980 3 2363 DAWGCKLRRLRPTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEBDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTWKEELLDDATMMEFKDVIVPERGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLRNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECMQLMEACWDG DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST 5981 1 2519 GRRHSAAMERFWGAADGLSRWFGGGLULLLULLPFSTLSQDRL DAPPPPAAPLPRWSCPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVQBSTGV	, ,			FORLPSYRSWRTQHIGNOE\ENKSKNRNSNVIPYDYNRVPLKHE
EGKCTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTNWSVEQLPABBYKELISMIQVVKQKLPQKNSSEGNKHHKSTPL LIHCRDGSQQTGIFCALLNLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQBDKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEBLLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEGSEKLRHLSTFSHQVLQTRLVDBAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIGELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFPHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTFIHMAPELFTGKYDNSVDVVAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECMQLMEACNDG	EGKCTYGDIEVDLKDTDKSSTYTLRVFELRHSKRKDSRTVYQYQ YTMWSVEQLPABPKELISMIQVVKQKLPQKNSSBGMKHHKSTPL LIHCRDGSQOTGI FCALLINLLESAETBEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRPTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVTIYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEI IDSSTRRMESERSPLYRQLLIDIGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKENELYESLMN IANRKQEEMKOMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELI ISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAABSURQLEAGHSGRLEKTEDLWURVRK DHAPRLARLSLESRSLQDVLLHKKPKLGQELGRGQYGVVVLCDN WGGHFFCCALKSVVPPDEKHWNDLALEFHYMRSLEPHHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSGCLVHRDIKLRNVLLDKQNRAKITDLGFCKPEA MMSGSIVOTPIHMAPELFTGKYDNSVDVVAFGILFWYICSGSVK LPEAFFERCASKOHLWNNVRRGARPERLPVTDEECMQLMEACWDG DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST 1 2519 GRRHSAAMERFØGAADGLSRWPHGUGLLLLLQLLPPSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\CGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV				LEMSKESEHDSDESSDDDSDSEEPSKYINASFIMSYWKP\EVMI
YTNWSVEQLPABPKELISMIQVVKQKLPQKNSSEGNKHHKSTPL LIHCRDGSQQTGIFCALLINLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQPLYDVIASTYPAQNGQVKKNHQEDKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLFFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLBVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSHWN CGAPGQDTKAQSMLVEGSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMW IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEGIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGGFFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTFIHMAPELFTGKYDNSVDVVAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACNDG	YTNNSVEQUPABPKELISMIQVVKQKLPQKNSSBGNKHHKSTPL LIHCRDGSQOTGIFCALINLLESAETEEVVDIFQVVKALRKARPP GMVSTFEQVQFLYDVIASTYPAQNGQVKKNNHQEDKEIFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCOGLR PTVDVLGDLVNDFLPVTTYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQDQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLINTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFYGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPATTLEWKRKVAQEAIESLSASKLAK SICSGPRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVKK DHAPRLARLSLESRSLQDVLHRKPKHGGELGRGQYGVVVLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQELVHRDIKTKNVLLDKQNRAKITDLGFCKPEA MMSGSIVOTPIHWAPELFTGKYDNSVDVVAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVPDEECWQLMEACWDG DPLKRPLIGIVQPMLOGIMNRLCKS\NSEQPNRGLDDST 1 2519 GRRHSAAMERFWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV				FGYOTYCDIEUDI YDUDYCOUNT DUDE DUGGEICAQYWG
LIHCRDGSQOTGIFCALLNLLESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFPMQRDLQITPKRLEYTRKKBRELYESLMW IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIFFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPBLFTGKYDNSVDVVAFGILFMYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACNDG	LIHCRDGSQQTGIFCALLNILESAETEEVVDIFQVVKALRKARP GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQBDKIEFDNEVD KVKQDANCVMPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYRSFP VFFFKVPKLGSEIIDGSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKIRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKEMELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLMEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFMYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG DPLKRPLIGIVOPMLQGIMNRLCKS\NSEQPNRGLDDST 1 2519 GRRHSAMERPWGAADGLSRWPHGLGLLLLQLLPFSTLSQDRL DAPPPPAAPLPRMSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV				YTNWSVEOLPARDYELTSMIONUWOVI POVYCCEGOVYUWOWE
GMVSTFEQYQFLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKBNELYESLMM IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYWRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMGGSIVGTPIHMAPELFTGKYDNSVDVVAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACNDG	GMVSTFEQYOPLYDVIASTYPAQNGQVKKNNHQEDKIEFDNEVD KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCOGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQPRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLMLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHMDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLIMERLHRDLYTGKAGLTLETRLQIAL DVVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG DPLKRPLLGIVOPMLQGIMNRLCKS\NSEQPNRGLDDST 5981 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLEWWGDSTGV				LIHCRDGSOOTGIFCALLNILESAFTERWOIFOWWALDWARD
KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRIRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLBVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATMMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFFYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMGGSIVGTFIHMAPELFTGKYDNSVDVVAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACNDG	KVKQDANCVNPLGAPEKLPEAKEQAEGSEPTSGTEGPEHSVNGP ASPALNQGS DAWGCKLRRIFFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEGELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCTRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHKKPKLGGELGRGGYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG DPLKRPLIGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST 5981 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLQLLPFSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV				GMVSTFEQYOFLYDVIASTYPAONGOVKKNNHORDKIEDNEUD
ASPALNOGS DAWGCKLRRIRFTYGTOTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTFIHMAPELFTGKYDNSVDVVAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECMQLMEACNDG	ASPALNOGS DAWGCKLRRIRFTYGTOTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFTNQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATTMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQPRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGGELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFHHSQGLVHRDIKLRNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG DPLKRPLIGIVOPMLOGIMNRLCKS\NSBQPNRGLDDST 5981 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLQLLPFSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV				KVKQDANCVNPLGAPEKLPEAKEOAEGSEPTSGTEGDRUCINGD
DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLEVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVLGDLVNDFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLSSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATNMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGGELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIFFLISQGLVHRDIKLRNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVVAFGILFMYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACNDG	DAWGCKLRRLRFTYGTQTRVSLALPGQYELVHTLVAHQGNWETI PEEDLBVQENNEDAAHDLTELEVTMHHALLQEVDVVVAPCQGLR PTVDVUGDLVADFLPVITYALHKDELSERDEQELQEIRKYFSFP VFFFKVPKLGSEIIDSSTRRMESERSPLYRQLIDLGYLGSSHWN CGAPGQDTKAQSMLVEQSEKLRHLSTFSHQVLQTRLVDAAKALN LVHCHCLDIFINQAFDMQRDLQITPKRLEYTRKKENELYESLMN IANRKQEEMKDMIVETLNTMKEELLDDATMEFKDVIVPENGEP VGTREIKCCIRQIQELIISRLNQAVANKLISSVDYLRESFVGTL ERCLQSLEKSQDVSVHITSNYLKQILNAAYHVEVTFHSGSSVTR MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLINSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG DPLKRPLLGIVOPMLOGIMNRLCKS\NSEQPNRGLDDST 5981 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLLLLPFSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV			į	ASPALNQGS
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MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGGELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACNDG	MLWEQIKQIIQRITWVSPPAITLEWKRKVAQEAIESLSASKLAK SICSQPRTRLINSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG DPLKRPLLGIVQPHQGIMNRLCKS\NSEQPNRGLDDST 5981 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLQLLPPSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV				ERCLOSTEKSODASAHITANAN KATANAN MANANTANAN MA
SICSQFRTRLNSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGQELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACNDG	SICSQFRTRINSSHEAFAASLRQLEAGHSGRLEKTEDLWLRVRK DHAPRLARLSLESRSLQDVLLHRKPKLGGELGRGQYGVVYLCDN WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLRNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST 5981 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLQLLPFSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV			İ	MLWEOIKOIIORITWUS DDAITH EWYD WIR OF A TROIT
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WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG	WGGHFPCALKSVVPPDEKHWNDLALEFHYMRSLPKHERLVDLHG SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETRLQIAL DVVEGIRFLHSQGLYHRDIKLKMVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWDLMEACWDG DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV			1	DHAPRLARLSLESRSIODVIJARKERI GOELGEGOVGITUT COM
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DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDIGFCKPEA MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG	DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA MMSGSIVGTPIHMAPBLFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECMQLMEACWDG DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST 5981 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV				SVIDYNYGGGSSIAVLLIMERLHRDLYTGLKAGLTLETPIOTAL
MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG	MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK LPEAFERCASKDHLWNNVRGGAPERLPVFDEECWQLMEACWDG DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST 5981 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV	1 1			DVVEGIRFLHSQGLVHRDIKLKNVLLDKQNRAKITDLGFCKPEA
LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG	LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWQLMEACWDG DPLKRPLIGIVQPHUQGIMNRLCKS\NSBQPNRGLDDST 5981 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLQLLPFSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV				MMSGSIVGTPIHMAPELFTGKYDNSVDVYAFGILFWYICSGSVK
	DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST 5981 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV				LPEAFERCASKDHLWNNVRRGARPERLPVFDEECWOLMEACWDG
DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST	981 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLLQLLPPSTLSQDRL DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV				DPLKRPLLGIVQPMLQGIMNRLCKS\NSEQPNRGLDDST
5981 1 2519 GRRHSAAMERPWGAADGLSRWPHGLGLLLLLOLLPPSTLSODRL	DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV	5981	1	2519	GRRHSAAMERPWGAADGLSRWPHGLGLLLLLOLLPPSTLSODRI.
DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP	G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV				DAPPPPAAPLPRWSGPIGVSWGLRAAAA\GGAFPRGGRWRRSAP
G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV	ILVLTTFHVPI.VTMTFGGGKT.VDGEDVGKNEKDITTDI INDIMETE				G\EDEECGRVRDFVAKLANNTHQHVFDDLRGSVSLSWVGDSTGV
TTTT MADERAL	THE TOTAL PROPERTY OF THE PROP	. 1	1	1	ILVLTTFHVPLVIMTFGOSKLYRSEDYGKNFKDITDLINNTETE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
<u> </u>	sequence		\=possible nucleotide insertion)
			TEFGMAIGPENSGKVVLTAEVSGGSRGGRIFRSSDFAKNFVQTD LPFHPLTQMMYSPQNSDYLLALSTENGLWVSKNFGGKWEEIHKA
	1		VCLAKWGSDNTIFFTTYANGSCKADLGALELWRTSDLGKSFKTI
			GVKIYSFGLGGRFLFASVMADKDTTRRIHVSTDQGDTWSMAQLP
1			SVGQEQFYSILAANDDMVFMHVDEPGDTGFGTIFTSDDRGIVYS
			KSLDRHLYTTTGGETDFTNVTSLRGVYITSVLSEDNSIQTMITF
			DQGGRWTHLRKPENSECDATAKNKNECSLHIHASYSISQKLNVP
			MAPLSEPNAVGIVIAHGSVGDAISVMVPDVYISDDGGYSWTKML
			EGPHYYTILDSGGIIVAIEHSSRPINVIKFSTDEGQCWQTYTFT
			RDPIYFTGLASEPGARSMNISIWGFTESFLTSQWVSYTIDFKDI LERNCEEKDYTIWLAHSTDPEDYEDGCILGYKEQFLRLRKSSVC
			QNGRDYVVTKQPSICLCSLEDFLCDFGYYRPENDSKCVEOPELK
			GHDLEFCLYGREEHLTTNGYRKIPGDKCQGGVNPVREVKDLKKK
			CTSNFLSPEKQNSKSNSVPIILAIVGLMLVTVVAGVLIVKKYVC
			GGRFLVHLYSVLQQH\AEA\NGVDGVDALDTASHTNKSGYHDDS
5000		222	DEDLLE
5982	56	2316	ATRPPRGSSWCRQFSRTASAAPGRSNMLRIPVRKALVGLSKSPK
		1	GCVRTTATAASNLIEVFVDGQSVMVEPGTTVLQACEKVGMQIPR FCYHERLSVAGNCRMCLVEIEKAPKVVAACAMPVMKGWNILTNS
			EKSKKAREGVMEFLLANHPLDCPICDQGGECDLQDQSMMFGNDR
			SRFLEGKRAVEDKNIGPLVKTIMTRCIQCTRCIRFASEIAGVDD
			LGTTGRGNDMQVGTYIEKMFMSELSGNIIDICPVGALTSKPYAF
			TARPWETRKTESIDVMDAVGSNIVVSTRTGEVMRILPRMHEDIN
			BEWISDKTRFAYDGLKRQRLTEPMVRNEKGLLTYTSWEDALSRV
			AGMLQSFQGKDVAAIAGGLVDAEALVALKDLLNRVDSDTLCTEB
			VFPTAGAGTDLRSNYLLNTTIAGVEEADVVLLVGTNPRFEAPLF NARIRKSWLHNDLKVALIGSPVDLTYTYDHLGDSPKILODIASG
			SHPFSQVLKEAKKPMVVLGSSALQRNDGAAILAAVSSIAQKIRM
			TSGVTGDWKVMNILHRIASQVAALDLGYKPGVEAIRKNPPKVLF
			LLGADGGCITRQDLPKDCFIIYQGHHGDVGAPIADVILPGAAYT
İ			EKSATYVNTEGRAQQTKVAVTPPGLAREDWKIIRALSEIAGMTL
			PYDTL\DQVRNRLEEVSPNLVRYDDIEG\ANYFQQANELSKLVN
			QQLLADPLVPPQLTMKDFYMTDSISRASQTMAKCVKAVTEGAQA VEEPSIC
5983	248	1763	EARGDGGRRHRASGRRAGRGEP\AGLKSQGQRAVPKRAVARGG
			RQ\YSAAIALLEPAGSEIADDLSILYSNRAACYLKEGNCSGCIO
			DCNRALELHPFSMKPLLRRAMAYETLEQYGKAYVDYKTVLQIDC
			GLQLANDSVNRLSRILMELDGPNWREKLSLIPAVPASVPLQAWH
			PAKEMISKQAGDSSSHRQQGITDEKTFKALKEEGNQCVNDKNYK
			DALSKYSECLKINNKECAIYTNRALCYLKLCQFEEAKQDCDQAL
			QLADGNVKAFYRRALAHKGLKNYQKSLIDLNKVILLDPSIIEAK MELBEVTRLLNLKDKTAPFNKEKERRKIEIQEVNEGKEEPGRPA
			GEVSTGCLASEKGGKSSRSPEDPEKLPIAKPNNAYEFGQIINAL
			STRKDKEACAHLLAITAPKDLPMFLSNKLEGDTFLLLIQSLKNN
			LIEKDPSLVYQHLLYLSKAERFKMMLTLISKGQKELIEQLFEDL
			SDTPNNHFTLEDIQALKRQYEL
5984	755	1193	SSVCMACTYVSNLGKKQRSVSFLASGLMRVSTGPELRLHHSFVL
1			TGDVGRRICRLLVGLFTKGDTSSKRVHPFSPGPCFLLCDLARVG
			SSPKINVSPFYQN\QTSTQRSCTVFVWQRCSLVGPFQVTVFTMY FHHSLRSISRFSSG
5985	22	1408	RRVARPGTAEPAKARRTVRRGRARRDLAGAERKAGVSERGDSGR
			RRPNPSIPSAAAGMSHIQIPPGLTELLQGYTVEVLRQQPPDLVE
			FAVEYFTRLREARAPASVLPAATPRQSLGHPPPEPGPDRVADAK
1			GDSESEEDEDLEVPVPSRFNRRVSVCAETYNPDEEEEDTDPRVI
			HPKTDEQRCRLQEACKDILLFKNLDQEQLSQVLDAMFERIVKAD
			EHVIDQGDDGDNFYVIERGTYDILVTKDNQTRSVGQYDNRGSFG
1			ELALMYNTPRAATIVATSEGSLWGLDRVTFRRIIVKNNAKKRKM
			FESFIESVPLLKSLEVSERMKIVDVIGEKIYKR/DGERIITQGE
			K\ADSFYIIESGEVSILIRSRTKSNKDGGNQEVEIARCHKGQYF GELALVTNKPRAASAYAVGDVKCLVMDVQAFERLLGPCMDIMKR
	İ		NISHYEEQLVKMFGSSVDLGNLGO
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Predicted Predicted en Predicted en Predicted en Predicted en Docationing Contemporary Contempo	670	1 5 37	1 5 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7	
Sociation location corresponding corre	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cortisponding Cofreeponding Cofreeponding Cofirst Cofirs	1		· ·	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Corresponding	NO:	L		Glutamic Acid, F=Phenylalanine, G=Glycine,
To first				H=Histidine, I=Isoleucine, K=Lysine,
amino acid residue of amino acid anino acid anino acid anino acid anino acid anino acid acquence compared to the compared to t	[l.	L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence 5986 1806 484 1806 484 1806 484 1806 484 1806 484 1806 484 1806 484 1806 484 1806 484 1806 484 1806 484 1806 484 1806 484 1806 484 1806 484 1806 484 1807 5902 5902 5902 5902 5902 5902 5902 5902 5902 5902 5902 5902 5902 5902 5902 5902 5907 1806 484 5902 5907 1806 484 5902 5907 1806 484 5902 5907 1806 484 5902 5907 1806 484 5902 5907 1806 484 5902 5907 1806 484 5902 5907 1806 484 5902 5907 1806 484 5902 5907 1806 484 5902 5908 5908 1806 484 5902 5908 5908 1806 484 5902 5908 5908 1806 484 5902 5908 1806 484 5902 5908 5908 1806 484 5902 5908 5908 1806 484 5902 5908 5908 1806 484 5902 5908 5908 1806 484 5908 5908 5908 1806 484 5908 5908 5908 1806 484 5908 5908 5908 1806 5908 1806 484 5908 5908 5908 1806 484 5908 5908 5908 1806 5908 1806 484 5908 5908 5908 1806 484 5908 5908 5908 1806 484 5908 5908 5908 1806 5908 1806 484 5908 5908 5908 1806 5908 1806 5908 1806 484 5908 5908 5908 1806 5908 1806 484 5908 5908 5908 1806 484 5908 5908 5908 1806 5908 1806 5908 1806 5908 1806 484 5908 5908 1806 5908 1806 5908 1806 5908 1806 5908 1806 5908 1806 5908 1806 5908 1806 5908 1806 5908 1806 18	i		1	P=Proline, Q=Glutamine, R=Arginine,
Sequence Codon, /=possible nucleotide deletion,				S=Serine, T=Threonine, V=Valine,
Sequence				W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1806 1806 1806 1806 1806 1806 1806 1806 1806 1806 1807 1806 1806 1806 1806 1807 1806 1806 1807 1807 1806 1807			sequence	Codon, /=possible nucleotide deletion,
SPECERFORPROPPRIEGLICALMAEDGVRGSPPURSCHPMERS GLRRYTKSPLDPDSGLSCTLPHGYGGGSPDGRESLAPDASI LISNVCSIGHVAGELFGGSGLJMAEEARROGEN\AGGHSPLRS EHVYCVGSILDSFLOYVSLIFLSTEVYKLED FYGGSFTF SRKGLVLGLIGSTGRMGRMAVRGFRVAYKRIVLTMDDLGTLYG QNEMDOWMBMYGLUMDTVJEEN\HFRSFPY\DELFTKYDG VKRHTKNYDIFNKELLIJEPHLEVSMFLISVDVWKLED FYGGSFTF SRKGLVLGLIGSTGRMGRMAVRGFRVAYKRIVLTMDDLGTLYG QNEMDOWMBMYGLUMDTVJEEN\HFRSFPY\DELFTKYDG VKRHTKNYDIFNKELLIJEPHLEVSMFLISVDVWRAGNN DSDCGAFVLGYCKHLALSQPFSFTQDDMFKLRGIYKELCHCKL TV 5987 1806 484 DAMKSTSLTFHKELMGRHGGRRGLAIFENNHLSPGGGAFTGVDF SPCCRFDSPRGSPPPBERJGLIGLAIMAEDGVGRSPVDVSEDPMERD GLRRTFKSPLDPDSGLLISCTLHNGFGGGGGFDGRBFLAPPDASI LISNVCSIGHVAGEPGGSGLOFDGVGSPDYSED GLRRTFKSPLDPDSGLLISCTLHNGFGGGGGFDGRBFLAPPDASI LISNVCSIGHVAGEPGGSLGVARFRYSHVANDHLATLY GNMLDDVMMWYGDLWNDTVUER\VHFPSSFFY\DKLFKGYDG SRKGLVLGLIGSTGRMGNAWGFRYWAYKHVLTHDLGLTLYG ONMLDDVMMWYGDLWNDTVUER\VHFPSSFFY\DKLFKGYDG SRKGLVLGLIGSTGRMGNAWGFRYWAYKHVLTHDLGLTLYG ONMLDDVMMWYGDLWNDTVUER\VHFPSSFFY\DKLFKGYDG SRKGLVLGLIGSTGRMGNAWGFRYWAYKHVLTHDLGTLYG ONMLDDVMMWYGDLWNDTVUER\VHFPSSFFY\DKLFKGYDG SRKGLVLGLIGSTGRADHGVGRAYFWWARQNN DSDCGAFVLGYCKHLAKTGLARAKKRILDPHGGWGYFWAWARQNN DSDCGAFVLGYCKHLAKTGLARAKKRILDPHGGWGYFWAWARQNN DSDCGAFVLGYCKHLAKTGLARAKKRILDPHGWKGYFWAWARQNN DSDCGAFVLGYCKHLAKTGLARAKKRILDPHGWKGYFWAWARQNN DSDCGAFVLGYCKHLAKTGLARAKKRILDPHGWKGYFWAWARQNN DSDCGAFVLGYCKHLAKTGLARAKKRILDPHGWKGYFWARQNA FKXYFLGFELDHLARAKLLFGLESALARAKKRILDPHGWKGYFWARQNA PGRADHILTYGLARAKKRILDPHTALMATHTYPOGT RLDCYTYLARAKKRILDPHTALMATHALKALLARAKKRILTPHOGT ALVALPHQKRSELMPLIXYLSATTGLFGRAYGTFAGKALLARAKKRILTPHOGT ALVALPHQKRSELMPLIXYLSATTGLFGARGTATAKLSISPE NODMULAWATTSLGMGDITACHGTFTVTGAWGFKRHAVIA ACSETYRMLFVDOWHULDISANAGGCT ASSAGROTTSKALARAKKRILDPHTAGAGLAGGCAALARAK FRYCKLLEERKHLECHGCAGGAGGAGAFVKERGGGLENGGA ACSETYRMLFVDOWHULDISANAGGCT ASSAGRAGTTSKALARAKKRILDPHTAGKSCHAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA				\=possible nucleotide insertion)
GLRNTKSPLDPOSCLISCTLPNGFCGQGSDPGERSLAPDAS; LISNVCSIGHHAGENGGSLIAMBERERORKNINGSPGHPIERE ENTYCVGSILDEFLQTYVGSLIPLSTDEVVFKLEDIPQGEFSTEP SRKGLVLQLIQSGYGMFGMWAGGERVAYKRINLTHODLATLYG QNMLNIOQMBMYGGLWGTVVER\VHFRISPFY\DKLETYGYGG VERRITKNDT FYRELLIP INLEVWBRISFY\DKLETYGYGG VERRITKNDT FYRELLIP INLEVWBRISFY\DKLETYGYGG RTLNRGCPRILLIP INLEVWBLISVPURGTTTYPDSO RTLNRGCPRILLIP INLEVBRISLSVPURGTTYPDSO RTLNRGCPRILLIP INLEVBRISLSVPURGTTYPDSO RTLNRGCPRILLIP INLEVBRISLSVPURGTTYPDSO RTLNRGCPRILLIP INLEVBRISLSVPURGTTYPDSO RTLNRGCPRILLIP INLEVBRISLSVPURGTTYPDSO RTLNRGCPRILLIP INLEVBRISLSVPURGTTYPDSO RTLNRGCPRILLIP INLEVBRISLSVPURGTTYPOSCOGATTOVP SPCCRFTSPRGPPPRIGLICALMAEDGVGGPPVPSGPPMEDI GLRNTKSPLDPDSOLLSGTLPRGFGGGGGGFGRALAPFORST LISNVCSIGNFVAQELPQGSDLGMAEARRRGKKAQGGATTQVP SPCCRFTSPRGPPPRIGLICALMAEDGVGGPPVPSGPPMEDI GLRNTKSPLDPLOTY\COGNAPCAGRACHAPFORST LISNVCSIGNFVAQELPQGSDLGMAEARRRGKKAQGGATTQVP SRKGUVLGLIQSTGRPGONAVGGRVAKRHVITMOLICATIV CONLADOMBMYGGLWGTVAGGATTAGATAGATAGATAGATAGATAGATAGATAGA	5986	1806	484	DAWKSTSLTFHWKLWGRHRGRRRGLAHPKNHLSPQQGGATPQVP
LISNYCS IGOHVAQGELTQCSGLIGMAERAERGEK\AGQHSPLERE EHVTCVQSILDERLIGTY TYSSLIPLISTDEVVEKLIG PQGPSTP SRKGLVLQLIGSYGMPGNAMYGFEVAYKSHVLTINDLIGTYTY QNEMINDOVMMYGDLVMDTVPEK.VISFENSFY, KNEKTKGYDG VKRHTENVDIFNRELLIJPHLEVHSIJSVDVRERTITYTYSG RTINRECKHIAKVIQAEAVKKDLEPHGGKGKYSYKMVARGNN DSDGGAFVLQYCKHLALSGPFSFTOQDMFKLRGIYKELCHCKL TV 5987 1806 484 DAMKSTSLTPHMKLIGRHRGERKGLAHPKHLSPQOGGATPQDV SPCCRDSPROPP PBRIGLIGAHARDGVYGSS PPSGOPBMED GLRHTFKSPLDPDSGLISGTLPHOFGGSGGPGGERSLAPPDBAE GLRHTFKSPLDPDSGLISGTLPHOFGGSGGPGGERSLAPPDBAE LISNYCSIGDHVAQLEVQSDLAMBAEBARGEK\AGQUSSPLRE EHVTCVQSILDBELGTLYNGSLPASTERVEKLEDIFQQPSTD SRKGLVLQLIGGSVGMRGNAMVRGABEABRGEK\AGQUSSPLRE EHVTCVQSILDBELGTLYNGSLPASTERVEKLEDIFQQPSTD SRKGLVLQLIGGSVGMRGNAMVRGABEABRGEK\AGQUSSPLRE EHVTCVQSILDBELGTLYNGSLPASTERVEKLENDIGUPSTT SRKGLVLQLIGGSVGMRGNAMVRGABEABRGEK\AGQUSSPLRE EHVTCVQSILDBELGTLYNGSLPASTERVEKLENDIGUPSTT SRKGLVLQLIGGSVGMRGNAMVRGABEABRGEK\AGQUSSPLRE EHVTCVQSILDBELGTLYNGSLPASTERVEKLENDIGUPSTT SRKGLVLQLIGGSVGMRGNAMVRGABEABRGEK\AGQUSSPLRE EHVTCVQSILDBELGTLYNGSLPASTERVEKLENDIGUPSTT SRKGLVLQLIGGSVGMRGNAMVRGABEABRGEK\AGQUSSPLRE EHVTCVQSILDBELGTLYNGSLPASTERVEKLENDIGUPSTT SRKGLVLQLIGGSVGMRGAMVRGABEABRGERVEKTYTELSTORGERVARCH LISNYSSLUNGLUNGSGLAMBAEAGVURHARGINARA ENGARATIONAL SALENDIGUPSTTATATATATATATATATATATATATATATATATATAT				
BENTCVGSILDEFLOTY YSSLIPLISTDEWVEKLED POGGESTS SRKSLVLDLIGS (ORMENDAMORENVAYKHULTINDLIGTLY) ONMENDOWNMYGOLVMDTVPEK VSFENSFFY (DKLRITGS) VKRHTNNTD FINELLIL PIHLEVHSLIS VDWERTITTYFDSQ KTLINRECPKHIAKYLOABAYKORLDFHOGKKYYFKMWARGNN DSDCGAFFLOGVCHIALSOPES FTOOMPKLERGIYKLCKL TV DAWKSTSLTFHWILMGRIRGEREGLAHPENILSPOGGARPGVP SPCCRFDSPRGPPPPRIGLIGALMARDGAYRGS PVPSGPPRESE GLRRTDKSPLDPDSGLISCTLENDFOGGGARBERAP PDASI LISMVCSIGDHVAQGLPGGSDLGMARERAR RGEK (NOGSPLERE BHYTCVGSILDEFLOTY) VSGLIP LESTDEVVEKLEDIFQGESTAP SRKOLVLOLIGS VGRMFGHAWKGFRWAYKRHVLIMDLGTLYG ONMENDOWNMYGDLWDTVPEK VHIFRNSFFY (NKLRTKUTFDSQ KTLINRCVRHIAKYLOABAVKGRLIPHQGWKS YFKMWARGN) DSDCGAFFLOGVCHARDLAWGTVPEK (VHIFRNSFFY) (NKLRTKUTFDSQ KTLINRCVRHIAKYLOABAVKGRLIPHQGWKS YFKMWARGN) DSDCGAFFLOGVCHARDLAWGTVPEK (VHIFRNSFFY) (NKLRTKUTFDSQ KTLINRCVRHIAKYLOABAVKGRLIPHQGWKS YFKMWARGN) DSDCGAFFLOGVCHARDLAWGTVPEK (VHIFRNSFFY) (NKLRTKUTFTDSQ KTLINRCVRHIAKYLOABAVKGRLIPHQGWKS YFKMWARGN) DSDCGAFFLOGVCHARDLAWGTVERLGHTGYTH (NELLIL PHILARTHILVWMFTCRFQ RLDCTYLMGSIHPHGWILM KALLFGLFS \ABGLITGGDKYTRECHCKL TV 5988 1292 410 FKKYFLSFLGLLESSHSRDRIHNLVLMFLLATHILVWMFTCRFQ RLDCTYLMGSHFRANKANA LGTALTHNITGILLSPEH WITHOUTHSTRARKSN FSLEDFOHISKGEPYSSKYATOLLSVALANNFMQGLISVLAW LGTALTHNITGILLSPEH WITHOUTHSTARAKSLS FSLEDFOHISKGEPYSSKYATOLLSVALANNFMQGLISVLAW LGTALTHNITGILLSPEH WITHOUTHSTARAKSLSDF ANDPOHISGNVLEGLONGORGGGLCCCTFYVONWHFRAHKAVLA ACSSFYRMLEVDOKVHLDISNAGLGGVULERWTAKLSJSP NVDDVL\AVATELONDOLITACHALKSLABPATS PGGNABALAL BGGGKNAGEKVATSTISKLSQAGSTGFT IGFSRCHKSEGGQAQ SAASGAGCTEKADAPREPPYELKDDPTSGMAARABAALEESS DQEMEVFBAKGEEPOKGERGEGEGEAAPAVKGERGAPAKGENGA FFINGEGEGGKSTTLISLINLIKKRNISGRAYXGGVIH KCEBCGKFFTTGNKRHTHITTGCHOPKYHATAKLSLSPA ANGKOTEKADAPACHYTAKLSLSDF PENNNESSAGTBGGGLAGSAGAPAVKGEAAPARVUNDLISH ITTORKEY LCDKGGGFRYRODHKHHTHTGRKPY CHORGAGAPATACHYTACHYTACHYTACHYTACHYTACHYTACHYTACH				GLRWTPKSPLDPDSGLLSCTLPNGFGGQSGPEGERSLAPPDASI
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SRKGLVLOLIGSYGMMGRNAWRGFRVAYKRUTIONDIGSTUR QNMLNDOVMMYUGDLVMDTUPEK, VIFENSFFY, DKARTKGYDG VKRHTENVDIFNRELLLIPHLEVHRSLISDVRRRTITTPEGG RITLINRECKHIARVQAEAVKADLEPHQGKGKATYKAMVARGNN DSDGGAFVLQYCKHLALSQPFSTOQDMPKLRRQIYKELCHCKL TV 5987 1808 484 DAMKSTSLTPHMKLMGRHRGGRRGLAHPEKHILSPQGGGATPAPVE GCRETDSRRGPPPPBFIGLIGLAHARDGVRGSPPVEGGGAPPWED GLRHTPKSPLDPDSGLLSCTLPMGFOGGGSPRGREALAPPDASI LISNVCSIGDHVAQELFOGSDLGMAEARRGEKVAGUBSHER EHYTCVQSILDBFLLTVYGSLIFISTDEVVEKLBEDIFQGEFSTP SRKGLVLQLIQSYGMMGRAWKGFRVAYKRHYLIMDDLGTLYG (DNILMDQVMMWIGVAGDLWMDTVPEK VVEFNSFFY) CHKRKYDG VKWWTKNUDIFNKELLIPHHLEVHSLISVDVRRRTITYTPOG RITLINRECHRILAKTQAEAVKKUDLPPAGVKGFYRMYARGNN DSDCGAFVLQYCKHLALSGPFSTFOQDMPKLRRQIYKELCHCKL TV 5988 1292 410 FKXYFLSFLGLLESSHSRRIHNLVLMFLLATHNLVWMFTLGCKKLK TV EKXYFLSFLGLLESSHSRRIHNLVLMFLLATHNLVWMFTLGCKKLK FKXYFLSFLGLLESSHSRRIHNLVLMFLLATHNLVWMFTLGCKKLK FKXYFLSFLGLLESSHSRRIHNLVLMFLLATHNLVWMFTLGCKKLK FKXYFLSFLGLLESSHSRRIHNLVLMFLLATHNLVMFTLTGDKITTAG LGEVFETUVGGHILLSVALARMFMOGLYSNNAC FSTALTNLTYGILPPFIWTLLMPAILLLRYPANAFTLTFYNGT ALVMLPHQKPESIDLLSVALARMFMOGLYSNNAC BGTALTNLTYGILPPFIWTLLMPAILLLSVALARMFMOGLYSNNAC BGTALTNLTYGILPPFIWTLLMPAILLLAVALARMFMOGLYSNNAC BGTALTNLTYGILPPFIWTLLMPAILLLAVALARMFMOGLYSNNAC BGTALTNLTYGILPPFIWTLLMPAILLLAVALARMFMOGLYSNNAC BGTALTNLTYGILPPFIWTLLMPAILLLAVALARMFMOGLYSNNAC BGTALTNLTYGILPPFIWTLLMPAILLLAVALARMFMOGLYSNNAC BGTALTNLTYGILPPFIWTLLMPAILLAVALARMFMOGLYSNNAC BGTALTNLTYGILPPFIWTLLMPAILLAVALARMFMALTLTPYNGT ALGEFFKHLFVOQNOVHLDISNAAGLGOVLBRMYTAKLSLSP SSEMPHLEVOQNOVHLDISNAAGLGOVLBRMYTAKLSLSP SSEMPHLEVOQNOVHLDISNAAGLGOVLBRMYTAKLSLSP BGDKRAKERSKVATSTISSLGOAGRST DIEGRGULKEGGGAG SAASGAGTEKALADORDITTACHKSLALBAPATSPARAKATL EGSDRAACERSKVATSTISSLGOAGRST DIEGRGULKEGGGAG SAASGAGTEKALADARDFPPVELKOPOGTSGREGGGULKEGGAG SAASGAGTEKALADARDFPPVELKOPOGTSGREGGGULKEGGGAG SAASGAGTEKALADARDFPPVELKOPOGTSGREGGGULKEGG GCGLETTTGGNLKRHLÄURIGKERGEGGAGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				EHVTCVQSILDEFLQT\YGSLIPLSTDEVVEKLEDIFQQEFSTP
ONMINDOWNMYGOLVMDTVERK_VIFFENSFFY_DKLRYKEGY VKRYKTNYDIFNELLIJPHILEUPHSLISTDVTMERTITYFDSO RTIMRECKHIAKYIQABAYKORLDFHQGKKGYFKMWARQIN DSDCGAFVLQYCKHLALSQPFSFTQQDMFKLRFQTYKELCKOL TV DAWKSTSLFFHMKIMGENEGEREGLAHERNILSPQGGATFQVP SPCCRFDSBRGPPPPRIGLIGAMAEDGVRGSPPVPSGPPMEED GLRWTPKSPLDPDSGLISCTLPMGFGGSGFBGERSLAPPDSI LINNYCSIGHVAGELPGGSLGMEABEARREGK-KAGNEPLRE BHYTCVGSILDBFLQTY_YSSLIFLSTDEVVEKLEDIFQGFSTYG CNMLDDQWMMYGOLWDTVPEK\VUFFNSFFY\DKLERKUFTYFOSG RTIMRECKHIAKYIQABAYKKORLDPFAQCHKGYFKMWARQIN DSDCGAFVLQYGKHALSQPPSFTQDMFKLARFQTYRELGHKA TV SP88 1292 410 EKKYFLSFLGLLESSHSRDRIHNLVLMFLATHNLVWFTCSFG RLDCTYLMAGIMPROLINIKALLFGLFS\ARGLLTCGGNITHTOGD LQEVFTDVFGIRJ LITELEGLALGHDSGLJHVTSGRWARKS FSLEDPGISKGKEPYSSSYATDLLSVALARNFNQGLYSNVAC PGTALTNLTYGILPPTFWTLMPTSGRWARKS FSLEDPGISKGKEPYSSSYATDLLSVALARNFNQGLYSNVAC PGTALTNLTYGILPPTFWTLMPTSGRWARKS FSLEDPGISKGKEPYSSSYATDLLSVALARNFNQGLYSNVAC PGTALTNLTYGILPPTFWTLMPTJANTSGRWARKS FSLEDPGISKGKEPYSSSYATDLLSVALARNFNQGLYSNVAC PGTALTNLTYGILPPTFWTLMPTJANTSGRWARKS FSLEDPGISKGKEPYSSSYATDLLSVALARNFNQGLYSNVAC PGTALTNLTYGILPPTFWTLMPTJANTSGRWARKS FSLEDPGISKGKEPYSSSYATDLLSVALARNFNQGLYSNVAC PGTALTNLTYGILPPTFWTLMPTJANTLFYNGT ALWALFHGKDSSLAPLIKTLSATTGFGRNYIHTGOMLDEDTAE KYTQKLLELERHIRVTIQKTUNGARISGSCU-LGCHGRAN FSCEDPGHSKGKEPYSSSYATDLLSVALARNFNQGLYSNVAC PGTALTNLTYGILPPTFWTLMPTJANTLSVALARNFNQGLYSNVAC PGTALTNLTYGILPPTWTLMPTJANTLSVALARNFNQGLYSNVAC PGTALTNLTYGILPPTWTLMPTJANTLSVALARNFNQGLYSNVAC PGTALTNLTYGILFRUNGGTILAGTGGGTVATAKSULA ACSSTFMLEVQXNVAHUDISMAGLGGVLEPMTTALLSSP NVUDVILAVATELHQDGJTANGKGGLARSTGGNABALAT EGGDRAAREKVATSTISRLEQAGRSTF1GPSRUKELEGS SASAGACTEKADAPERPPVELKDDFTSGMAABLAGSS FSCEMWEPAAKGEEGKERGEGGGEGGSSTLISHTAKKSTAGATSTATTGGRWARLAT EGGDRAARGERGVCGCGGGSGREGGGGRGAGAPAYKEGGGLENGER PENNESSAGTOSQGCLGSBARGGGTGGTGGTGTGTGTY CCCCCCCCCCCCCCCCCCCCCC	1			SRKGLVLQLIQSYQRMPGNAMVRGFRVAYKRHVLTMDDLGTLYG
VKRWTENVDIPNEELLIJ PHILEVHRSLISVDVRERTITTENG RTILNRECREHIARVIQABAVKEDELPHQGKGATEVENNVARGNN DSDGGAFVLOYCRILALSGPESTOODMPKLREQIYKELCHCKL TV 5987 1806 484 DAMKSTSLTPHMKLIGERRGLAHPENNLSPQOGGATPQU SPCCRTDSREDPEPRIGLIGARMAEDGVRGS PVPSGPPMED GLRWTEKSPLDPDSCLISCTLENDFOGGGEBGERSLAPPENDL LISMVCSIGDHAGELVGSDLGMAEDGWRGSKAAQHSPLRE BHYTCVGSILDBEACT\YGGLIPLSTDEVVEKLEDIFQGESTLAPPENDL LISMVCSIGDHAGELVGSDLGMAEBAERGEK\AQGHSPLRE BHYTCVGSILDBEACT\YGGLIPLSTDEVVEKLEDIFQGESTS SRKGLVLGLIGSYQRMFGRAMVRGFRVAYKRHILMDDLGTIVG CNMLNDOVMMUTGDLWMTVDEFX\WFFNSFY\LKMRTYGYDG VKWNTKNUDIFNEELLIPHLEVHSLISVDVRRXTITYFDGO RTILNRECKHIAARVIQAEVKKOULDFAQCWKGYFKNYARGNN DSDCGAFVLOYCKHLALSGPESTOODMPKLRRQIYKELGHCKL TV 5988 1292 410 FKXYFLSFLGLESSHSRDIHNILVIMFLLATHNILWMFTCRF RLDCTYLMAGIHPNEQLIXILATICHSPANAFTTPYNGTT ALVMLFHQKPBSLILVSVANKRHYDGWITYGERXGNAKNA FSLEDPOHISKGREYSSSKYATULSVALNRHYNDMLDEDTAE KFYYGKLLELBKHIRVTIQKTINGAKLISVALNRHYNDMLDEDTAE KFYQKLLELBKHIRVTIQKTINGARLISCALLSVALNRHYNDMLDEDTAE KFYQKLLELBKHIRVTIQKTINGARLISCALLSVALNRHYNDMLDEDTAE KFYQKLLELBKHIRVTIQKTONGAGIGLICCTFFVUGWIFFANKAVLA ACSSYFKHLSVDOKOVHLDISNAAGLGQVLRMYTAKLSLSP SASSGAGTEKALDADERSPPVELKDPSGMAAABABAAALSESS SCHWEVERSAKGERGERGERGERGERGARGATGGRALAR BEGDRAACERKVATSTISSLEQAGRSTP IGFSRDLKEERGGQAQ SASASGAGTEKALDARSPP POELKERDPSGMAAABABAALSESS SCHWEUSPARKGERGKERKVATSTISSLEQAGRSTP IGFSRDLKEERGGALEGE PERSTREESAGTDSGGELGSBRGAGFFF IGFSRDLKEERGGALEGE CGCKEFTTITGMFRHIRLITHGGRAFPSGTCKKAFSSPAACK AHRKHISPLKPYGCERGCKSTRLISLINLEKGRISGEARYGRGA KCEDCGKEFTITGMFRHIRLITHGGRAFPYCERGCGKRVGS SCLAMHTRHEDITHRIKSCVSCKSTRANABALGESS COMMUTEARALARATAVTUTUVYQHAAAVABAETHTGGERFY LCCKGGGGFRAVDALBSHVKTVUQGKAGIKHLITHGGEFY LCCKGGGGFRAVDALBSHVKTVUQGKAGIKHLITHGGEFY LCCKGGGGFRAVDALBSHVKTVUQGKAGIKHLITHGGEFY LCCKGGGGFRAVGHARMAVADAGDESISSLELVRAMRPYCLU SCHOOLGARPPOONSOGGEBERVAS FSQOILAGELDNCVSIPPD MHLACPBERDKATAARMAVPAAGDESISSLELVRAMRPYCLU CSEKGGISLNEEREKLBACHLKYREVYGVVKKFORPAARAAA GSGARRIGBRKKSKERGPAACVEGVARRIBRSSRGGOTVGTETYS QUDNICARGPOORSOGGEBERVAS FSQOILAGELDNCVSIPPD MLHACPBERDKATARMAVPAAGDESISSLELVRAMRPYCLU CSEKGGISLNEEREKLBSACLLKK				QNWLNDQVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLRTKGYDG
SP87 1806 484 DAWKSTSLTFHIKLMCRIRGERGILAIPKINTYRELCHKK, TV	ļ	1	ļ	VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVRRRTITYFDSO
DSDCGAFVLQVCKHLALSQPFSTTQQDMPKLRRQIYKELCHCKL TV 1987 1806 484 DAMKSTSLTFHKKLMGRRGGRAGILHPKNHLSPQCGGATPOVP SPCCRFDSPGPPPPRICLICALAMAEDOVRGS PVPSOPPMED GLRRTPKSPLDPDSGLLSCTLPNGPGQSOPEGERSLAPPDASI LISNVCSIGHVAQLELQGSDLGMAEBERFGEK\AGGISHER EHVTCQSILDEPLTYTGSLIFLSTEVVEKHEDIFQGPSTS SRKGLVLQLIQSVGMRONAMVGGRVAYKRHVLTMDLGTLYG QNMLNDQVMRNTQDLWMTVPEK\HPFNSFTY\DKLRTKGYDG VKRWTKNVDIFNELLLIPHLEVWBSLISVDVRRRTITYFDSQ RTLNRCCKHLASQPFSSTQQDMPKLRRQIYKELCHCKL TV 5988 1292 410 EKXYFJSFLGLLESSHSEDRINNLVLMFLLATHRLUWBFTCGF RLDCYLNARG IMPNOLINITALLFGLFS\ABGILTYGDKITAG RLDCYLNARG IMPNOLINITALLFGLFS\ABGILTYGDKITAG RLDCYLNARG IMPNOLINITALLFGLFS\ABGILTYSKNAC PGTALINITYG IMPNOLINITALLFGLFS\ABGILTYGDKITAG RLDCYLNARG IMPNOLINITALLFGLFS\ABGILTYGDKITAG RAWLFHGKRESINFLLKYLSATTGFGRYITHTYKNGDLDEDTAR KFYQKLLELKHRRYTIQKTMARALGLUTTSRRARKSIN RSLSPFKHLEVYDOKYVHLDINAGLGGLGLCCTFVVVGWHFKAKAVLA ACSSYFKHLEVYDOKYVHLDINAGLGGLGLCCTFVVVGWHFKAKAVLA ACSSYFKHLEVYDOKYVHLDINAGLGGLGLCCTFVVVGWHFKAKAVLA ACSSYFKHLEVYDOKYVHLDINAGLGGLGLCCTFVVVGWHFKAKAVLA ACSSYFKHLEVYDOKYVHLDINAGLGGLGLGCTFVVGWHFKAKAVLA ACSSYFKHLEVYGOKYGLGLAGGRSTP TOPSGLLKEBEGGGAA SAASGAGTEKADARBPPPVLIKDPTSGMAABABAALGESS EQURMYEDAKGESKOKSOKGEBEGAAPAEVKEEGGQLEGGA PENENEESAGTDSQQELGSERAGAPAEVKEEGGGLEGGA PENENEESAGTDSQQELGSERAGAPAEVKEEGGGLEGGA PENENEESAGTDSQQELGSERAGAPAEVKEEGGGLHGGA PENENEESAGTDSQQELGSERAGAPAEVKEEGGGCHAGE KCCDCGREFTHTGNFKHIR HITGEKFFSCREGSKAYGSVIH KCCDCGREFTHTGNFKHIR HITGEKFFSCREGSKAYGSVIH KCCDCGREFTHTGNFKHIR HITGEKFFSCREGSKAYGSVIH KCCDCGREFTHTGNFKHIR HITGEKFFSCREGSKAYGSVIH KCCDCGREFTHUNGNFKHIR HITGEKFFSCREGSKAYGSVIH KCCDCGREFTHUNGNFKHIR HITGEKFFSCREGSKAYGSVIH KCCDCGREFTHUNGNFKHIR HITGEKFFSCREGSKAYGSVIHGG FFTSGNLKRHILRHGGREFYCCDVGGREGARTSGRACKGRTVGGSG FTTSGNLKRHILRHGGREFYCCDVGGREGARTSGRACKGRTVGGSG FTTSGNLKRHILRHGGREFYCCDVGGRAGALGERVFREGREFTHUNG SQLANHIRHDNIRPHKCSVCSKAFVAVAGDISKHII HITGEKFF LCCKGREFFRAYCKOT VKOQEBPPTHILVACDSCCDKFIDGAATAGDLETEV VKOQEBPTHILVACDSCCDKFIDGAATAGDLETEV VKOQEBPTHILVACDSCCBCKFTARRINGSSRGGVULHEEAGD SGFVSLSRLGPBLRKDLEMELINLQDETLLGTMGSYFNATH CERKIGGLANGERFTARAFTAAT				RTLNRRCPKHIAKYLOAEAVKKDRLDFHOGWKGYFKMNVARONN
5987 1806 484 DAMKSTSLTFHNKLMGRHRGRRGLAHFKNHLSPQQGGATPQVP SPCCRFOSPRGPPPPRLGLLGALMAEDGVRGSPPVPSGPPPWED GLRRFTCKFDDSGLLGCTLPWGFQGSQFPEGBSLAPPDASI LISNVCSIGDHVAQELFQGSDLGMAEGAER FOEK (AGGISPLRR EHVTCVQSILDEPLGT)YGSLIPLSTDEVVEKLEDIFQGFSTP SRKGLVGLILGSYGMMFGNAWMGGRVAYKRTHDDLGTLYG ONMLNDOVMMYGDLVMDTVPEK\VHFPNSFFY\DKLRFKGYDG VKRWTKNDIFNEELLIPHALEVWBLISLVFMDLGTLYG RTLMRRCPKHLAKYLQABAVKKDRLDPHQGWKGYFKMNVARQNN DSDCGAFVLQYCKHLALSGPFSTYQDMPKLRRGIYYKELCHCKL TV FKKYFLSFLGLESSHSRDBIHNLVLMFLLATHNLVWWFTCRFDG RLDCIYLNAGIMPNGQINTKALLFGLESVAGGLLTGSDKITAGG RLDCIYLNAGIMPNGQINTKALLFGLESVAGGLLTGSDKITAGG RLDCIYLNAGIMPNGQINTKALLFGLESVAGGLLTGSDKITAGG RLDCIYLNAGIMPNGQINTKALLFGLESVAGGLLTGSDKITAGG RLDCIYLNAGIMPNGQINTKALLFGLESVAGGLTTSSTKARSEN FSLEDFQHSKKGKFYSSSKYATDLLSVALINNFQQGLTSSNVAG PGTALTNLTYGLPFFYWTLLMPAILLLFRPANAFTLTFYRGTE ALMWFHQKRSSINDLIKUTLATTGRTNYHNFQQGTYSNVAG PGTALTNLTYGLPFFYWTLLMPAILLLFRPANAFTLTYTYGTE ALMWFHQKRSSINDLIKUTLATTGRTNYHNFQQGTYSNVAG ACSEYKHLFYDOKOVHLDISNAAGLGQVLEPMYTAKLSLSPE NVDDVL\AVATFLOMQDIITACHALKSLAEPATSPGGGARALAT EGGDKRAEBKVATSTISHEQAGRSTPIGSFBLKEERGQQAG SAASGARQTEKADAPREPPPVELKPDTTSGMAABAEAALESSS EQGMEVEPARKGEEROKGOSGEGEGAGPAWGTEKSMYGSVIH KCBCGKEFTITHONFKHIR INTHEKEPFSCESCAGFSDLKEERGQCAG SAASGARQTEKADAPREPPPVELKPDTTSGMAABAEAALESSS EQGMEVEPARKGEEROKGOSGEGEGAGPAWGTSKAGVIH KCBCGKEFTITHONFKHIR INTHEKEPFSCESCAGFSVIHANA RKHTHSPLKPVGCEGCGKSYRLISLLINKKRHSGEARVRCD CGKLFTTSGNLKRHQLHYSGEBERGGAGABVCSVIH KCBCGKFFTHINFNSKHIR HITTGERFSFCEGCKAFSDFAACK AHKKHTSPLKPVGCEGCGKSYRLISLLINKKRHSGEARVRCD CGKLFTTSGNLKRHLRHDNIRHKCSVCSKAFVNVODLSKHIIINTGERFS SQLANHIRHIDNIRHKCSVCSKAFVNVODLSKHIIINTGAGGAG FTTSGNLKRHLRHDNIRHKCSVCSKAFVNVODLSKHIIINTGAGAG FKPCQCVMCGKAFTQASSLLAHVRQAGAIKLHGEGSGSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLRAGISKA VKOVGEBPPTHIIJACDSGGGKKLADASLAGHTTAAQALM FGTDADFYQOYGFGGTBFAGAQVLQAGGLVFRPRDAGGQDALE TSTTAPECPPPAE 5990 2 4700 FGGGPDSGGGARGSGWGSRSQAPYGTLGAUSGGCVLLHEEAGD SGVVSLSRGLISHSENDESSPSPFETESSKYLFRAQPKYTLI CESKEGGISINSEKLDSACLLKPPEVVSPVPKPCDGVPANAAA GSGYARKKRKKSKEQPAACVEGYARRLRSSSRQGSVLETVIST QVDNLGKCPOREDGKKRGARAR				DSDCGAFVLQYCKHLALSOPFSFTOODMPKLRROIYKELCHCKI.
SPCCRPDSPRGPPPPRIGILGALMARDGVRGSFPVPSGPPMEND GLRNTPKSPLDPDSGLISCTLPNNFGGGSGPEGREKALPDASI LISNVCSIGDBVAQELFGGSSLOMABEARRGEK\AGGHSPLAR EHVTCVQSILDEFLGT\YGSLIPLSTDEVVEKLEDIFQGETSTP SRKGLVLQLIGSVGRNFGRAVVGRFRAVVLTMDLGTLYG ONMINDQVMNNYGGLVMDTVPEK\VHFPNSFFY\DKLRTKGYDG VKRHTKNVID INKELLIP HILEVHNSLIVDVBRATITYPDSO RTINRCFKHLAKYLQAEAVKKDRLDFHQGKGVFRMNVARONN DSDCGAFVLQVYCKHLALSQPFSFTQDMFKLRGIVYKLCICKL TV FKKYFLSFLGLLESSHSRDRIHNLVUMFLLATHNLVWMFTCRFQ RLDCIYLNAGIMNPQGLNIKALLFGLFS\ABGILTTGDKTTADG LQEVFSTDVFGHFILTRELEPLLCHSDNPSQLIVTSSRNAKSN FSLEDFOGISKKEKPYSSSKATDLLSVALNFOQGLYSNVAC PGTALTNLTYGILPPFINTLIMPAILLIRFPANAFTLTPYNGTE ALVULFHQKFSINPLIKYLSATTGGRNTPQGGLYSNVAC PGTALTNLTYGILPPFINTLIMPAILLIRFPANAFTLTPYNGTE ALVULFHQKFSINPLIKYLSATTGGRNTPQGGLYSNVAC PGTALTNLTYGILPPFINTLIMPAILLIRFPANAFTLTPYNGTE ALVULFHQKFSINPLIKYLSATTGGRNTPQGGLYSNVAC PGTALTNLTYGILPPFINTLIMPAILLIRFPANAFTLTPYNGTE ALVULFHQKFSINPLIKYLSATTGGRNTPQGGLYSNVAC PGTALTNLTYGILPPFINTLIMPAILLIRFPANAFTLTPYNGTE ALVULFHQKFSINPLIKYLSATTGGRNTPQGGLYSNVAC PGTALTNLTYGILPPFINTLIMPAILLIRFPANAFTLTPYNGTE ALVULFHQKFSINPLIKYLSATTGGRNTPQGGTSNAALST EGGDKRAVERSENJENISTALSATTORGGVLEFMYTTAKLSISPE NVDDVI\AVATFILQMDDITACHAKSLAEPATSPGGRAALLAT EGGDKRAVERSKVATSTLERELGAGRSTT JGGSRALLAT EGGDKRAVERSKVATSTLERELGAGRSTT JGGSRALLAT EGGDKRAVERSKVATSTLERELGAGRSTT JGGSRALLAT EGGDKRAVERSKVATSTLERELGAGRSTT JGGSRALLAT EGGDKRAVERSKVATSTLERELGAGRST JGGSRALLAT EGGDKRAVERSKVATSTLERELGAGRST JGGSRALLAT EGGDKRAVERSKVATSTLERELGAGRST JGGSRALLAT EGGDKRAVERSKVATSTLERELGAGRST JGGSRALLAT EGGDKRAVERSKVATSTLERELGAGRST JGGSRALLERERAYGSVL KCDGCKFTTTIONKRHIR HINGGEPEVELCHOPSFADALCKARGLUC GEKLFTTSGNIKRHLHRIHGHENFEGSKAFSDPTSKMRHLE THDTDKEHKCPHCDKKFNQVGNIKAHKKHIHADGELKCRECGKQ FTTSGNIKRHLHRIHGHENFEGSKAFSDPTSKMRHLE THDTDKEHKCPHCDKKFNQVGNIKAHKKHIHADGELKCRECGKQ FTTSGNIKRHLHRHHNNIRPHKCSVCSKAFVNVGJOLKSHTYNLHTGALAM VKOVGEBPHTHILYACDSCOSKFLDANAVATADETSVLKREJISKA VKOVGEBPHTHILYACDSCOSKFLDANAVATADETSVLKREJISKA VKOVGEBPHTHILYACDSCOSKFLDANAVATADETSVLKREJISKA VKOVGEBPHTHLIVACDSCOSKFLDANAVATADLERSPKNDALLE LITHASLEDBLIGGERMSLIPGSSGLLUKYBRYVEROMPR				
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GLRYTKSPLDPDSGLISCTLPNDFGQGGPGGREAPDENS, LISNVCS IGDRIVAQEIP, GOGGSLORMAEBARPOKK, AGGRSLRE BHUTCUQSI LIDEPLQTI, YGSLIPLSTDEVUEKLEDIFQQEPSTP SRKGLVUQLIQSYQRMPGNAWNGFRVAYKRHUTUNDLUGTLYG QNMINDQWMNYGGLWMDTVPEK, VHEFRYSFY YDKLRYKGYCG VKRWTKNVDIFNKELLIT HILEVHNSLISUDVRATTITYPDSG RTINRCYKHTAYYLQAEAVKKORLDPJGKYFYFWAYKARQNN DSDCGAFVLQYCKKILAISQPFSTQOMPKLRRQIYKELCHCKL TV 5988 1292 410 FKXYFLSFLGLESSISGRRIHNLVIMFILATHILWWFTCCFQ RLDCIYLNAGIMPNPQLNIKALLFGLFS\ABGLITYGDKITADG LQEVFSTDVFGHFILITELBFLLCHSDMPSQLIWTSSKNARKSN FSLEDPGHSKKEPYSSSKYATDLISVALNNINNQGLYSNVAC PGTALTNLTYGILPPSHWTLMPAILLIFFANAFTLTPYNGTE ALWALPHQKPSSINPLIKYLSATTGGRNYIMTQKDLDEDTAE KFYQKLLELEKHRVVIQKTMONARLSGCI HEMYTAGLISSPE NVDDVL\AVATFLQMDDI ITACHAKSLAEAFSTPGGNARALAT EGGDKRAKERKYATSTLSVALNNINNGQLYSNVAC PGTALTNLTYGILPPSHWTLMPAILLIFFANAFTLTPYNGTE ALWALPHQKPSSINPLIKYLSATTGGRNYIMTQKDLDEDTAE KFYQKLLELEKHRVVIQKTVANQARLSGCI HAMPOPHSGCI HAMPOPHSGNALEKHRVATUKATAGLSVPHKARAVLA ACSSYFKMLFVQDKDVVHLDISTRAGLGQVLEMTYTAGLSISSP NVDDVL\AVATFLQMDDI ITACHAKSLAEAFSTPGGNARALAT EGGDKRAKERKVATSTLSRLEQAGRSTP IGGSBDLKERGGQAQ SAASGAGTERADAREPPYDVELKDPPTSGGNABAEBAALSESS EQEMEVEPARRGEEGOKROEGSBEBGAGPARVKEGSGLINGRA PERNNERSSATTSGGGIGERGARGLAGGTVGCKSGCOK GRENNERGGGAAGACK AHEKTHS PLRPYGCEEGGKSVFLISLINLRKRHSGSRAVGCH CGGLFTTSGGNLRKHLIHTSGERFSYCOTYCGRSFSDPTSKMRHLE THITDKEHKCPHCDKKFNQVGNIKAHLKIHADGILKREGGGA FTTSGGNLRKHLIHTSGERFYVCHCRGCKRFVQG SGLANHIHMLNITRHKGVCSCAFVYONGGASFSDPTSKMRHLE THITDKEHKCPHCDKKFNQVGNIKAHLKIHADGILKREGGGA SGLANHIHMINTRPHKCSVCSKAFVNONGARATLAGILKA VKQVGBEDPNTHLITACDSGGKFLDANSLAGNIKHTTAGALM VKQVGBEDPNTHLITACDSGGKFLDANSLAGNIKHTTAGALM VKQVGBEDPNTHLITACDSGGKFLDANSLAGNIKHTTAGALM VKQVGBEDPNTHLITACDSGGKFLDANSLAGNIKHTTAGALM VKQVGBGFPPAGA VKQVGBGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG				
LISNVCSIGDHYAGELFOGSDLOMAERARROSEK/AGOSEPLER BHYTCVGSILDERICTY/SILPLESTBEVEKLEDTFOGEPSTB SRKGLVLQLIGSYGRMEGRAWYRGFRAYKHVLTMDDLGTLYG ONMINDOWMYGDLAWDYDEK/VHFPNSFFY/DKLRTKGYDG VKRWTKNVDIFNKELLIPIHLEVHRSLISTDVRRRTITYFDSG RTIMRCPRHTAKYLQAEAVKKORLDFHQGWKGYFRWAYAQNN DSDCGAFVLQYCKHLALS/GPSFTTQOMPEKLRGYIYKELGICKL TV S988 1292 410 FKXYFLSFLGLLESSHSRDRIHNLVLMFILATHNLVWMFTCRFC RLDCIYLNAGIMPNPQLNIKALLFGLFS\ASGLLTGGKLTTAGG LQFVFETDVPGHPILLREBLELCHSDNIFTSRNAKSN FSLEDFOHSKKKEPYSSSXYATDLLSVALNRNPNQGGLYSNVAC PGTALTNLTYGILPPFIWTILMFAILLRFFANAFTLTYNGFE ALWEFHGKPSSINPLIKYLSATTGGRRNYIMTQKNDLDEDTAE KFYQKLLELEKHIRVTIQKTDNQARLSGSCI AMPFPHSSHINPLIKYLSATTGGRRNYIMTQKNDLDEDTAE KFYQKLLELEKHIRVTIQKTDNQARLSGSCI AMPFPHSGNVAFFLGMONGGGLGLCCTFVVDGVHFKAHKAVLA ACSSYFKMLFYDQKDVVHLDISNAAGLGQVLEFMYTAKLSLSPE NVDDVL\AVAFFLQMDDITACHALSLSAGAGAGVLEFMYTAKLSLSPE NVDDVL\AVAFFLQMDDITACHALSLSAGAGAGAGAFAFROEBSAGAGAS SAASGAGTERADAPEDPPVELKPDDPTSGMAABAGAGA SAASGAGTERADAPEDPPVELKPDDPTSGMAABAGAGS PENNEBSAGTDSGGELGSEAAGLRSGTYGDRTESKAYGSVH KCBCCKEFTITIONFKRHIRHGSKEPTSCRCSKAFSDPAACK AHEKHISPLRPYGCEECKSYRLISLINLRKRKHSSEARVRCDL CGKLFTTSGNIKRHQLVISGEFPYCQTVCGHCRGCKGAFTDAACK AHEKHISPLRPYGCEECKSYRLISLINLRKRKHSSEARVRCDL CGKLFTTSGNIKHRHJRHSGEEPYCTCHCORPDALQPHVRIHTG EKCQCVWCGKAFTQASSLIAHVRQHTGEKPYVCTECGKRPYQS SQLANHIRHIDNIRPHKCSVCKSKAFAVNYGDLSKGHITHTGEKPY VODMYTLATERALAATAVYQLTVVPYGAAVTADETEVLKASISKA VKOVEEDPITHILIYACDSCOKPLDANISHITAGALWH FOTDADFYQQYGFGGTWPAGQVLQAGELVFRPDGAEGQPALAE TSTAPECPPPAE 5990 2 4700 FGFGPDSGGGARSSKGGRSQAYGTLGAVSGGQVLLHEEAGD SGFVSLSRLGPSLRDKDLEMBELMLQDETLLGTMGSYNDALISI LIEDGSGLGSEVENSLPPDFSNDFSPSPSPSSFRSPRSR PRMGGSPPRQORDGEEEEVASFSGGILAGELDNCVSSIPPDF MHLACPEEEDKATAARMAVYAGDESISSALQLEHPRYCLDAALISI LIEDGSGLGSEVENSLPPDFSNDFSPSPSPSSPSPTSKMFTSCL LTHLSSLEDELGGGPODLTT.PGGCVVLEIVGQAATAGDLETPV VVGVSPGPPPAL 5990 2 4700 FGFGPDSGGGARSSKGGRSQAYGTLGAVSGGQVLLHEEAGD SGFVSLSRLGPSLRDKDLEMBELMLQDETLLGTMGSYNDALISI LEEDGGLGSCFFATAGRAWAYAGAGBSISTSSPLANDALISI LCEKGGLSLANSEKLDSACLLKPERVYEPVVPKEPONPANAA GSGPARKGRKKSKSDAACVGVARRRSSSGGSTVOTETTS QVDNLQKQPOELQKESGPLQKKKPGAA]		
BHYTCVQSILDEFICT\YQSILPISTDEVVEKLEDIFQQEFSTP SRKGLVLQILQISYQRMPGAMYGREFAYADILATINADIQGTLYG ONMLNDQWANNYGGUWDTVDEX\VHFPNSFFY\DKLRTKGYDG VKRWTKNYDI FNKELLI I PIHLEVHWSLISUDVRRTTITYPDSG RTLNRCRFRH:AKYLQARAVKKRDLDFIQGKGYFKMWYARQNN DSDCGAFVLQYCKHLALSQPFSFTQDMFKLRRQIYKELGICKL TV 5988 1292 410 FKXYFLSFLGLESSHSRDRIHNLVUMFLLATINLVWMFCRFC LQEVFSTDVPGHFILLRELEPLLCHSDNPSQLIWTSSRNARKSN FSLDCYTLNAG MYMPQLAIN KALLPGLIPS\AGGLITGGKITADG LQEVFSTDVPGHFILLRELEPLLCHSDNPSQLIWTSSRNARKSN FSLDCYTHNAG MYMPQLAIN KALLPGLIPS\AGGLITGGKITADG LQEVFSTDVPGHFILLRELEPLLCHSDNPSQLIWTSSRNARKSN FSLDCYHNAG HYMPQLAIN KALLPGLIPS\AGGLITGGKITADG LQEVFSTDVPGHFILLRELEPLLCHSDNPSQLIWTSSRNARKSN FSLDCYHNGHERPRINLIYSLSATTGGRNYIMTQKMDLDEDTAE KYPQKLLELEKHRIVIYGKTNOARLISGST ALMWEPKQKEPYSSKYATILISVALNRINNOQGLISNNAR FYPGKLELEKHRIVIYGKTNOARLISGST ALMWEPKQKEPSLEHRIVIYGKOVUHLDISNAGLIQOVLEHNYTAKLSLSP NVDDUL\AVATFLOMQDIITACHALKSLAEPATSPGGNABALAT EGGDKRAXEKVATSTLSRLEQAGRSTPIGGSBDLKERGGQAQ SAASGAGTEKADAREPPVELKDDPTSGMAABELBALISES EQEMEVEPARKGEEGKRQESQEBGARQHASVERGGGLENGEA PERNNERSSATTSGGGLEGSBARGLISGYDTSGMAABELBALISES EQEMEVEPARKGEEGKRQESQEBGARQHASVERGGGLENGEA PERNNERSSATTSGGGLEGSBARGLISGYDTSGMAABELBALISES CGKLFTTSGNLKRHQLVHSGEKFYLGTCGCKSKFYUGS SQLANHIRHMIRHSGERFYLCHORGPADPGALQRIVRHING EKCCCVWCGKBFTGASSLIAHVRQHTGEKFYVCCERCKRFYUG SQLANHIRHMIRHSGERFYLCHORGPADPGALQRIVRHING EKCCVVCGKBFTGASSLIAHVRQHTGEKFYVCCERCKRFYUG SQLANHIRHMIRHSGERFYLCHORGPADPGALQRIVRHING EKCCVVCGKBFTGASSLIAHVRQHTGEKFYVCCERCKRFYUG SQLANHIRHDNIRPHKCSVCSKAFVNOGGRGAIKILEPEGGSFSVVT VDDMYTLATEALAATAVTOJTVVPVGAAVTADETEVLKAEISKA VKQVQBEDPNTHILYACDSGCKFILDANSALGHVRIHTGADLM FOTDADFYQQYGGGTWBAGQVLQAGELVFRPRDGABGQPALAE ESTAPACFPPAB 5990 2 4700 FGFGFDSGGGRGSSGKGSRSGAPFYTLIAVSGGGVLLHEEAGD FFGGGLGSVENSHAPPSSR FREGGLIAGRELINCOSYBDPP MHACPEEBBKATABABMAVPAAGDESISSLEVEAWHPYCLPN LTHLASLEDELGGCPPDLTLPGGCVVLEIVGQAATAGLETVIS VVRQVSPCRPFVLLDDSLEFTSSALQLLMFTLLEFTSSALLVEAWHPYCLPN LTHLASLEDELGGCPPDLTLTPGGCVVLEIVGGAATAGENSFN LCESKGGSFAKEGRLDAYFRANGFSALLLKTHUSAGAS PMYDSVLADGSSPLOUGKGKFRAMARAMAALENSSFN LCESKGGSFAKEGRLDLYFRLDGSSTLEV	1	1		LISNVCSIGDHVAOELFOGSDLGMAFFAFFBGFK\ AGOUGHT DE
SRKGLVLQLIQSYQRM@SNAWQGFRVAYKRHULMDDLGTLYG QNMLNDQVNMYMGGLWDMTYPEK\UPEFFY\DKIGYDG VKRMTKNVDIPMKSLLLIPJHLEVBWSLISVDVRRTITYFDGQ RTLNRRCPKHIAKYLQAEAVKURGLDPHQCWKGYFKMYARQNN DSDCGAFVLQVCKHLALSQPFSFTQDMPKLRRQTYRELCHCKL TV FKKYFLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWMFTCFFC RLDCIYLNAGIMPKPQLNIKALLFGLFS\ABGLLTGDK1FAKA LQEVFETDVYGHFILIRELEPLLCHSDNPSQLIWTSSRNARKSN FSLEDFQHSKKRPYSSSKYATDLLSVALRRWFNQQGLYSNVAC PGTALTNLTYGILDPFIWTLLMPAILLLRFPANAFTLTPYNGTE ALWULFHQKPSSLMPLIKKISATTGFRYNIMTQKMDLDEDTAE KFYQKLLELEKHRVTIQKTDNQARLGGSCL AMPFQHSOFVLEGLNQRQCLGLLCDCTFVVDGVHFKAHKAVLA ACSSYFKMLFVDQXDVVHLDISNAAGIGGVLEPMTTAKLSLSPE NVDDVL\AVAFFLMMODIITACHALKSLAEPAFSGGNARALAT EGGDKRAKEKVANSTISLBCAGRSTPGVKEGGGQAQ SAASGAEQTEKADAPREPPPVELKPDTSGMAARALASESS EOMEWEFARKGEERGKOREOEBEERGAPWKEGGGQAQ SAASGAEQTEKADAPREPPPVELKPDTSGMAARALASESS EOMEWEFARKGEERGKOREOEBEERGAPWKEGGGAQ SAASGAEQTEKADAPREPPPVELKPDTSGMAARALASESS EOMEMEPARKGEERGKOREOEBEERGAPWKEGGGAQ SAASGAEQTEKADAPREPPPVELKPDTSGMAARALASESS EOMEMEPARKGEERGKOREOEBEERGAPWKEGGGAQ SAASGAEQTEKADAPREPPPVELKPDTSGMAARALASESS EOMEMEPARKGEERGKOREOEBEERGAPWKEGGGAQ SAASGAEQTEKADAPREPPPVELKPDTSGMAARALASESS EOMEMEPARKGEERGKOREOEBEERGAPWKEGGGAQ SAASGAEQTEKADAPREPPPVELKPDTSGMAARALASESS EOMEMEPARKGEERGKOREOEBEERGAPWKEGGGAQ SAASGAEQTEKADAPREPPPVELKPDTSGMAARALASESS EOMEMEPARKGERGAPWARGASCHONGA AHEKTHSPLRYGGEGGARGARGARGARVERGGAQLAGRAVEHING KCEDCOKEFTTSGNLKRRQLVHSGERFYQCDYGGSFSPTSKMRHLE THOTDKERKKCHCDKKPQVUNGAGRAVRODESKHILTHTGEKPY LCDKCGRGFNNVDNLRSHVKTVHGGKAGIKLLADGFLKCRGRCFYQG SQLAMHIRHHDNIRPIKCSVCSKAFNVODLSKHILTHTGEKPY LCDKCGRGFNNVDNLRSHVKTVHGGKAGIKLLADGFLKCRGSKFYQG SQLAMHIRHHDNIRPIKCSVCSKAFNVODLSKHILTHTGEKPY LCDKCGRGFNNVDNLRSHVKTVHGGKAGIKLLADGFLVCRGRAFQG SQLAKSHILRHDNIRPIKCSVCSKAFNVODLSKHILTHTGEKPY LCDKCGRGFNNVDNLRSHVKTVHGGKAGIKLIKEPERGEGEVSVTT VDMVTLATATALATATATATATATATATATATATATATATATA	i			EHVTCVOSILDEFLOT\YGSLIPLSTDEVVEKLEDIFOOEFSTD
ONMENDOWNINT GERELLI PHILEWING SUPWRRITTY PDSO VKRWTKNVDI PKKELLI PHILEWING SUPWRRITTY PDSO RTLMRCPHIAKYLQAEAVKKORLDPHQGKGYFKMNVARQIN DSDCGAFYLQYCKHLALSOPFSFTQOMPKLRRQTYKELCHCKL TV 5988 1292 410 FKXYFLSFLGLLESSHSRDRIHILVLMFLLATHILVWMFTCRFG RLDCIYLMAG IMPROLUIN KALIFOLSY-\ABGULTOGKITAICA LQEVFETDVFGHFILIRELEPLLCHSDNPSQLIWTSSRNARKSN FSLEDPQHISKKKEPYSSSKYATÜLLSVALMNIPROQGLYSINVAC PGTALTINLTYGLIPPFIWILMPALLIYAFNANFTLTPYINGTE ALWULFHQKPSSLMPLIKVLSATTOFGRNYIMTQKMDLDEDTAE KYPQKLLELEKHIRVITQINDPALSGSCI 5989 194 2610 AMDFFQHSQHVLEQLNQQRQLGLLCDCTFVVDGVHFKAHKAVLA ACSSYFKMLFVDQKOVHUDISINAAGLGQVLEFMTAKLSLSPS VNDDVL\AVATFLQMDJITACHALKSLAEPATSPGGNARLAT EGGDKRAKSEKVATSTLSILEQAGRSTP 1GPSGDLKEERGGQAQ SAASGAGTCEKADAPREP PPVELKEPGMAABAEBAALSESS EQEMEVE PARKGEEEQKEQEEGGAGPAEVKEEGGGLENGA PEENEMEESAGTDSGGELGSEARGLRSGTYGGRTESKAYGSVIH KCEBCOKEFTTITONFKHIRTHTGEKEPTYCOKGRAFABAEBAALSESS EQEMEVE PARKGEEEQKEQEEGGAGPAEVKEEGGGLENGAA PEENEMESSAGTDSGGELGSEARGLRSGTYGGRTESKAYGSVIH KCEBCOKEFTTITONFKHIRTHTGHEKPYVCERGCKSKASTSPAACK AHEKTIS PLRPYGGEEGGKSYRLI SILINLRKKRHSGEARVRCD CGGKLPTTSGNLKRHQLVHGSGEFYOCKGRSFSDDTSKMRHLE THDTDKEHKCPHCDKKFNQVUNLKAHLKH HADGEJKCRECKKQ FTTSGNLKRHLRI HISGEKPYVCHCRGKRFYOCS SQLANHIRHHDIN RPHKCSVCSKAFAVVODLSKHI II HTGEKPY LCDKCGGFGFNEVDILLESHVKTVHQGKAG IK ILLEPEEGSEVSVYT VDDMVTLATEALAATAVTQLTVVPVGAATTADETEVLKAEISKA VKQVGEEDPNTHLIYACDSCGBK/LDANSLAGHVHITTAGALVM FOTDADFYOQYGGGGTWPAGGVULAGELVYFRPROGAEGQPALAE TSFTAPECPPPAE FGFGPDSGGGARGSGWGSSGARSTQAPYGTLGAVSGGEQVILHEEAGD SGFVSLSRLIGPSIRNDLEMBEIMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVENSLDDPSMDFSFPFLETSSPKLPSMRPRSR PRHGGSPPTQOSTGGEEEEEVAFFSGULAGELDINCVSSI IPPOP MHLACPEEEDKATAABMAVPAAGDESISSLEELVRAHPYCLIP LTHLASLEDELQEQPDDLTIPEGCVVLETVGAATAGDDLETPV VVRQVSPPRPVULDUSLETSSALQLUMTLESSTEAAVFUTL CSEKEGLSLNSEEKKLDSACLLKFREVVEFVUFVERPGOPPPANAAP GSGPARKGRKKKSKEGPAACCGVARRESSRGGGTVGTEVTS QVDNLQKGPOPELVRLAGGVVVDGVUFVERPGOPPPANAAP GSGPARKGRKKKSKEGPAACCGVARRESSRGGGTVGTEVTS QVDNLQKGPOPEVLAGGVVVDGVUFDAGATSSSELVEPLPA				SRKGLVLOLIOSYORMPGNAMVRGFRVAVKRHVLTMDDLCTLVC
VKRWTKNVDI PNKELLLI PIHLEVENSLI SUVDKRATITYPDSQ RTIMRCFENHIAKYLQARAVKKORLDPHQOWKGYPKMVARQNN DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL TV FKYYFLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWMFTCRFC RLDCIYLNAG IMPNPQLNIKALIFGLPS\ABGILTGGKTANDA LOEVFETDVFGHFLIRELEPLLCHSDQLLWTSSRNARKSN FSLEDFOHSKKKEPYSSSKYATDLLSVALNRNFNQQGLYSNVAC PGTALTNLTYGILPPFIWTLLMPAILLLRFPANAFTLTPYNGTE ALMWLPHQKPSSLNPLIKYLSATTOFGNYIHTQMCDLDEDTAE KFYQKLLELEKHIRVTIQKTDNQARLSGSCL AMPPFOHSHOWLEGLNORQKJCELLGCTFVVDGVHFKAHKAVLA ACSSYFKMLFVDQKDVVHLDISNAGLGGQULGFMYTAKLSLSPE NVDDVL\AVATFLQMQDIITACHALKSLAEPTSGGNARALAT EGGDRRAKEEKVATSTLSRLEQAGRSTP IOPSRDLKEERGGQAQ SAASGAEQTEKADAPREPPPVELKPDTSGMAARAEAALSESS EQEMEVEPARKGEERGKGEOEGEEGAPVKGEGSQLEGLRGA PERNENESSAGTDGGCLGSRARGLRSGTYGDRTSSKAYGSVIH KCEDCAKFTTTGNFKRNLIKHITGKFPYGCRSKAYGSVIH KCEDCAKFTTTGNFKRNLIKHITHTGKFPYSCRCSKAFSDPAACK AHEKTHSPLKPYGCECGKSTRLISLINLRKKRHSGEARVRCED CGKLFTTSGNLKRRQLVHSGEKPYCCTYGGSFSDPTSKMRHLE THOTDKEINKCHCHKNYQVGNLKAHLHADGFLKCRECGKQ FTTSGNLKRHLRHSGEKPYCCTHCORQPADGALQRIVKHTMG EKPCCVOWGGAPTOASSLLAHVQCHTGSKPYVCTERCGKRPYQS SQLANHIRHHDNIRPHKCSVCSKAFNVODLSKHITITHTGEKPY LCDKCGGFPNRVDNLRSHVKTVHQGKAGIKLHEPEGSEVSVTT VDDMYTLATEALARTAVTLOTVVPVGAGGLIKLEPEGSEVSVTT VDDMYTLATEALARTAVTLOTVVPVGAGGLINGELDGGAGGQPALLAE TSPTAPECPPDAE 5990 2 4700 FGFGFDSGGGARGSGWGSRSQAPYGTLGAVSGGGQVLLHEEAGD SGFVSLSRLGFSLRNDLEMEELMLQDGFLLGFMOASSLIS LIEDFGSLGFVRNLDDLEMEELMLQDGFLLGFMOASILS LIEDFGSLGFVRNLDDLEMEELMLQDGFLLGFMOASILS LIEDFGSLGFVRNLDDLEMEELMLQDGFLLGFMOASILS LIEDFGSLGFVRNLDDLEMEELMLQDGFLLGFMOASILS LIEDFGSLGFVRNLDDLEMEELMLQDGFLLGFMOASILS LIEDFGSLGFVRNLDDLETSSALQLHKFLSSTEALWFVLL CCSKRGLSLRSGERVBSLDFDSWDFSFPSFLETSSPKLFSMRPRSR PRHGGSPPPQONSDGREEEEVASFSGJGLGLDNCVSS IPDPP MHLACPEEEDKATAAEMAVPAAGDES ISSLSELVRAMHPYCLPN LTHLASLEDBLQGCPDDLTLJEGGCVVLEUVGGAATAGDDLETPV VWRQVSGPOPRPVLLIDSLETTSSALQLHTESSTEALWFVTL CCSKRGLSLRSERKLDSACLLKRPEVVEPVVVKEPGNPPANAAP GSGPARKKKSKEGDFAACGGVARKSTSSELVEPLPA PMYDSVEADPTAVGPULAGGVVDGFULDLASTSSELLEPLPA PMYDSVEADPTAVGPULAGGVVDGFULDLASTSSELLEPLPA				ONWLNDOVMNMYGDLVMDTVPEK\VHFFNSFFY\DKLPTKGVDG
RTIMRRCPKHIAKYLQABAVKKORLDPHQGWKYFKMVARQNN DSDGGAFVLQYCKHLALSQPFSFTQQDMPKLRRQYYKELCHCKL TV FKKYPLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWMFTCRPQ RLDCIYLNAGIMPNPQLNIKALLIFGJFS\ABGLITQGDKITADG LQBYFSTDVPGHFILIRELBPLLCHSDNSSQLIWTSSRNARKSN FSLEDFOHSKGKEPYSSKYATDLLSVALNRNPNQQGIYSNVAC PGTALTNLTYGILPPFWTLLMFALLLRFPANAFTLTPYNGTE ALWWLFHQKPBSLMPLIKYLSATTGGRNYUTMTQKMDLDEDTAE KFYCKLLELEKHIRVTTQKTNDQARLGSGCI LMWLFHQKPBSLMPLIKYLSATTGGRNYUTMTQKMDLDEDTAE KFYCKLLELEKHIRVTTQKTNDQARLGSGCI ACSEYFKMLFVDQKDVVHLDISNAGILGQVLEFMYTAKLSLSPE NVDDVL\AWATFLOMQDIITACHALKSLAEPATSPGGNARALAT EGGDKRAKERVATSTLISRLEQAGRSTFIGSPGDLKERGGQAQ SAASGAGGTEKADAPREPPPVELKPDPTSGMAAREBRALSESS EQEMEVEPARKGEEGQKEQEEGEGAGPAVKEEGSQLENGEA PEENENEESAGTDSGQLEGSEARGLRSGTYGDRTESKAYGSV'H KCEDCGKEFTHTGMFKHRIRIHTGEFPSCRECKARSPDRACK AHEKTISPLKPYGCEEGKSYRLISLLNIKKRHSGEARYRCED CGKLFTSGNLKRHQUHSGERPYCQDYGGSFSDDTSKMPKLE THDTDKEHKCPHCDKKRNQWBLKAHLKIHIADGPLKCRECGKQ FTTSGNLKRHLGHISGEKPYCCHCQRSFADPGAQRHWRIHTG EKCQCVMGKRPTQASSLIAHVGRTGEKPYVCERGKRFVQS SQLANHIRHHDNIRPHKCSVCSKAFVNVODLSKHIITHTGERY LCDKCGRGFNRVDHLAESHVXTVHQGKGAIKILDPEBGSEVSVUT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQEEDPNTHILIYACDSCGKFLOANSLAQHVRIHTAQALVM FOTDADPYQQYGGGTPAPAGQVLQGKGAIKILDPEBGSEVSVUT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQEEDPNTHILIYACDSCGKFLYARSCAGGPALLAE TSFTAPECPPPAE 5990 2 4700 FGFOFDSGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD SGFVSLSRLGPSLRDKDLEMEELMLQDETLLGTMGSYMBASLIS LIEDFSSLGEVEMSLPPPSSFLETSSFKLPSMRPPRSR PRHQGSPPPAKGEREEEVASFELTSSFKLPSMRPPKSR PRHGGSPPPQSRSGEEEVASFELTSSFKLPSMRPPKSR PRHGGSPPPPQGRSGEEEVASFELTSSFKLPSMRPPKSR PRHGGSPPPPQGRSGEEEVASFELTSSSRQATATGDTLEPTY CCEKEGLSLNSEEELDSACLLKPREVVEPVOPKEPONPPANAAP GSGPARKGRKKKSEGPLALVERSSRGQOTLAGELDNCVSSITPPY MHLACPEBEDKATARMAVPARGDESISSLSELVPAMHPYCLPN LTHLASLEDELQEQPDDLTLPEGCVVLEINGSSRGQTVATTETTS QUUNLQKQPQEELQKSGPLACVEGVARKRASSRGARASPKNT	1			VKRWTKNVDIFNKELLLIPIHLEVHWSLISVDVPPRTTTVFDGO
DSDCGAFVLQYCKHLALSQPFSFTQQDMPKLRRQIYKELCHCKL TU FKKYFLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWWFTCRFQ RLDCIYLNAG IMPNPQLNI KALLFGLFS \ASELLTQGENTTAGG LQEVFETDVFGIFF LIFEBEPLLCHSDNSQLIWTGSRNARKSN FSLEDFOHSKGKEPYSSSKYATDLLSVALNRNPNQQGLYSNVAC PGTALTNLTYGILPPFIWTLIMPAILLIRFPANAFTLTPYNGTE ALWUFHQKPBSLHPLIKYLSATTGFGRNYIMTQKMDLBOTAE KFYQKLLELEKHIRVTIQKTDNQARLSGSCI AMPPPONSOPULGELDQCGCLGLCDCTPVUDGVHFKAHKAVLA ACSEYFKMLFVDQKDVVHLDISNAGLGQVLEFMYTAKLSLSPE NVDDVL\AVATFLQMQDIITACHALKSLAEPATSPGONABALAT EGGDKRAKEEKVATSTLSFLEQAGRFJGSTYGDRTESKAYGSVH KCEDCGKEFTHTGNFKHIRIHTGEKPFSCESCKAFSDPAACK AHEKTISPLKPYGGEGGGSYRLISLALIRKKRNSGEARYRCED CGKLFTTSGNLKKHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE THDTKEHKCPHCDKKRNQVGBUKAHLKHLADGPLKCECCKQ FTTSGNLKHHLGVHSGEKPYVQCDYCGRSFSDPTSKMRHLE THDTKEHKCPHCDKKRNQVGBUKAHLKHLADGPLKCECCKQ FTTSGNLKHRHDNIRPHKCSVCSKAFVNVGDLSKHIIHTGEKPY LCDKCGRGFNRVDNLRSHWKTVHQGKAGIKLLEPEEGSSEVSVVT VDDMVILATEALAATAVTQLTVPVGAAVTADETEVLKAEISKA VKOVGEDPNTHILIYACDSGCDKFLDANSLAQHVHTHTG EKPCQCVMGGKAPTQASSLIAHVQCHTGEKPYVCERGGKEPVQS SQLANHIRHDNIRPHKCSVCSKAFVNVGDLSKHIIHTGERPY LCDKCGRGFNRVDNLRSHWKTVHQGKAGIKLLEPEEGSSEVSVVT VDDMVILATEALAATAVTQLTVPVGAAVTADETEVLKAEISKA VKOVGEDPNTHILIYACDSGCOKFLDANSLAQHVH HTAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPDGAEGGPALAE TSTAPECPPPAE 5990 2 4700 FGFGPDSGGGARGSGGGRSGQAPYGTLGAVSGGEQVLLHEEAGD SGFVSLSRLGPSLRDKDLEMELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSWDPSPPSPSRLFTSSPKLPSKRPFRSR PRMGGSPPPOQRSGEEEEVASFSGQILAGELDNCVSSIPDFP MHLACPEEDKATAARMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQDDDLTHJPEGVELVQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKBGLSLNSEEKLDSACLLKFREVVEPVVYEPQNPPANAAP GSGNARKGKKKSKEGPDAACVEGVARRIRASSSGOGTVTTETTS QVDNLQKQPQPELQKKSGPLACVEGVARRIRASSSGOGTVTTETTS QVDNLQKQPPEELQKKSGPLACVEGVARRIRASSSGOGTVTTETTS QVDNLQKQPQPELQKKSGPLACVEGVARRIRASSSGOGTVTTETTS QVDNLQKGPPEELQKAGRPACVEGVARRIRASSSGOGTVTTETTS QVDNLQKGPPEELQKAGRPACVEGVARRIRASSSGOGTVTTETTS QVDNLQKGPPEELQKAGRPACVEGVARRIRASSSGOGTVTTETTS QVDNLQKGPPEELQKAGRPACVEGVARRIRASSSGOGTVTTETTS QVDNLQKGPPEELQKAGRPALAGEPLAGARAAAALBENSSPAN LERSAGGSPAKEDPLAUGPLA	1			RTLNRRCPKHIAKYLOAEAVKKDRLDFHOGWKGYFKMNYAPONN
5988 1292 410 FKXYFLSFLGLLESSHSRDRIHNLVLMFLLATHNLVWWFTCRFQ RLDCIYLNAGIMPNPQLNIKALLFGLFS\ABGLLT\COBKITAGG LQEVFETDVFGHFILIRELEPLLCHSDNESQLIWTSSRNARKSN FSLEDFOHSKGKEPYSSSKYATULSVALNNFNQGGLYSNVAC PGTALTNLTYGLIPPFIWTLLBVALNNFNYQGGLYSNVAC PGTALTNLTYGLLPFIWTLLMFAILLLEVALNNFNYQGGLYSNVAC PGTALTNLTYGLLPFIWTLLMFAILLLEVALNNFNYQGGLYSNVAC PGTALTNLTYGLPFIWTLLMFAILLLEVALNNFNYQGGLYSNVAC PGTALVMLFFQKPESLNPLIKYLSATTGFGRNYIMTQKMDLDDTAE KFYQKLLELEKHIRVTTQKTDNQARLSGSCL AMPFPCHSQHVLEQLNQQRQLGLLCDCTFVVUGYHFKAHKAVLA ACSEYFKMLFVDQNOVHLDISNAGQVLEFWHYAKLSLSFE NVUDVL\AVATFLQMQDITTACHALKSLAEPATSPGGNAEALAT EGGDKRAKEKVATSTLSRLEQAGRSTFIGSFROLKEERGGQAQ SAASGAEQTEKADAPREPPFVELKDPTTSGMAAALABAALSESS EQEMEVEPARKGEEROKEQEEGEEGAGFAFVKEGGGLENBEA PERNEMEESAGTDSGQELGSEARAGTVGDPTGSKAYGSVIH KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDFAACK AHEKTHSPLKFYGCEEGGKSYRLISLLMIRKRHSGEAFYRCED CGKLFTTSGNLKRHQUHSGEKFYCQCVCGSSFSDPTSKMRHLE THDTDKEHKCPHCDKKFNQVGNLKAHLKHHADGPLKCRECCKQ FTTSGNLKRHQUHSGEKFYVCERGGKRFVQS SQLANHIRHHDNIRPHKCSVCSKAFVNYGDLSKHIIHTGEKPY LCDKCGGFGNRVDNLRSHWXTVHQGKGGIKTLEPERGSEVSVVT VDDMVTLATEALAATAVTQLTVPVGNAVTADETEVLKAEISKA VKQVQEEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM FOTDADFYQQYGGGTWPAGQVLQAGELVFRPRGRAGGPALAE TSFTAPECPPPAE 5990 2 4700 FGFGPDSGGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEERGD SGFVSLSRLGPSLRKDLEMEELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPDFSWDFSPPSFLETSSFKLPSMRPPRSR PRRGGSPPPQGSTGBEEEEVASFLIAGSSINGSTVLSPIPP MHLACPEEEDKATAARMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELGEGPDDLTT-PERGCVVLEIVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAPVRVTI CSEKEGLSLNSEEKLDSACLLKFREVVEPVVPREPONPPANAAP GSGVARKGKKKSKEGPLALKFRSSSRGGSTVGTFETTS QUDNLQKQPQEELQKKSGPLACVENTARLSSSRGGSTVGTFETTS QUDNLQKQPGEPLQKKSGPLACVENTARLSSSRGGSTVGTFETTS QUDNLQKGPPREPLARGPPLLYPKLATGTVFPTPTPHLSLVDVSAQAS PMPVDSVEAPDPTANGEVLAGGPVLDGAATGTTPTPTPTHSLVDVSAQAS PMPVDSVEAPDPTANGEVLAGGPVLDGLATAGTDDLEASSELVEPLPA				DSDCGAFVLOYCKHLALSOPFSFTOODMDKT.PROTVKRLCUCVI
S988 1292 410				
RLDCIYLNAGIMPNPQLAIKALLFGLFS\ABGLLTQGDKITADG LQBVFETDVPGHFILIRBLEPLLCISDNPSQLIWTSSRNARKSN FSLEDPCHSKGKEPYSSKYATDLLSVALNRINPNQGLYSNVAC PGTALTNLTYGILPPFIWTLIMPAILLIRFANNAFTITFYNGTE ALWULFPQKPBSLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAE KFYQKLLELEKHIRVTIQKTDNQARLSGSCI 5989 194 2610 AMPPCHSORVLEQUNQQRQLGLLCDCTYVDGWFFKAHKAVLA ACSSYFMILFVOLKDVHULDISNAAGIGQVLEMYTTAKLSLSPE NVDDVL\AVATFLONQDIITACHALKSLAEPATSPGGNARALAT EGGDRKAKEEKVATSTLSRLEQAGRSTY 1GPSRDLKEERGGQAQ SAASGAEQTEKADAPREPPPVELYBDTSGMAAARAEAALSESS EQEMEVEPARKGEEGKBGEBGEBGAGPAEVKEEGSQLENGEA PEENENESAGTDSRGELSBARGLRSGTYORTESKAYGSVIH KCEDCGKETTHTGNYKRHIRITHGEKPFSCRECSKAFSDPAACK AHEKTISPLKPYGCEECKSVRLISLINLKKKHSGEARYRCED CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE THDTDKEHKCPHCDKKFNQVGNKAHLKIHLAGPLKCRECGKQ FTTSGNLKRHLRHINGERPYVCHCGRGFADFALAGRHVRINTG EKPCQCWGGKAFTQASSLIAHVQHTGERPYVCERCGKRPVQS SQLANHIRHHDNIRPHKCSVCSKAFWVGDLSKHIIHTGERPY LCDKCGRGFNRVDNLRSIVKTVHQGKAGIKILIPPEEGSSVSVVT VDDMVTLATEALAATAVTQTAVQAAVTADETSULKAEISKA VKQVQEEDPNTHILYACDSCGDKFLDANSLAQHVRIHTAQALVM FQTDADFYQQYGPGGTWBAGQVLQAGELVFRPRDGAEGQPALAE TSFTAFECPPPBE 5990 2 4700 FGPGPDSGGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD SGFVSLSRLIGPSLRDKDLEMELMLQDETILGTMGSYMBASLIS LIEDFGSLGEVEMSLPPSWDFSPFSFETSSFKLFSKRENGENFORM PRWGQSPPPQORSDGEBEEEVASFSGQILAGELDNCVSSIPDFP MHLACPEBEDKATAARMAPAADESISSLSLVRAMHPYCLPN VVRQVSPGFRPVLLDDSLETSSALQLLMPPLESETEAAVRVTL CSEKEGLSLNSEEKLDSACLLKPREVVEPVKEPGNFPARAAF GSQRARKGRKKKSKEQPAACVEGVYARELRSSSRGGSTVGTEVTT QVNNLQKGPGELQKESGPLQGKGKFRAMARAWAAALENSSFKN LERSAGGSSPAKEGPLDLYRLADTIQTNTPTHLSLVDSAQAS PMYDDSVEADPTAVGPVLAGFUVPUFDGLUDLASTSSELVEPLPA	5988	1292	410	FKKYFLSFLGLLESSHSRDRIHNI,VI,MFLJ,ATHNI,VWWFTCDFC
LQEVFETDVPGHFILIRELEPLLCHSDNPSQLINTSSRNARKSN FSLEDFQHSKGKEPYSSSKYATDLLSVALNRNPNQQGLYSNVAC PGTALTNLTYG LLPPFIWTLLMPAILLLRPPANAFTLTPYNGTE ALWALPFQKPSSINPLIKYLSATTGFGRNYIMTQKMDLDEDTAE KFYQKLLELEKHIRVTIQKTDNQARLSGSCL 5989 194 2610 AMPFQHSQHVLEQLNQQRQLGLCDCTFVVDGVHFKAHKAVLA ACSEYFKMLFVDQKDVVHLDISNAAGLGQVLERWYTAKLSLSPE NVDDVL\AVATFLQMQDIITACHALKSLAEPATSPGGNARALAT EGGDKRAKEEKVATSTLGRLEQAGRSTPIGPSRDLKEERGGQAQ SAASGAEQTEKADAPREPPPVELKPDFTSGMAAAEAEAALSESS EQEMEVEPARKGEEEQKEQEEGEEGAGPAEVKEEGSQLEMGEA PEENEMEESAGTDSQELGSEARGLRGGTGDRTESKAYGSVIH KCEDCCKEFTHTGNNFKRHIRTHTGEKFPSCRECSKAFSDPACK AHEKTHSPLKPYGCEECGKSYRLISLINLRKKRHSGEARYRCED CGKLFTTSGNLKRHCLVHSGEKPYQCTYCGRSFSDPTSKMRHLE THDTDKEHKCPHCDKKFRQVGNLKAHLKIHLAGPLKCEECKQ FTTSGNLKRHLRHSGEKPYVCIHCQRGFADPGALQRHVRIHTG EKPCQCVMGGKAFTQASSLIAHVQQHTGEKPYVCERCGKRFVQS SQLANNIRHHDNIRPHKCSVCSKAFVWVGDLSKHIIIHTGERPY LCDKCGGFDRYDDHLRSIVKYTUNVQPVGRAVTADETEVLKAEISKA VKQVQEEDPNTHILVACDSCDKFAJOANSLAGNVRIHTAQALVM FQTDADPYQQYGGGTWPAGQVLQAGELVFRPRDGAEGQPALAE TSPTAPECPPPAE 5990 2 4700 FGFGPDSGGGARGSGWGSRSQAPYGTLGAVSGGQOVLLHEERGD SGFVSLSRLGPBLRKDLEMEELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWRPFRSR PRWGSPPPQORSGEEEEEVAFSGGILAGGLDNCVSSIPDPP MHLACPEEDKATAAEMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQFDDLITLPEGCVVLETVGQAATAGDDLEIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKEQPAACVEGVYARLRSSSRQGSTVGTEVTTS QVDNLQKQPQEELQKESGPLQGKKPRAMARWAAALENSSPKN LERSAGQSSPARGGRLAKESTSSLOLLMPTHLESETEAAPKSTTTS QVDNLQKQPQEELQKESGPLQGKKPRAMARWAAALBNSSPKN LERSAGQSSPARGGPLDLYPKLADTIQTNTPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGFUVPUPGLOUNDLASTSSELVEPLPA			·	RLDCIYLNAGIMPNPOLNIKALLEGI.ES\ARGLITOCDKITADO
FSLEDFOHSKGKEPYSSSKYATDLLSVALNRRNPNQGLYSNVAC PGTALTMITYGILPPFIWTLIMPAILLIRFPANAFTITPYNGTE ALVWLFHQKPESLNPLIKYLSATTGGRNYIMTQKMDLDEDTAE KFYQKLLELEKHTRVTIQKTDNQARLGGSCL AMDPPOHSGPIVLEQLNQQRQLGLLDCTTFVVDGVHFKAHKAVLA ACSEYFKMLFVDQKDVHLDISNAAGLGQVLERMYTAKLSLSPE NVDDVL\AVATFLQMQDITTACHALKSLAEPATSPGGNARALAT EGGDKRAKEEKVATSTILSLAGARSTPIPGSPDLKEERGQAQ SAASGAEQTEKADAPREPPPVELKPDPTSGMAABEAEAALSESS EQEMEVEPARKGEERGKEQEEGEGEGABAEVKEEGSQLENGEA PEENEMESSASTDSGGELGSARLIKSGTYGDRTESKAYGSVIH KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK AHEKTHSPLKPYGCEECGKSYRLISLLNLRKKRHSGERSYRCED CGKLFTTSGNLKRHQLVHSGEYPQCDYGGRSFDPTSKRAFLE THDTDKEHKCPHCDKKFNQVGNLKAHLKHHADGPLKCRECGKQ FTTSGNLKRHLRHIBGEKPYVCHCQRGPADPGALQRRVRHINTG EKPCQCVMCGKAPTQASSLIAHVQHTGEKEPVCERCGKREFVQS SQLANHIRHIDNIRPHKCSVCSKAFVNVGDLSKHIIHTGEKPY LCDKCGRGFNRVDNLRSHVKTVHQGKAGIKILEPEEGSEVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQEEDPNTHLLYACDSCGDKFLDANSLAGHVRIHTAQALVM FQTDADFYQQYGPGGTWPAGQVLQAGELVFRPRGABGQPALAE TSSTAPECPPPAB 5990 2 4700 FGFGPDSGGGARSSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD SGFVSLSRLGPSLRDKDLEMEELHQDETLLGTMGSYMDASLIS LLIEDFGSLEEVEMSLPDPSWDPSPSFLETSSPKLJFSMRPPRSR FRWGGSPPPQGNSDGBEEEVASFSGQLLAGELDNCVSSIPDPF MHLACPBEEDKATAABAMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLBDELQEQPDDLTLPEGCVVLEIVQQAATAGDDLSIPV VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKEGLSLNSEEKLDSACLLKRFEVEVPVPVPKPQNPPANAAP GSQRARKGKKKSKQPAACVEGVARRLRSSSRQGSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGRPRAMARAMAALENSSPKN LERSAQGSSPAKKKKKSRQPAACVEGVARRLRSSSRQGSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGRPRAMARAMAAALENSSPKN LERSAQGSSPAKGKKSKSRQPAACVEGVARRLRSSSRQGSTVGTEVTS QVDNLQKQPQEELQKEGPLQGKGRPRAMARAMAALENSSPKN LERSAQGSSPAKGRKKSKRQPAACVEGVARRLRSSSRQGSTVGTEVTS QVDNLQKQPQEELQKEGPLQGKGRPRAMARAMAALENSSPKN				LOEVFETDVFGHFILIRELEPLICHSDNPSOLIWTSSDNAPKON
PGTALTHLTYGILPPFIWTLLMPAILLLRPPANAPTLTPYNGTE ALWWLFHQKPSINPLIKYLSATTGGRNYIMTQKMDLDEDTAE KFYQKLLELEKHTRVTIQKTDNQARLSGSCL 5989 194 2610 AMDPPOHSGHVLEGLNQQKGLGLLCDCTFVVDGVHFKAHKAVLA ACSEYFKMLFVQQKDVVHLDISNAAGLGQVLEFMYTAKLSLSPE NVDDVL\AVATFLQMQDITTACHALKSLAEPATSPGGNABALAT EGGDKRAKEEKVATSTLSKLEQAGRSTPIGPSRDLKEERGGQAQ SAASGAEQTEKADAPREPPPVELKEDPTSGMAAAEALAETSE EQEMEVEPARKGEEGKEQEEGEEGAGPAEVKEEGGQLENGEA PEENEMEESAGTDSGGGLGSEAGGRSGTYGDRTESKAYGSVIH KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK AHEKTISPLKPYGCEECGKSYKLISLLNINKKRHSGEARYRCED CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE THDTDKEHKCPHCDKKFNQVGNLKAHLKHIADGPLKCRECGKQ FTTSGNLKRHRIHGSEKPYVCTHCQRGFADGALQRRWINTG EKPQCVMCGKAFTQASSLLAHVRQHTGEKPYVCTECGKRFVQS SQLANHIRHHDNIRPHKCSVCSKAFVNDDLSKHILHTGEKPYV LCDKCGRGRNVDNLRSHVKTVHQGKAGIKILEPEEGSESVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQEDDPNTHLLYACDSCGDKFLDANSLAQHVRIHTAQALVM FQTDADPYQQYGFGGTWPAGQVLQAGELVFRPRDGAEGGPALAE TSPTAPECPPPAE 5990 2 4700 FGGFDSSGGARGSGGRSGAPYGTLGAVSGGGQVLLHEEAGD SGFVSLSRLGFSLRNKDLEMEELMLQDETLLGTMGSYMDASLIS LIEDFGSLGEVEMSLPDPSWDFSPPSFLETSSPKLPSWRPPRSR PRWGSPPPQRSDGEEEEEVASFSGQILAGELUVRAMHPYCLPN LTHLASLEDELQEQPDDLTLPEGCVVLEIVQAATAGDDLEIPV VVRQVSPGRPPVLLDDSLETSSALQLLMPTLESSTEAAVPKVTL CSEKEGLISLNSEKLLDSACLLKPREVVPPVVPKEPQNPPANAAP GSQRAKGRKKKSKEQPAACVEGYARRLRSSSRQGSTVGTEVTS QVDNLQKQPQEELQKESGPLQQKGRPRAWARAMAALENSSPKN LERSAGQSSPAKEGPLALYPRIPLTSLSTSELLVBAAS PMPVDSVEADPTAVGPVLAGFOPPOLDALSTSSELVEPLPA		•	'	FSLEDFOHSKGKEPYSSSKYATDLLSVALNRNFNOOGLVSNVAC
ALWALFIQKESLNPLIKYLSATTGFGRNYIMTQKMDLDEDTAE KFYQKLLELEKHIRVTIQKTDNQARLSGSCU AMDFPQHSQHVLEQLNQQRQLGLLCDCTFVVDGVMFKAHKAVLA ACSEYFMLFVDQKDVVHLDISNAAGLGQVLEFMYTAKLSLSPE NVDDVL\AVATFLQMQDIITACHALKSLAEPATSPGGNABALAT EGGDKRAKEKEVATSTISHERQAGRSTPIGPSRDLKEERGGQAQ SAASGAEQTEKADAPREPPPVELKPDPTSGMAAAEAEAALGESS EQEMEVEPARKGEEEQKQEEQEEEGAGPABVKEEGSQLENGEA PEENEMEESASTDSGQELGSEARGLRSGTYGDRTESKAYGSVIH KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK AHEKTHSPLRPYGGEEGKSYRLISLINIRKKRHSGERRYPCCD CGKLFTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE THDTDKEHKCPHCDKKFNQVGNLKAHLKIHTADGPLKCRECGKQ FTTSGNLKRHQLVHSGEKPYQCDYCGRSFSDPTSKMRHLE EKPQCVMCGKAPTQASSLIAHVRQHTGEKPYVCERCGKRYVQS SQLANHIRHHDNIRPHKCSVCSKAFVWGDLSKHIITHTGEKPY LCDKCGRGFNRVDNLRSHVKTVHQGKAGIKILEPEEGSEVSVVT VDDMVILATEALAATAVTQLTVVPVGAVTADETEVLKAEISKA VKQVQEEDPNTHLIYACDSCDKFLDANSLAQHVRIHTAQALVM FQTDADPYQQYGPGGTWPAGQVLQAGELVFRPRDGAEGQPALAE TSSTAPECPPPAE 5990 2 4700 FGPGPDSGGARGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD SGFVSLSRLGPSLRDKDLEMEELMLQDETLLGTMQSYMDASLIS LIEDFGSLGEVEMSLPPPSNDFSPPSFLETSSPKLPSWRPPRSR PRWGQSPPPQWSDEGEEEVASFSGQILAGELDNCVSSIPDFP MHLACPEEEDKATAABMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQPDDLTLPEGCVVLEIVGQAATAGDDLEIPV VVRQVSPGRPPVLLDDSLETSSALGLLMPTLESETEAAVPKVTIL CSEKEGLSLNSEEKLDSACLLKPREVVEPVYPKEPQMPPANAAP GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPGEELQKRSGPLQGKGKRAWARAMAAALENSSPKN LERRSAGQSSPAKSGPLLDLYPKLADTIQTNFIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDFGLUDLASTSSELVEPLPA				PGTALTNI-TYGTL-PPFIWTI-I-MPATI-I-I-PERANA FTT TRANSCORE
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194 2610 AMDPPQHSQHVLEQINQQRQLGILICDCTFVVDGVHFKAHKAVLA ACSEYFKMLFVDQKDVVHLDISNAAGIGQVLEMYTAKLSISPE NVJDVL\AVATFLQMQDIITACHALKSLAEPATSPGGNAEALAT EGGDKRAKEEKVATSTLSRLEQAGRSTPIGPSRDLKEERGGQAQ SAASGAEQTEKADAPREPPPVELKEDPTSGMAAAEAEAALESSS EQEMEVE PARKGEEEQKEGEQEEGAGPAEVKEEGSQLEMGEA PEENEMEESAGTDESQELGSEARGLRSGTYGDRTESKAYGSVIH KCEDCGKEFTHTGNFKRHIRIHTGEKPFSCRECSKAFSDPAACK AHEKTHSPLKPYGCEECGKSYLISLLNIKKKHSGEARYKCED CGKLFTTSGNLKRHQUVISGEKPYQCDYCGSFSEDPTSKMRHLE THDTDKEHKCPHCDKKFNQVGNLKAHLKIHIADGPLKCRECGKQ FTTSGNLKRHGUVISGEKPYQCDYCGSFSEDPTSKMRHLE THDTDKEHKCPHCDKKFNQVGNLKAHLKIHIADGPLKCRECGKQ FTTSGNLKRHGUVISGEKPYVCHCQRQFADPGALQRHVRIHTG EKPQCVCMCGKAFTQASSLIAHVRQHTGEKPYVCERCGKRFVQS SQLANHIRHHDNIRPHKCSVCSKAFVNVODLSKHIIIHTGEKPY LCDKCGGRFNRVDNLRSIVKTVHQGKAGIKILEPEEGSEVSVVT VDDMVTLATEALAATAVTQLTVVPVGAAVTADETEVLKAEISKA VKQVQEEDPNTHILYACDSCDKFLDANSLAGHVRIHTAQALVM FQTDADPYQQYGPGGTWPAGQVLQAGELVFRPRDGAEGQPALAE TSPTAPECPPPAE 5990 2 4700 FGGGPDSGGGGGGGGGGGGGGGGGGGAGSGWGSRSQAPYGTLGAVSGGEQVLLHEEAGD SGFVSLSRLGPSLRDKDLEMEELMLQDETLLGTMQSYMDASLIS LIEDFGGLGEVEMSLPDPSWDFSPFSFLETSSFKLPSWRPPRSR PRWQSPPPQQRSDGEEEEVASFSGQILAGELDNCVSSIPDFP MHLACPEBEDKATAAEMAVPAAGDESISSLSELVRAMHPYCLPN LTHLASLEDELQEQDDDLTLPEGCVLETVGQAATAGDDLEIPV VVRQVSPGPPPVLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKEGLSLNSEEKLDSACLLKPREVVSPVVPKPEPNTAAP GSQRARKGRKKKKEQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPGEELQKESGPLQGKKPRAWARAWAAALENSSPKN LERSAGQSFAKEGGPLLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	1			
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VVRQVSPGPRPVLLDDSLETSSALQLLMPTLESETEAAVPKVTL CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	[[LTHIASLEDELOFODDDLTLDFGGTTT ETTGGAATAGDS
CSEKEGLSLNSEEKLDSACLLKPREVVEPVVPKEPQNPPANAAP GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA	, 1			AMBOACOCODO DATA DOCTOR DE CONTROL DOCUMBRATA DE LA COMPANSA DEL COMPANSA DE LA COMPANSA DE LA COMPANSA DE LA COMPANSA DEL COMPANSA DE LA COMPANSA DE LA COMPANSA DE LA COMPANSA DE LA COMPANSA DE LA COMPANSA DE LA COMPANSA DE LA COMPANSA DEL COMPANSA DEL COMPANSA DE LA COMPANSA DE LA COMPANSA DE LA COMPANSA DEL COMPANSA DEL COMPANSA DE LA COMPANSA DE LA COMPANSA DEL COMPANSA DE LA COMPANSA DEL COMPANSA DEL COMPANSA DE LA COMPANSA DE LA COMPANSA DEL COM
GSQRARKGRKKKSKEQPAACVEGYARRLRSSSRGQSTVGTEVTS QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA				CCERECI CI NCEEN DOS OF A DESCRIPTION OF THE SETEMAN PROTECTION OF THE
QVDNLQKQPQEELQKESGPLQGKGKPRAWARAWAAALENSSPKN LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA]	ļ	,	
LERSAGQSSPAKEGPLDLYPKLADTIQTNPIPTHLSLVDSAQAS PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA				
PMPVDSVEADPTAVGPVLAGPVPVDPGLVDLASTSSELVEPLPA			!	
			1	
EPVLINPVLADSAAVDPAVVPISDNLPPVDAVPSGPAPVDLALV				
	Ŀ <u></u>			DEVITAEVHADSAAVDPAVVPISDNLPPVDAVPSGPAPVDLALV

Y		Predicted end	Amino acid segment containing signal peptide
	Predicted		1
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1			P=Proline, Q=Glutamine, R=Arginine,
1	to first	amino acid	
i i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
1	amino acid	sequence	
	sequence		\=possible nucleotide insertion)
			DPVPNDLTPVDPVLVKSRPTDPRRGAVSSALGGSAPQLLVESES
			LDPPKTIIPEVKEVVDSLKIESGTSATTHEARPRPLSLSEYRRR
- 1			ROOROAETEERSPOPPTGKWPSLPETPTGLADIPCLVIPPAPAK
		1	
Į.			KTALQRSPETPLEICLVPVGPSPASPSPEPPVSKPVASSPTEQV
1		1	PSQEMPLLARPSPPVQSVSPAVPTPPSMSAALPFPAGGLGMPPS
ļ		1	LPPPPLQPPSLPLSMGPVLPDPFTHYAPLPSWPCYPHVSPSGYP
i		l .	CLPPPPTVPLVSGTPGAYAVPPTCSVPWAPPPAPVSPYSSTCTY
į			
Ì			GPLGWGPGPQHAPFWSTVPPPPLPPASIGRAVPQPKMESRGTPA
ł		1	GPPENVLPLSMAPPLSLGLPGHGAPQTEPTKVEVKPVPASPHPK
ì		1	HKVSALVQSPQMKALACVSAEGVTVEEPASERLKPETQETRPRE
		1	i
i		1	KPPLPATKAVPTPRQSTVPKLPAVHPARLRKLSFLPTPRTQGSE
I			DVVQAFISEIGIEASDLSSLLEQFEKSEAKKECPPPAPADSLAV
1			GNSGGVDIPQEKRPLDRLQAPELANVAGLTPPATPPHQLWKPLA
		1	AVSLLAKAKSPKSTAQEGTLKPEGVTEAKHPAAVRLQEGVHGPS
		i	
		1	RVHVGSGDHDYC\VRSRTPPKK\MPALLIPEVGSRWNVKRHQDI
.		i	TIKPVLSLGPAAPPPPCIAASREPLDHRTSSEQADPSAPCLAPS
1		1	SLLSPEASPCRNDMNTRTPPEPSAKQRSMRCYRKACRSASPSSQ
		1	GWOGRRGRNSRSVSSGSNRTSEASSSSSSSSSSSSRSRSRSLSPP
			HKRWRRSSCSSSGRSRRCSSSSSSSSSSSSSSSSSSSSSSSS
.			1 5
			PSPRRSDRRRRYSSYRSHDHYQRQRVLQKERAIEERRVVFIGK
			IPGRMTRSELKQRFSVFGEIEECTIHFRVQGDNYGFVTYRYAEE
		1	AFAAIESGHKLROADEOPFDLCFGGRROFCKRSYSDLDSNREDF
	}	ļ	DPAPVKSKPDSLDFDTLLKQAQKNLRR
ļ			
5991	334	1379	RLSSHFSQCSPSIYC\TKFDKQGNVTSFERKKTELYQBLGLQAR
		1	DLRFQHVMSITVRNNRIIMRMEYLKAVITPECLLILDYRNLNLK
1	1	1	QWLFRELPSQLSGEGQLVTYPLPFEFRAIEALLQYWINTLQGKL
		i	SILOPLILETLDALGDPKHSSVDRSKLHILLQNGKSLSELETDI
	1	1	
			KIFKESILBILDEEELLEELCVSKWSDPQVFEKSSAGIDHAEEM
	ł		ELLLENYYRLADDLSNAARELRVLIDDSQSIIFINLDSHRNVMM
		1	RLNLOLTMGTFSLSLFGLMGVAFGMNLESSLEEDHRIFWLITGI
	Ł		MFMGSGLIWRRLLSFLGR/LARSSIASYGMKDMVHGGIVEGL
5992	2	609	AGPDFRLVCGVSGSGFPGGRQGQATEWRPLRPWNGAMEKLRRVL
	1		SGQDDEEQGLTAQDSQINL/SEVLDASSLSFNTRLKWFAICFVC
	1	1	GVFFSILGTGLLWLPGGIKLFAVFYTLGNLAALASTCFLMGPVK
	1		OLKKMFEATRLLATIVMLLCFIFTLCAALWWHKKGLAVLFCILQ
	1		~
	İ		FLSMTWYSLSYIPYARDAVIKCCSSLLS
5993	1650	594	AEGLGSWAVWAGLGWAGRHMEAGGATGALGVGCKLPSAFCFPGS
-			SVAMDMFQKVEKIGEGTYGVVYKAKNRETGQLVALKKIRLDLEM
		ł	EGVPSTAIREISLLKELKHPNIVRLLDVVHNBRKLYLVFEFLSQ
		[DLKKYMDSTPGSELPLHLIKSYLFQLLQGVSFCHSHRVIHRDLK
			PONLLINELGAIKLADFGLARAFGVPLRTYTHEVVTLWYRAPEI
	Į.		LLATRFYTTAVDIWSIGCIFAEMVTRKALFPGDS\EIDQ\LFRI
ł	1		FRMLGTPSEDTWPGVTQLPDYKGSFPKWTRKGLEEIVPNLEPEG
ĺ	1		
1			RDLLMQLLQYDPSQRITAKTALAHPYFSSPEPSPAARQYVLQRF
İ			RH
5994	394	1934	AGEVQLHVWIRGMRIQPQ/KAAAIIDLDPDFEPQSRPRSCTWPL
	1	1	PRPEIANOPSKPPEVEPDLGEKVHTEGRSEPILLPSRLPEPAGG
i		ļ.	
i			PQPGILGAVTGPRKGGSRRNAWGNQSYAELISQAIESAPEKRLT
İ			LAQIYEWMVRTVPYFKDKGDSNSSAGWKNSIRHNLSLHSKFIKV
1	1	1	HNEATGKSSWWMLNPEGGKSGKAPRRRAASMDSSSKLLRGRSKA
Į.	1	·	PKKKPSGLPAPPEGATPTSPVGHFAKWSGSPCSRNREEADMWTT
l		I	
1	1	1	FRPRSSSNASSVSTRLSPLRPESEVLAEEIPASVSSYAGGVPPT
I			LNEGLELLDGLNLTSSHSLLSRSGLSGFSLQHPGVTGPLHTYSS
1		1	SLFSPAEGPLSAGEGCFSSSQALEALLTSDTPPPPADVLMTQVD
Į.		1	PILSQAPTLLLLGGLPSSSKLATGVGLCPKPLRAPGPSSLVPTL
l .	1 '	l	
1		i	SMIAPPPVMASAPIPKALGTPVLTPPTEAASQDRMPQDLDLDMY
		I	MENLECDMDNIISDLMDEGEGLDFNFEPDP
		\$	
5995	2	2437	RPPGPGPASGAWLCTRARGSAAFVPPLPRPPSRGARRRRLPGR
5995	2	2437	
5995	2	2437	GVAALRRGPGSAPGLPRGRAERSAAGSGRGPSREERGAAAAAAA
5995	2	2437	

750	I beadlesed	I Deadisted and	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	l ·		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	residue of	amino acid	
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	1	\=possible nucleotide insertion)
	 		ISDYFERRVEOPLYGLDGSAAKEATEEQSALPTLMSVMLAKPRL
			DTEOLAORGAGLCFTFVSAOONSPSSTGSGNTEHSCSSOKOISI
i			1
i	1	1	QHRQT\QSDLTIEKISALENSKNSDLEKKEGRIDDLLRANCDLR
		1	RQI\DEQQKMLEKYK\ERLNRCFDNEPRNFLIEKSKQEKMACRD
	1		KSMQDRLRLGHFTTVRHGASFTEQWTDGYAFQNLIKQQERINSQ
		1	REEIERORKMLAKRKPPAMGOAPPATNEOKORKSKTNGAENETL
}		1	TLAEYHEQEEIFKLRLGHLKKEEAEIQAELERLERVRNLHIREL
	1		**
	i	1	KRIHNEDNSQFKDHPTLNDRYLLLHLLGRGGFSEVYKAFDLTEQ
1			RYVAVKIHQLNKNWRDEKKENYHKHACREYRIHKELDHPRIVKL
ľ		1	YDYFSLDTDSFCTVLEYCEGNDLDFYLKQHKLMSEKEARSIIMQ
l	1		IVNALKYLNEIKPPIIHYDLKPGNILLVNGTACGEIKITDFGLS
}			KIMDDDSYNSVDGMELTSQGAGTYWYLPPECFVVGKEPPKISNK
i .		İ	
1	1	1	VDVWSVGVIFYQCLYGRKPFGHNQSQQDILQENTILKATEVQFP
			PKPVVTPEAKAFIRRCLAYRKEDRIDVQQLACDPYLLPHIRKSV
1			STSSPAGAAIASTSGASNNSSSN
5996	1612	981	DOOACLIGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCE
1	1	1	LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
			AFLTCLLYLALDVYFPOISSVKDRKK\AVLSGHPVVSGEPHPAA
i	1		
Į			FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
Ì	1		FFSIFTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5997	1612	981	DOOACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB
1 333.			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
ŀ	i	i	AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
ļ	l		FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
Į	•		FFS1FTWSLTAALAVRRFKDLSFQEEYSTLFP\ASAQP
5998	1612	981	DOQACLLGLMLTLEFGILEFDPSWIGSWTQR/SWVSWRSRPGCB
1			LFSIVVFGSIVNEGYLNSASEGEEFCIYNRNPNACSYGVAVGVL
ļ			AFLTCLLYLALDVYFPQISSVKDRKK\AVLSGHPVVSGEPHPAA
1		1	The state of the s
		1	FWAFLWFTGDSCYL\ANQWQVSKPKDNPLNEGTDASPGRPSPFS
Ì		l	FFSIFTWSLTAALAVRRFKDLSFQEEYSTLPP\ASAQP
5999	2	1790	RPPMEKARRGGDGVPRGPVLHIVVVGFHHKKGCQVEFSYPPLIP
1		1	GDGHDSHTLPEEWKYLPFLALPDGAHNYQEDTVFFHLPPRNGNG
			ATVFGISCYR\QIEAKALKVRQADITRETVQKSVCVLSKLPLYG
1		ł	
•		[LLQAKLQLITHAYFEEKDFSQISILKELYEHMNSSLGGASLEGS
		į.	QVYLGLSPRDLVLHFRHKGLILFKLILLEKKVLFYISPVNKLVG
1	1	i	ALMTVLSLFPGMIEHGLSDCSQYRPRKSMSEDGGLQESNPCADD
1			FVSASTADVSHTNLGTIRKVMAGNHGEDAAMKTEEPLFQVEDSS
. .			KGOEPNDTNOYLKPPSRPSPDSSESDWETLDPSVLEDPNLKERE
		1	OLGSDOTNLFPKDSVPSESLPITVQPQANTGQVVLIPGLISGLE
			T
ŀ			EDQYGMPLAIFTKGYLCLPYMALQQHHLLSDVTVRGFVAGATNI
i			LFRQQKHLSDAIVEVEEALIQIHDPELRKLLNPTTADLRFADYL
1	1		VRHVTENRDDVFLDGTGWEGGDEWIRAQFAVYIHALLAATLQLV
1			LFRIVNVAKKIGNVMVTT\SRNVVQTGK\AVGQSVGGAFS\SAK
1		1	TA\MSSWLSTFTTSTSQSLTEPPDBKP
			
6000	101	1561	TEPCRTAENCTATMSENNKNSLESSLRQLKCHFTWNLMEGENSL
1			DDFEDKVFYRTEFQNREFKATMCNLLAYLKHLKGQNEAALECLR
			KAEELIQQEHADQAEIRSLVTWGNYAWVYYHMGRLSDVQIYVDK
1			VKHVCEKFSSPYRIESPELDCEEGWTRLKCGGNQNERAKVCFEK
1	1		ALEKKPKNPEFTSGLAIASYRLDNWPPSQNAIDPLRQAIRLNPD
1	ł	(NQYLKVLLALKLHKMREEGEEEGEGEK\LVEEALEKAPG\VTDV
1	1		LRSAA/KFYRGKDEPDKAIELLKKALEYIP/NNAYLHCQIGCCY
			RAKVFQVMNLRENGMYGKRKLLELIGHAVAHLKKADEANDNLFR
1	1	1	VCSILASLHALADOYEDAEYYFQKEFSKELTPVAKQLLHLRYGN
I		1	FOLYOMKCEDKAIHHFIEGVKINQKSREKEKMKDKLQKIAKMRL
ļ		}	
1	i	1	SKNGADSEALHVLAFLQELNEKMQQADEDSERGLESGSLIPSAS
	1	1	SWNGE
6001	176	1038	AFAHSPSRGHRHTHIHTPRHTPRCTMAESHLQSSLITASQFFEI
	1		WLHFDADGSGYLEGKELQNLIQELQQARKKAGLELSPEMKTFVD
I			
1			QYGQRDDGKIGIVELAHVLPTEENFLLLFRCQQLKSCE\EFMKT
			WRKYDTDHSGFIETEELKNFLKDLLEKANKTVDDTKLAEYTDLM

SEO	Predicted	Predicted end	Amino acid company
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid E-Dhamalal :
	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	corresponding	to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first		L=Leucine, M=Methionine, N=Asparagine,
ŀ	amino acid	amino acid	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	<u> </u>	\=possible nucleotide insertion)
			LKLFDSNNDGKLELTEMARLLPVQENFLLKFQGIKMCGKEFNKA
}			FELYDQDGNGYIDENELDALLKDLCEKNKQDLDINNITTYKKNI
		1	MALSDGGKLYRTDLALILCAGDN
6002	977	81	LAPPGGGLHIPPRTPLSHSRPPPSHHAPHPSPLPLPPADLHPHS
			SMAQRSDLLELDCQLTRDRVVVVSHDENLCRQSGLNRDVGSLDF
1			EDLPLYKEKLEVYFSPGHFAHGSDRRMVRLEDLFQRFPRTPMSV
l i	İ	ł	EIKGKNEELIREQ/VLVRRYDRNEITIWASEKSSVMKKCKAANP
1		-	EMPLSFTISRGFWVLLSYYLGLLPFIPIPEKFFFCFLPNIINRT
1		1	VEDECCCCI NOLLA MILICIALI TARRAS TERR
			YFPFSCSCLNQLLAVVSKWLIMRKSLIRHLEERGVQVVFWCLNE
6003	140	4000	ESDFEAAFSVGATGVITDYPTALRHYLDNHGPAARTS
0003	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP
			APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA
1 1			FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR
1			SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA
1			HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
			RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLOEWOTHSLE
			RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY
	•		NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSOESLNRPFSS
1 1			KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK
1			AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
			RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT
			TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSREASPSRLSV
			ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS
1 1			TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVEEA
1 1			VADALLLGDIRTKKKPARRYESYGMHSDDDANSDASSACSERS
]]			YSSRNGSIPTYMRQT\EDV\AEVLNRCASSNWSERKEGLLGLQN
1			LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI
			OVERDI ODEL ETT I TOLL KANGA DI L'EGGE TETTE DE L'EGGE T
			QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES
1 1			FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD
i I			FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFBLNTPE
1			FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
1			RSPANWSSPLTSPTNTSQNTLSPSAFDYDTENMNSEDIYSSLRG
1			VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA
			GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSIS
1	,		PFNKSALKEAMFDDDADQFPDDLSLDHSDLVAELLKELSNHNER
			VEERKIALYELMKLTQEBSFSVWDEHFKTILLLLLETLGDKEPT
1			IRALALKVLREILRHQPARFKNYAELTVMKTLRAHKDPHKEVVR
ſ			SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT
			KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
			HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
	1	ĺ	GQS
6004	140	4098	GKLRAFRGMRRLICKRICDYKSFDDEESVDGNRPSSAASAFKVP
! !			APKTSGNPANSARKPGSAGGPKVGAGASKEGGAGAVDEDDFIKA
]			FTDVPSIQIYSSRELEETLNKIREILSDDKHDWDQRANALKKIR
1			SLLVAGAAQYDCFFQHLRLLDGALKLSAKDLRSQVVREACITVA
1	ļ		HLSTVLGNKFDHGAEAIVPTLFNLVPNSAKVMATSGCAAIRFII
			RHTHVPRLIPLITSNCTSKSVPVRRRSFEFLDLLLQEWQTHSLE
1		ĺ	PHANULUETI ENGLISHED PRESENTATION OF THE PROPERTY OF THE PROPE
1 1	ŀ		RHAAVLVETIKKGIHDADAEARVEARKTYMGLRNHFPGEAETLY
1 1		,	NSLEPSYQKSLQTYLKSSGSVASLPQSDRSSSSSQESLNRPFSS
1 1			KWSTANPSTVAGRVSAGSSKASSLPGSLQRSRSDIDVNAAAGAK
	1		AHHAAGQSVRSGRLGAGALNAGSYASLEDTSDKLDGTASEDGRV
	ļ		RAKLSAPLAGMGNAKADSRGRSRTKMVSQSQPGSRSGSPGRVLT
			TTALSTVSSGVQRVLVNSASAQKRSKIPRSQGCSRBASPSRLSV
			ARSSRIPRPSVSQGCSREASRESSRDTSPVRSFQPLASRHHSRS
			TGALYAPEVYGASGPGYGISQSSRLSSSVSAMRVLNTGSDVERA
]			VADALLLGDIRTKKKPARRRYESYGMHSDDDANSDASSACSERS
Í	1	1	YSSRNGSIPTYMRQT\EDV\ABVLNRCASSNWSERKEGLLGLQN
			_ , - · · · · · · · · · · · · · · · · · ·
		ŀ	LLKNORTLSRVELKRLCEIFTRMFADPHGKRVFSMFLRTIJDDT
. [LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI OVHKDDLODWLFVLLTOLLKKMGADLLGSVOAKVOKALDVIDES
			QVHKDDLQDWLFVLLTQLLKKMGADLLGSVQAKVQKALDVTRES
			LLKNQRTLSRVELKRLCEIFTRMFADPHGKRVFSMFLETLVDFI QVHKDDLQDWLFVILTQLLKKMGADLLGSVQAKVQKALDVTRES FPNDLQFNILMRFTVDQTQTPSLKVKVAILKYIETLAKQMDPGD FINSSETRLAVSRVITWTTEPKSSDVRKAAQSVLISLFELNTPE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
			Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
[amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
 			FTMLLGALPKTFQDGATKLLHNHLRNTGNGTQSSMGSPLTRPTP
			RSPANWSSPLTSPTNTSONTLSPSAFDYDTENMNSEDIYSSLRG
1			VTEAIQNFSFRSQEDMNEPLKRDSKKDDGDSMCGGPG\MSDPRA
1			GGDATDSSQTAL\DNKASLLHSMPTHSSPRSRDYNPYNYSDSIS
1			PFNKSALKEAMFDDDADQFPDDLSLDHSDLVAELLKELSNHNER
1		j	VEERKIALYELMKLTQEESFSVWDEHFKTILLLLLETLGDKEPT
1			IRALALKVLREILRHQPARFKNYAELTVMKTLEAHKDPHKEVVR
1 1		ļ	SAEEAASV\LATSI\SPEQCIKVLCPIIQTADYPINLAAIKMQT
l i		[KVIERVSKETLNLLLPEIMPGLIQGYDNSESSVRKACVFCLVAV
1			HAVIGDELKPHLSQLTGSKMKLLNLYIKRAQTGSGGADPTTDVS
i l			GQS
6005	133	5955	RSSGRRQEQLGQFPGRERKGMASGLGSPSPCSAGSEEEDMDALL
] [1	NNSLPPPHPENEEDPEEDLSETETPKLKKKKKPKKPRDPKIPKS
			KROKKERMLLCROLGDSSGEGPEFVEEBEEVALRSDSEGSDYTP
			GKKKKKLGPKKEKKSKSKRKEEEEEDDDDDDDSKEPKSSAOLL
1 1			BDWGMEDIDHVFSEEDYRTLTNYKAFSQFVRPLIAAKNPKIAVS
1		}	KMMMVLGAKWREFSTNNPFKGSSGASVAAAAAAAVAVVESMVTA
			TEVAPPPPPVEVPIRKAKTKEGKGPNARRKPKGSPRVPDAKKPK
		Į.	
1		1	PKKVAPLKIKLGGFGSKRKRSSSEDDDLDVESDFDDASINSYSV
1		i	SDGSTSRSSRSRKKLRTTKKKKKGEEEVTAVDGYETDHQDYCEV
		<u>[</u>	CQQGGEIILCDTCPRAYHMVCLDPDMEKAPEGKWSCPHCEKEGI
i l			QWEAKEDNSEGEEILBEVGGDLEEEDDHHMEFCRVCKDGGELLC
			CDTCPSSYHIHCLNPPLPEIPNGEWLCPRCTCPALKGKVQKILI
			WKWGQPPSPTPVPRPPDADPNTPSPKPLEGRPERQFFVKWQGMS
		}	YWHCSWVSELQLELHC\QVMFRNYQRKNDMDEPPSGDFGGDEEK
	1	İ	S\RKRKNKDPKFAEMBERFYRYGIKPEW\MMIHRILNHSVDKKG
1			HVHYLIKWRDLPYDQASWESEDVEIQDYDLFKQSYWNHRELMRG
			EEGRPGKKLKKVKLRKLERPPETPTVDPTVKYERQPEYLDATGG
			TLHPYOMEGLNWLRFSWAQGTDTILADEMGLGKTVQTAVFLYSL
1		ì	YKEGHSKGPFLVSAPLSTIIN\WEREFEMWAPDMYV\VTYVGDK
		i	DSRAIIRENEFS\FEDNAIRGGKKASRMKKEASVKFHVLLTSYE
	1	1	LITIDMAILGSIDWACLIVDEAHRLKNNQSKFFRVLNGYSLQHK
ł]]	LLLTGTPLONNLEELFHLLNFLTPERFHNLEGFLEEFADIAKED
	1	ł	QIKKLHDMLG\PHMLRRLKADVFKNMPSKTELIV\RVELSPM\Q
1	1	İ	KKYYK\YILHSKFLKALN\ARGGGNQVSLLNVVMDLKKCCNHPY
		}	LFPVAAMEAPKMPNGMYDGSALIRASGKLLLLQKMLKNLKEGGH
			RVLIFSQMTKMLDLLEDFLEHEGYKYERIDGGITGNMRQEAIDR
Ì		i	
	1	1	FNAPGAQQFCFLLSTRAGGLGINLATADTVIIYDSDWNPHNDIQ
		1	AFSRAHRIGQNKKVMIYRFVTRASVEERITQVAKKKMMLTHLVV
	1		RPGLGSKTGSMSKQELDDILKFGTEELFKDEATDGGGDNKEGED
		1	SSVIHYDDKAIERLLDRNQDETEDTELQGMNEYLSSFKVAQYVV
1			REEEMGEEEEVEREIIKQEESVDFDYWEKLLRHHYEQQQEDLAR
		1	NLGKGKRIRKQVNYNDGSQEDRDWQDDQSDNQSDYSVASEEGDE
	[DFDERSEAPRRPSRKGLRNDKDKPLPPLLARVGGNIEVLGFNAR
1			QRKAFLNAIMRYGMPPQDAFTTQWLVRDLRGKSEKEFKAYVSLF
1		!	MRHLCEPGADGAETFADGVPREGLSRQHVLTRIGVMSLIRKKVQ
1	1	1	EFEHVNGRWSMPELAEVEENKKMSQPGSPSPKTPTPSTPGDTQP
			NTPAPVPPAEDGIKIEENSLKEEESIEGEKEVKSTAPETAIECT
1			QAPAPASEDEKVVVEPPEGEEKVEKAEVKERTEEPMETEPKGKG
1		1	AADVEKVEEKSAIDLTPIVVEDKEEKKEEEEKKEVMLQNGETPK
1			DLNDEKOKKNIKORFMFNIADGGFTELHSLWONEERAATVTKKT
1	1		- "
1			YEIWHRRHDYWLLAGIINHGYARWQDIQNDPRYAILNEPFKGEM
1			NRGNFLEIKNKFLARRFKLLEQALVIEEQLRRAAYLNMSEDPSH
1			PSMALNTRFAEVECLAESHQHLSKESMAGNKPANAVLHKVLKQL
1	1	1	EELLSDMKADVTRLPATIARIPPVAVRLQMSERNILSRLANRAP
L	L		EPTPQQVAQQQ
6006		965	DNDFLRNTVHRHBPPVTAEPIRLLAENEDVVVVDKPSSIPVHPC
	1	, , , ,	
	1		GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAAVS
	1		GRFRHNTVIFILGKEHQLKELHPLHRLDRLTSGVLMFAKTAAVS ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKVGV
ļ	1		
	1		ERIHEQVRDRQLEKEYVCRVEGEFPTEEVTCKEPILVVSYKVGV

Predicted the process of the proce			1 B 32 - L . 3 4	Amino acid segment containing signal peptide
No:	SEQ	Predicted	Predicted end	
Cotation Corresponding	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Cotation Corresponding	NO.		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
corresponding to first smino acid residue of amino acid residue of amino acid sequence solve of sequen				
to first amino acid residue of amino acid amino acid amino acid amino acid sequence ##Tryptophan, Y=Tyrosine, X=Unknown, *-Stop Codon, /-possible nucleotide deletion, \{-possible nucleotide insertion} ##Tryptophan, Y=Tyrosine, X=Unknown, *-Stop Codon, /-possible nucleotide deletion, \{-possible nucleotide insertion} ##Tryptophan, Y=Tyrosine, X=Unknown, *-Stop Codon, /-possible nucleotide insertion) ##Tryptophan, Y=Tyrosine, X=Unknown, *-Stop ##Tryptophan, Y=Tyro				l · · · · · · · · · · · · · · · · · · ·
amino acid residue of amino acid sequence Seq	ì		1	
menidue of amino acid sequence (Codon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion) 803D/ULDICCRGIS.PSG/ULDTATASSEGNER/BUBERIAANA\QKME		to first		
residue of amino acid sequence Codon, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide deletion, /-possible nucleotide insertion) SUMPARAPOELDITALASEKAVETUVNNO\RQT\TLCEPPAGATG SLAPRCOVECTUL BERGOVETUTELL SERVEROPETORIUS SLAPRCOVECTUL REPORT SLAPRCOVECTUL REPORT SLAPRCOVECTUL REPORT SLAPRCOVECTUL REPORT SLAPRCOVECTUL REPORT SLAPRCOVECTUL REPORT SLAPRCOVECTUL REPORT SLAPRCOVECTUL REPORT SLAPRCOVECTUL REPORT SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SCHEME SPEEKLAVEDARIO SCHEME SPEEKLAVEDARIO SCHEME SCHEME SPEEKLAVEDARIO SCHEME SC	i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence Codon, /=possible nucleotide deletion,	1			W=Truptophan, Y=Turosine, X=Unknown, *=Stop
Sequence V-possible nucleotide insertion				
GSLDYLDLCSGDLSPGLTDSTAPSSELGKDDLSRIAAAAQUME VARAAPGELDTIALASKKAVETUMOKQRTYTLCKPYAGATG SLAPRPCOVPTOPTI BILGOVEVYPTOKTGTITENEMOFRECSINGHKYGEINGRLVPE GPTDDSSEGNLSYLSSLSHINNLSHLTTSSSFRSPERNETELIK EHDLFKAVSLCHTYGUINVOTCOTGOPMOSNLABSOLLSYNAS SPDEKALVRAAARIGIVFIGNESETMEVKTLGKLERYKLIHILE PDSSRRNSVIVOAPSKEKLLFKAGASSILDKYGGGGIEKTRI HVDEFALKGURTLCLAYRKFYSKEYERIDKRIFFARTALQGA\E EKLAAMPOPIERDLIGATAVEDELDGWYRETTERLEMGIKV WUTGGRHETAVSVSLSGGHFHRTMILLELINGKSDSBCAEGLAR GLARRITEDHIVJGRUVUTOGISLSLAREHEKLEMPUSKTYRIAGIKV GLARRITEDHIVJGRUVUTOGISLSLAREHEKLEMPUSKTYRIATI VQYFFYRNVCFITPQLTQYFVCLFSGOTLYDSYVLTLY\NICFT SLPILIYSLLEGHUPPHILOKNETIVJBLISKRILSITHSTUFVT TLGFSRAFIFFGSYLLIGKTSTLLKSGOMFORMTEGTLYFTVM VITTVYKMALETHFRITMINHUTWOSLIDISKRILSITHSTUFVT LGSGNNYFVFIGLSSGSAFFAIILMVYTCLFLDIKKRSDSRCAEGLAR GROSPHISSRHSASDPFYTMORSITLTSTWOSSTC ASVERGARARGRGGRAADIKCLDSNCCFPGEGACASVGMLERVI GROSPHISSRHSASDPFYTMORSITLTSTWOSSTC ASVERGARARGRGGRAADIKACHSONCTOFTSADKRLERVI BYSTERKAQLITETNAGIKCLDSNCCFPGEGACASVGMLERVI GROSPHISSRHSASDPFYTMORSITLTSTWOSSTC ASVERGARRGRGGRAADIKACHSONCTORSTVANDYKTERCSACP FSSKFFSAYKSHFRNVISSDFERRILLINCDYCTFNADKRLERVI KKTYRDPLYSITURKHITYRRHOVILADPSTRRRRRCAPBEHAGPAR ASPRSOCTMFQLPVINLGSLRKARKTVKKILSDIGLEXCKEHIE DFKOFFRADYSKSHFRNVISSDFERRILLINCDYCTFNADKRLETH KKFFRADASAPSSISTFKNNKSHDERRRRRCAPBEHAGPAR ASPRSOCTMFQLPVINLGSLRKARKTVKKILSDIGLEXCKEHIE SRABERSSIEKRCRLUFHKSYBLAUGWYTEDHRICHYVYTAMIG HITNVVVPRSKYHERVINLABRORVSHGHEBRINVYSVYFRAGKSLAGAVYLKG KCTYRDPLYSITURKHITYRRHOVILADPSTRRRRRKRCAPBEHAGPAR PARAYSISTRYMKKINTERNOVILADPSTRRRRRKCAPVYCAMIG GROMBLISTRYBLINKHITYRRHOVILADPSTLARGKSLAGAVYLKG GSMRLISTSTQKKKICTICNSLFPRNYSVAHQANYCYXXAC GSMRLISTSTQKKKICTICNSLFPRNYSVAHQANYCYXXAC GSMRLISTSTQKKKICTICNSLFPRNYSVAHQANYCYXXAC TRINDVERMAJAHRAWHIDEBRGGRVAASTATICHLUMHLHIGLIGCCYCES TRINDVERMAJAHRAWHIDEBRGGRVAASTATICHLUKGCYTCMACH AVARGRAADRARVINLABRADDKARGKKYCVDCEKYXPOVL LLVATTURLABARASSISTGKRKYTROGESCLARKSFILKYFYKOPTY TRREIERLAASLWYNKACHDORGCKYAGAGRGGGGRVAAGRGFORMANS GOOGNAASERBORDASHOPAGARRTTIALHUNGRGGRGGRAAGH LLVA			sequence	
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#KILABYOPIEKDLILLGATAVEDELODKYRETIEALRHAGIKV WVITGRKHEITAVSUSLGGIPHETNINILELIGLOGSHOCADGLE QLARRITEDHVIQHGLVVDGTSLSLALREHERLEMEVCRICSAV LCCRMAPLQKAKVIRLIKISPEKPITLAVGDGANDVSMIQEAHV GIGIMKKBGROARRISDYATARFKFLSKLIPHGHFYYIRTATIL VQYFFYKRVCFITPOFLYGFYCLFSQOTLYDSVYLITVANLGFT SLPILIYSLLEGHVOPHYLONKFTIYRDISKRILSIKKFFLYWT ILGFSHARIFFFTWINIHLVMGSITFYFYSLFYGGILWPF LGSQNMYFVFJQLISSGSAWFAILMVVTCLFLDITKKVPOPHL HPTSTEKQLIETHFMTWINHLVMGSITFYFYSLFYGGILWPF LGSQNMYFVFJQLISSGSAWFAILMVVTCLFLDITKKVPOPHL HPTSTEKQLIETHANGIKCLBONCCPFPGERAVGARNLEKVI GRCSPTHISRSWGASDPFYTNDRSILTISTMDSSTC GRCSPTHISRSWGASDPFYTNDRSILTISTMDSSTC GRCSPTHISRSWGASDPFYTNDRSILTISTMDSSTC GRCSPTHISRSWGASDPFYTNDRSILTISTMDSSTC GRCSPTHISRSWGASDPFYTNDRSILTISTMDSSTC FSKKFPSAYKSHFRWNHSEDFERRILLNCPYCTFNADKKTLETH IKIFHAPRASAPSSSLSTFKDNNKNDGLKRKQDSVPQXVTYCK KCTYRDLYLEVILVKHITYBERPOVAPPIARRERCPAPEHAGPAR ASPRSGETMPGLPVNNLGSLKRARKTVKKILGDIGLEYCKEHIE DFKQFEPMFYLKNTTWEDVGLNOPSLKROORSTKAPCCSCAC FSKKFPSAYKSHFRWNHSEDFERRILLINCPYCTFNADKKTLETH IKIFHAPRASAPSSSLSTFKDNNKNDGLKRAGDASVQAVYCK KCTYRDLYLEVILVKHITYBERPOVAPAPIARGEKSLAGAVPLG SNARESSIHCKRCLFMPKSYBALVQNVIEDHERIGGVUTAMIG HTNVVYPRSKEDHLAPPKQDGKASMGLPFSIGLASGNV\RSLP SQCMVRRLSITKPNLNSTGVNNMSSVHLQONNYGVSVGQGSV GGSRRIGLGGARPVSIPQOSGYKGLLPSGROSGUSADSONV\SSLP SQCMVRRLSITKPNLNSTGVNNMSSVHLQONNYGVSVGQGSV GGSRRIGLGGARPVSIPQOSGYKGLLPSGROSGUSADSONV\RSLP SQCMVRRLSITKPNLNSTGVNNMSSVHLQONNYGVSVGCGSSKPAAA ATGPPONTSSTCKWICCTICHELFPRNVYVSHEKHKAEKVP AJANYIMKINNPTSKCLVCRV.PPTDTLLMHRLHGLSCCYCGS TFNDVKMAAHMRNVHIDEBMGPKTDSTLESPLLTVLOGGSHTNHH LLVITNINGAPABSVAYHAQNNPPVPPRQPKVQRADIPVKS SPQAAVPYKXDUKTLCFLCFSILKGFISDALSHLKKRKLDOGSBFILK GGCPTASTVKHCHTUKCHGUSTON GGOKTHAPSRLNOSPSLAPVKRTYPGOFFPLKKRKKLDOBSDS SFPEREPEEPVVLADPGMGFFISDASKYPTHNTDGOSHTUKCHGUSTON GGOKTHAPSRLNOSPSLAPVKRTYPGMFFIKKRKCVDOLCKYKROVL LGFRMKELKVKHEMPDFABGLFFHNDEKNSKTACCVBCCKYKROVL LGFRMKELKVKHEMPDFABGLFFHNDEKNSKTACCVBCFKKKOU QSQKRASENDERLSNOGSFPDVPEVEPKISINDNPBH VLKVIPEDASSERKLONGRSKYTHNTDGOGGTPASPG RNAGGSCPBSCHAPSRAFTNAFGGGGGGGGAGASTTTSVAL UNGKGCFPSSVFJOFFTINGKGRKTMCMCVSVSDVTG RNAGGSCPBSCTLFFTNYT	1		1	FDSDRRRMSVIVQAPSGEKLLFAKGAESSILPKCIGGEIEKTRI
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CLARRITEDHVIQHGLVVDGTSLSLAIREHERLEMPECVENCSAV LCCCMARAĮCKAKVIRLIK IS PERP ITITAVOGORANOVSMIQEAHV GIGIMKGERGAARNSDYALAR PKFLSKLLFVHGHEFYJRIATIL VQYFYYKNVCPITPQELYGFYCLPSQOTLYDSVYLTYLVINLEPT SLPILLYSLLEGNVDFHVLONKPTLYRD ISKRILFSKTLFYWT ILGESBARIFFFGSYLLIGKUTSLLGKOSHENSTRYLLYTUM VITVTVKHALETHFWTMINHLVMSSI IS FYFYSLFYGGILMPF LGSQNMYEVFIQLISSGSAWFAI LIMVVTCLFLDI IKKVFDRHL HPTSTEKAQLIETHFMTMINHLVMGSI IS FYFYSLFYGGILMPF LGSQNMYEVFIQLISSGSAWFAI LIMVVTCLFLDI IKKVFDRHL HPTSTEKAQLIETHANGIKCLDGMCCPFBGBASVGNMLERVI GRCSPTHISRSWSASDFYTMORSI LTLSTMDSSTC GROSPTHISRSWSASDFYTMORSI LTLSTMDSSTC GROSPTHISRSWSASDFYTMORSI LTLSTMDSSTC GROSPTHISRSWSASDFYTMORSI LTLSTMDSSTC FYSKFPSAYKSHFRANVHEDPERNELLINCDYCTPMADKITLETH IKIFHAPRASPSSLSSLSTFKDRNINDGLKPKQADSVGNNLEVEN PSKFPSAYKSHFRANVHSEDPERNELLINCDYCTPMADKITLETH IKIFHAPRASPSSLSSLSTFKDRNINDGLKPKQADSVQAVYCK KCTYRDPLYELVRKHITREHFORVAAPY LAKGGEKSLNGAVFLO SNAREBSSIHCKRCLPMFKSYBALVQHVIEDHERIGGVITAMIG HTNVVYPRSKENLLAPRPQDKSKRMGLPPSIGLASGNV\RSLD SQMWRRISTIKNILNSTGVIMMSSVHLQONNYGVKSVCQGYSV GQSMRIGLGGARPVSIPQOSGSVGKLLPSGNGSKOLSANAA ATGPFORTNSTGVMKICT CURLEPPRNVYSHYEKSHKARKVY APARYSLGSANASSLSSGUKKSPSLSGSQASRVLOGSSKAPAA ATGPFORTNSTGVMKICT CURLEPPRNVYSHYEKSHKRAKKVY AVANYIMKINHPTSKCLVCRYLPTDTLIANHLHGLSCYCRS TFNDVEKMAAMRAVHIDEBROKKTDSTLSPFLLQGGSHTNIH LLVTTVHLDADABSSVAHAQNNPSVPPKPGPKVOEKADIPVKS SPQAAPYTKDVOKTLCLCSTSLKMPTSCHAKKCVGROCKYKROVL GONKTHAPSKLNOSPSLAPVKRTYSCMEPFPLLKKRKLDDEDSS SFFEREPEPEPVLALDPKRGH VEDDSYBARKSFLKYFT\KQPYL GONKTHAPSKLNOSPSLAPVKRTYSCMEPFPLKKRKKLDDEDSS SFFEREPEPEPVLALDPKRGH VEDDSYBARKSFLKYFT\KQPYL GROMELINKVIHENDFDASCLFFRHDEKOSNASTADKKLM LGKEDDSSSDSFENLERSSNEGSFPPVPEVEPKISNDNPEBH VLKYTPEDASSERELLOXGROSF XYETHTLFURKMSTATDLKLM LGKEDDSSSDSFENLERSSNEGSFPPVPEVEPKISNDNPEBH VLKYTPEDASSERELLOXGROSF XYETHTLFURKSTLTSVATAGGSGTW BYDQDDVVEWENDGASBSGGRGGOGOVSPFEDDTCEMKFFTNSDE SQSGABARSSFRAAKKATHOGROKAWNSTATAKKLM LGKEDDSSSDSFRALERSSNEGSFPPVPEVEPKISNDNPEBH VLKYTPAGGGCCGAKSTSTAFTHYDTKGGRTTANGC*VSDSVTGG RAVAGGACFESTUTTAGGGGCGAKASTAFTTTOGGGTFKABGGSTW EVTLOHOVWAGAGAGGVCHOWEND PHYGLAGGTFTSVSL FYLAPQDGGGVPPV				
LCCMAPLOKAKUIRLIKISPERPITLAVGDGAADDUSMIOGRAHU GIGIMKGGGAARNENSTALREKFISKUHGHEYYIRLATU. VQYFFYKNVCFITPQFLYQFYCLFSQQTLYDSVYLTLY\NICPT SLPILLYSLLEQHYDDHYUQNKPTLYRDISKURLLSKTFLYWT ILGFSHAFIFFFGSYLLIGKUTSLLSLOQGMGNNTBYSTLVSTVW VITVTVKMALETHEWWINHLVTWGSIIFYEVFSLYSTVW VITVTVKMALETHEWWINHLVTWGSIIFYEVFSLYGILWPF LGSQNNYFVFTQLLSSGSAWPAILHWVTCFLDIIKKVFDRHL HPTSTEKAQLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVI GRCSPTHISRGWASDDFYTMORSIILISLDGILEYKKFDRHL HPTSTEKAQLTETNAGIKCLDSMCCFPEGEAACASVGRMLERVI GRCSPTHISRGWASDDFYTMORSIILISLDGILEYKKHENV GRCSPTHISRGWASDDFYTMORSIILISLDGILEYKKHENV ASRPSQETMPQLPVNNLGSLRKAKKTVKLDGIGLEYKKHEN DFKQFEPNDFYLRNTTWRDVGLWDPSLTKNQDYRTKPFCCSACP FSSKFFSAYKSHFRNVHSEDDENNILLNCPYCTFNAGKKLETH IKIFHAPNASAPSSISSTFKNKNNOSLEHKQGLSVEQAVYYCK KCTYRDPLYEIVKRHIYRRHONVAAPYIAKAGEKSLNAVPLG SNARESSICKCRLTMFKSYEALVQONIVAKSVOQGYSV GQSRTGLGGNAPVSIPQOSGVWOLLPSGNASYGLGSCORSQ APARYSLQSANASSLSSGQLKSPSLAVGNOSKYLOGGSSVNAGA ATGPPGNTSSTGWRKCTTCNELFPENVYSVHPEKEHKAKVP AVANYIMKIHNFTSKCLYCNSYLDFUTLLNIMLHENGEPYCRS TYNDVEKMAAMMRNVHIDERMGPKTDSTLFPUTLQOGSHTNIH LLVTTYNLRDAPABSVAYHAQNNPVPFKPQFKVQGASVEADIFVKS SPQAAVPYKKVOWKTLCCJCFSILKGFI SDALAHHLREEHQVI TYHPVEKKLTYKCHCLGVYTSNNTASTITLHLVHCRGVGTON GQDKTNASBRINGSPSLAPKRYTEXMEPFLIKKRKLDDDSDSP SFFEEKPEEPPVLALDPKGH\EDDSYEARKSFLIKVFPTVKOPY TRREIEKLAASLWVWK\SDIASHFNKKKCVDCCKKVPQVL LGFNMEERINGSPSLAPKRYTEXMPEPLIKKRKLDDDSDSP SFFEEKPEEPPVUKNORTLCCJCFSILKGFI SDALAHHLREEHQVI UKVIYEDASSEEKLDGCBGSXYETIHITEBTTLMMINSDS SYOGEDANSSENBARKKARMGGASCGFFKAARGSKYNACKKRI UKVIYEDASSEEKLDGCBGSXYETIHITEBTKLMMINSDS SYOGEDANSSENBARKSFRAMKKRATMGGRECLGANSVRASKTADKKLN LGKBGCFESSYLPGTIVYGKIGSLGSGGFFNAKAGGSCCHGVGSL NCHAUGULDVAVGSRSAACHARGGRECGFFNSKD OSONKASENDERISNPOTEMGASTFAAACROPCVMGLI NGKGGCFESSYLPGTIVYGKIGSLGSAYSTATHTEBTRYMNSDDE SKOGEDARSSERAKAKKARMGGRECGGFFNSKD OSONKASENDERISNPOTEMGASTGFTFAABCGGRCFGSPC HLVLGULPVAVASGRGGFSVATAARGGRECGFFNSKD OSONKASENDERISNPOTEMGASTGFTFAABCGGFF NGRGCGFFSVATAGRACHTHOLFF FRIUDAVCSSERH*DHFTAAAPLENSTIIS*VAPGSWQDHA VLOKVOASSVATGFFSSVATARAFTUSKIGGSCCGASSVARSPTOTORGOVMGLI NGKGGCFESSGYLFFOTYTAGGGCCLGAKSVRASVFT	1			1
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ATGPPPGNTSSTQKWKICTICNELFPBNVYSVHPEKEHKAEKVP AVANYIMKIHNFTSKCLYCNRYLPTDTLLNHMLIHGISCPYCRS TFNDVEKMAAHMRWAVHIDEBMGPKTDSTLSFDLTLQQGSHTNIH LLVTTYNLRDAPAESVAYHAQNNPPVPPREQPKVQEKADIPVKS SPQAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLUHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEPPLLKKRKLDDDSDSP SFFEEKPEEPVVLALDPKGH\BDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKCVRDCEKYKPGVL LGFMMKELNKVKHEMDFDAEGLFEHHDEKDSRVNASKTADKKLN LGKEDDSSDSFENLEESSNBEGSPPDVPEVEFKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGPGQQVSDFEDNTCEMKFGTWSDE SSQSEDARSSKPAAKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDSEOFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVVPVAQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLWMKGRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFTVIGKIQSLEAKVPLPVMGGTGERASPG NCRHIVDAVC*SEHH*DHFLAAPLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFMAHSPGLGGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFABVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*BQCGGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFFWRWGLSHRT	ì	1		APARYSLOSANASSLSSGOLKSPSLSOSOASRVLGOSSSKPAAA
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TFNDVEKMAAHMRNVHIDEBMGPKTDSTLSFDLTLQQGSHTNIH LLVTTYNLRDAPABSVAYHAQNNFPVPPKPQPKVQEKADIFVKS SPQAAVPYKKDVGKTCPLCFSILKGPISDALAHHLRERHQVIQ TVHPVEKKLTYKCIHCLGYYTSMMTASTITLHLVHCGSVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP SFFEEKPEBFVULALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEESNESGSPFDVFEVEPKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSSESGPSQQVSDFEDNTCEMKPGTWSDE SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLJSQQA 6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQFGVMGLL NGKRGGCFESGYLFGFIVIGKIGSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAKESPGLGGETTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVRPDSOPVP RPLRVGLLQVGPLVVRGGGRRVAGRGKCWRDLLFPWRWGLSHRT	1	1	1	
LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQPKVQEKADIPVKS SPQAAVPYKROVGKTLCPLCFSILKGFISDALAHHLRERHQVIQ TVHPVEKKLTYKCIHCLGYTSNMTASTITLHLVHCRGVGKTQN GQDKTNAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDDSDSP SFFEEKPEFPVVLALDPKGH\EDDSYEARKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNNKELNRVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPEEH VLKVIPBDASESEEKLDQKEEGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGFGSQVSDFEDNTCEMKPGTWSDE SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVETAGGGECLGAKSVRASVFTGNQPGVWGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GRNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT		I		
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TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTMAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDSDSP SFFEKPEEPVVLALDPKGH\EDDSYEAKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNMKELNKVKHEMPFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPEBH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGGGQVSDFEDNTCEMKPGTWSDE SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVWKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIGSLEAKVPLPVNGQTGERASPG NCRIHLVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFYHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVWAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQSVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKCKGRDLLFPWRWGLSHRT	ì	1		LLVTTYNLRDAPAESVAYHAQNNPPVPPKPQPKVQEKADIPVKS
TVHPVEKKLTYKCIHCLGVYTSNMTASTITLHLVHCRGVGKTQN GQDKTMAPSRLNQSPSLAPVKRTYEQMEFPLLKKRKLDDSDSP SFFEKPEEPVVLALDPKGH\EDDSYEAKSFLTKYFT\KQPYP TRREIEKLAASLWV\WK\SDIASHFSNKRKKCVRDCEKYKPGVL LGFNMKELNKVKHEMPFDAEGLFENHDEKDSRVNASKTADKKLN LGKEDDSSSDSFENLEEESNESGSPFDPVFEVEPKISNDNPEBH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMHNASDS EVDQDDVVEWKDGASPSESGGGQVSDFEDNTCEMKPGTWSDE SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLSNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGVLVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMFPIQRPPLVWKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIGSLEAKVPLPVNGQTGERASPG NCRIHLVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFYHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVWAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQSVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKCKGRDLLFPWRWGLSHRT	ļ		1	SPOAAVPYKKDVGKTLCPLCFSILKGPISDALAHHLRERHOVIO
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LGKEDDSSDSFENLEEESNESGSPFDPVFEVERKISNDNPEEH VLKVIPEDASESEEKLDQKEDGSKYETIHLTEEPTKLMINASDS EVDQDDVVEWKDGASPSESGPGSQQVSDFEDNTCEMKPGTWSDE SSQSEDARSSKPAAKKKATMQGDREQLKWKNSSYGKVEGFWSKD QSQWKNASENDERLISNPQIEWQNSTIDSEDGEQFDNMTDGVAEP MHGSLAGVKLSSQQA 6009 4272 1534 CHGLQHLTPFRELNLSLQG*EPH*AA*QAVRSEEKSIC*GSPSC HLVLGULVPVARQSSHSAGPAQSAFR*TGTGSGTPKAAEQSGYW EAYTLGHQHWNMPPIQRPPLVMKGRRIMCGKCEKG*VSDSVTGG RAVAGEQASQRRTVFTAGGGECLGAKSVRASVFTGNQPGVMGLL NGKRGGCFESGYLFGFIVIGKIQSLEAKVPLPVNGQTGERASPG NCRIHIVDAVC*SEHH*DHFLAAAFLENSTIIS*VAPGSWQDHA VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL FVLAPQDGEGVPFVEGQLTTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	1			LGFNMKELNKVKHEMDFDAEGLFENHDEKDSRVNASKTADKKLN
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FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT			1	1
I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	1	1		VLQKEVQASVRCRGFESVDTAPAGFWAHSPPGLQGEPTTTSVSL
I*KLGALDVAFLHLLTLVCSSFNVAYG*GKNGGTTLHQLFAEVN AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	1		1	FVLAPQDGEGVPFVEGQLVTVLGLVVPQSIRHTFVHHTQLFLHP
AVTRGSAVQRRPSITISSIHVDTKIQQELHDVMVAGADGVVQWG DPFVVGLAGIFHLIDDPLHQIELSFQRRV*EQCQGVKPDSQPVP RPLRVGLLQVGPLVRGGGRRVAGRGKRCWRDLLFPWRWGLSHRT	1	1	1	
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SEQ Predicted beginning nucleotide location nucleotide location corresponding to first amino acid segment containing signal peptic (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Cysteine, location corresponding to first amino acid residue of amino acid sequence Sequen
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence P=Proline, Q=Glutamine, N=Asparagine, V=Sequence P=Proline, Q=Glutamine, N=Asparagine, V=Sequence N=Introduced insertion) 1 **RGRLSGEWGCGLGRGELFQVSIGIGVSIVHIGQGDHEVIX AGLVERGALHATGGQVEALUQULLDVGPAGALGLCDGAALFQX GRVGQLPAEGLQVCITLVAQWRMHDGRELGGAEWPWQALIGAA CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRRWRVFTWRYGNPLINLL*GAVCCRLVILRWCGLLEVHGVYGT*IHC GSFPGRLWP*PFISQERPMGHCQWEFRLAVPSWKCRWSRWVFTWRYGNPLINLL*GAVCCRLVILRWCGLLEVHGVYGT*IHC GSFPGRLWP*PFISQERPMGHCQWEFRLAVPSWKCRWSRWVFTWRYGNPLINLL*GAVCGCGQGGGPLSTWQACTGPGQAF AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGII PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSATIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTAN VKTIKALDGDFSEDNRKCRIATAPLIEAVENLTAFASNPEFF IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKL PTWSVLAGHSHTVSDSIKSLITSIRDKAPGGRECDYSIDGINF IRDIEQASLAAVSQSLATRDDISVEALQEQITSVVQEIGHLII
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I **RGRLSGEWGCGLGRGELFQVSIGIGVSIVHIGQGDHEVIA AGLVERGALHATGQGVEALVQQLLDVGPAGALGLCDGAALFQC GRVGQLPAEGLQVCITLVAQWRMHDGRELGGAEWPWQALHGAA CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRWRGG* R*NGLTIHCFN*LI*GAVCCRLVILRWCGLLEVHGVYGT*IHC GSFPGRLWP*PFISQERPNGHCQWEFRLAVPSWKCRWSRWRVI TWRYGNPLINILL*GAWLGGAACGGQQGGPLSTWQACTGPGQAA LPPFQGACRPTQRCRTWVCPIAWRQLLAYTRD 6010 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGES AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIE PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSA TIVAKHTSALCNACRIASKTANPVAKRHFVQSAKEVANSTAN VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFV IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKI PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINW IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
AGLVERGALHATGQGVEALVQQLLDVGPAGALGLCDGAALFQQ GRVGQLPAEGLQVCITLVAQWRMHDGRELGGAEWPWQALHGAA CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRRWRG*? R*NGLTIHCFN*LI*GAVCCRLVILRWCGLLEVHGVYGT*IHC GSFPGRLWP*PFISQERPNGHCQWEFRLAVPSWKCRWSRWRVI TWRYGNPLINLL*GAWLGGAACGGQQGGPLSTWQACTGPGQAA LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGES AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIE PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTAN VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFV IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKI PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIGGIHN IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
GRVGQLPAEGLQVCITLVAQWRMHDGRELGGAEWPWQALHGAM CGVGGAILLKALSQYFLKGG*RLWCARGQ*PVKKRQRRWRG*T R*NGLTIHCFN*LI*GAVCCRLVILKWCGLLEVHGVYGT*IH GSFPGRLWP*PFISQERPNGHCQWEFRLAVPSWKCRWSRWRVI TWRYGNPLLNLL*GAWLGGAACGGQQGGPLSTWQACTGPGQAM LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGES AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGIB PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSM TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTAN VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFV IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKI PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINB IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
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R*NGLTIHCFN*LI*GAVCCRLVILRWCGLLEVHGVYGT*IHC GSFPGRLWP*PFISQBRPNGHCQWEFRLAVPSWKCRWSRWRVF TWRYGNPLLNLL*GAWLGGAACGGQQGGPLSTWQACTGPGQAF LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD 6010 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYPDCIESVMENSKVLGES AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGTI PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTAN VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFV IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKL PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINE IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
GSFPGRLWP*PFISQERPNGHCQWEFRLAVPSWKCRWSRWRVF TWRYGNPLLNLL*GAWLGGAACGGQQGGPLSTWQACTGPGQAX LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD 6010 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGES AGISQNAKTGDLPAFGECVGIASKALCGLTEAAQAAYLVGIB PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSX TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTAN VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFV IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKL PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINF IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
TWRYGNPLLNLL*GAWLGGAACGGQQGGPLSTWQACTGPGQAM LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD 6010 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGES AGISQNAKTGDLPAFGECVGIASKALCGLTEAAQAAYLVGII PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSA TIVAKHTSALCNACRIASSKTANPVAKRHPVQSAKEVANSTAN VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFV IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKL PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINF IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
LPPFQGACRPRTQRCRTWVCPIAWRQLLAYTRD 6010 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGES AGISQNAKTGDLPAFGECVGIASKALCGLTEAAQAAYLVGII PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSA TIVAKHTSALCNACRIASSKTANPVAKRHPVQSAKEVANSTA VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEF\ IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKL PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINF IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
6010 1 3533 IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGES AGISQNAKTGDLPAFGECVGIASKALCGLTEAAQAAYLVGIE PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTAN VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEF- IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKI PTWSVLAGHSHTVSDSIKSLTTSIRDKAFGQRECDYSIDGINF IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAQAAYLVGII PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTAN VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEN IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKI PTWSVLAGHSHTVSDSIKSLITSIRDKAFGQRECDYSIDGINN IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSQVLSA TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTAN VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEF\ IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKL PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINF IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTAN VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEF\ IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKL PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINF IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEF\ IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKL PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINF IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKI PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINF IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINF IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLII
IRDIEQASLAAVSQSLATRDDISVEALQEQITSVVQEIGHLII
TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLM
EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPR
TFVDYQTTVVKYSKALAVTAQEMMTKSVTNPEELGGLASQMTS
YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG
ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQAC
TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKT
KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGA
SIGSDDPETQVVLINAIKDVAKALSDLISATKGAASKEVDDPS
YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIK
ELTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQ
DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTE
TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQA
EAMKGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRA
PKQADETLDFEBQILEAAKSIAAATSALVKSASAAQRELVAQG
VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGH
SEEKLISSAKQVAASTAQILVACKVKADQDSEAMRRLQAAGNA
KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEE
LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6011 446 1835 LLQPAMRKSPGLSDCLWAWILLLSTLTGRSYGQPSLQDELKDN
TVFTRILDRLLDGYDNRLRPGLGERVTEVKTDIFVTSFGPVSD
DMEYTIDVFFRQSWKDERLKFKGPMTVLRLNNLMASKIWTPDT
FHNGKKSVAHNMTMPNKLLRITEDGTLLYTMRLTVR\AECPMA
GRDFPM\D\AHACPLKFGSYAYTRAEVVYEWTREPARSVVVAE
GSRLNQYDLLGQTVDSGIVQSSTGEYVVMTTHFHLKRKIGYFV
QTYLPCIMTVILSQVSFWLNRESVPARTVFGVTTVLTMTTLSI
ARNSLPKVAYATAMDWFIAVCYAFVFSALIEFATVNYFTKRGY
WDGKSVVPEKPKKVKDPLIKKNNTYAPTATSYTPNLARGDPGL
TIAKSATIEPKEVKPETKPPEPKKTFNSVSKIDRLSRIAFPLL
GIFNLVYWATYLNREPQLKAPTPHQ
6012 351 5013 PAELFQSFAIWHKELYDWRLGPWNQCQPVISKSLEKPLECIKG
EGIQVREIACIQKDKDIPAEDIICEYFEPKPLLEQACLIPCQQ
CIVSEFSAWSECSKTCGSGLQHRTRHVVAPPQFGGSGCPNLTE
QVCQSSPCEAEELRYSLHVGPWSTCSMPHSRQVRQARRRGKNK
REKDRSKGVKDPEARELIKKKRNRNRQNRQENKYWDIQIGYQT
EVMCINKTGKAADLSFCQQEKLPMTFQSCVITKECQVSEWSEW
PCSKTCHDMVSPAGTRVRTRTIRQFPIGSEKECPEFEEKEPCL
QGDGVVPCATYGWRTTEWTECRVDPLLSQQDKRRGNQTALCGG
IQTREVYCVQANENLLSQLSTHKNKEASKPMDLKLCTGPIPNT
QLCHIPCPTECEVSPWSAWGPCTYENCNDQQGKKGFKLRKRRI
NEPTGGSGVTGNCPHLLEAIPCEEPACYDWKAVRLGDCEPDNG:
BCGPGTQVQEVVCINSDGEEVDRQLCRDAIFPIPVACDAPCPKI
CVLSTWSTWSSCSHTCSGKTTEGKQIRARSILAYAGEEGGIRC
NSSALQEVRSCNEHPCTVYHWQTGPWGQCIEDTSVSSFNTTTTT
NGEASCSVGMQTRKVICVRVNVGQVGPKKCPESLRPETVRPCLI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:		_	H=Histidine, I=Isoleucine, K=Lysine,
1	location	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	1	bequest	\=possible nucleotide insertion)
L	sequence		PCKKDCIVTPYSDWTSCPS\SCKEGDSSIRKQSRHRVIIQLPAN
ļ	1	l l	•
1		1	GGRDCTDPLYEEKACEAPQACQSYRW\KTHKW\HRCQ\LVP\WS
Í	Í	ĺ	VQQDSP\GAQEGCGPGRQARAITCRKQDGGQAGIHECLQYAGPV
	1	1	PALTOACQIPCODDCQLTSWSKFSSCNGDCGAVRTRKRTLVGKS
1	1		KKKEKCKNSHLYPLIETQYCPCDKYNAQPVGNWSDCILPEGKVE
1	1	1	VLLGMKVQGDIKECGQGYRYQAMACYDQNGRLVETSRCNSHGYI
	1	1	
	†	i	EEACIIPCPSDCKLSEWSNWSRCSKSCGSGVKVRSKWLREKPYN
1	\$		GGRPCPKLDHVNQAQVYEVVPCHSDCNQYLWVTEPWSICKVTFV
1	†	1	NMRENCGEGVQTRKVRCMQNTADGPSEHVEDYLCDPEEMPLGSR
1	1		VCKLPCPEDCVISEWGPWTQCVLPCNQSSFRQRSADPIRQPADE
1	1		GRSCPNAVEKEPCNLNKNCYHYDYNVTDWSTCQLSEKAVCGNGI
	Į.		KTRMLDCVRSDGKSVDLKYCEALGLEKNWQMNTSCMVECPVNCQ
1			
1			LSDWSPWSECSQTCGLTGKMIRRRTVTQPFQGDGRPCPSLMDQS
1	i		KPCPVKPCYRWQYGQWSPCQVQEAQCGEGTRTRNISCVVSDGSA
1			DDFSKVVDBEFCADIBLIIDGNKNMVLEBSCSQPCPGDCYLKDW
	1		SSWSLCQLTCVNGEDLGFGGIQVRSRPVIIQELENQHLCPEQML
			ETKSCYDGQCYEYKWMASAWKGSSRTVWCQRSDGINVTGGCLVM
			SOPDADRSCNPPCSQPHSYCSETKTCHCEEGYTEVMSSNSTLEQ
1		i	CTLIPVVVLPTMEDKRGDVKTSRAVHPTQPSSNPAGRGRTWFLQ
		ł	
ı			PFGPDGRLKTWYYGVAAGAFVLLIFIVSMIYLACKKPKKPQRRQ
1			NNRLKPLTLAYDGDADM
6013	1161	710	GAFIAGVPVQPVLIRYPNSLDTTSWAWRGPGVLKVLWLTASQPC
1			SIVDVEFLPVYHPSPEESRDPTLYANNVQRVMAQALGIPATECE
1			FVGSLPVIVVGRLKVALEPQL/WGTGKSASEGWAVRWLCGRWGR
i	l .		ARPESNDQPGRVCQAATAL
L			
6014	2857	613	EAVAGGMEKSRMNLPKGPDTLCFDKDEFMKEDFDVDHFVSDCRK
	i		RVQLEELRDDLELYYKLLKTAMVELINKDYADF\VNLSTNLVGM
1		ì	DKALNQLSVPLGQLREEVLSLRSSVSEGIRAVDERMSKQEDIRK
1			KKMCVLRLIQVIRSVEKIEKILNSQSSKETSALEASSPLLTGQI
	1	1	LERIATEFNQLQFHACQSK\GMPLLDKVRPRIAGITAMLQQSLE
	1	İ	GLLLEGLOTSDVDIIRHCLRTYATIDKTRDAEALVGQVLVKPYI
	1		DEVIIEQFVESHPNGLQVMYNKLLEFVPHHCRLLREVTGGAISS
	1		EKGNTVPGYDFLVNSVWPQIVQGLEEKLPSLFNPGNPDAFHEKY
1	i		
	l		TISMDFVRRLERQCGSQASVKRLRAHPAYHSFNKKWNLPVYFQI
	i	i	RFREIAGSLEAALTDVLEDAPAESPYCLLASHRTWSSLRRCWSD
		1	EMFLPLLVHRLWRLHSGRFWARYSVFV\N\ELSLRPISNESPKE
	1		IKKPLVTGSKEPSITQGNTEDQGSGPSETKPVVSISRTQLVYVV
			ADLDKLOEOLPELLEIIKPKLEMIGFKNFSSISAALEDSQSSFS
1	į.		
			ACVPSLSSKIIQDLSDSCFGFLKSALEVPRLYRRTNKEVPTTAS
			SYVDSALKPLFQLQSGHKDKLKQAIIQQWLBGTLSESTHKYYET
İ			VSDVLNSVKKMEESLKRLKQARKTTPANPVGPSGGMSDDDKIRL
			QLALDVEYLGEQIQKLGLQASDIKSFSALAELVAAAKDQATAEQ
			p
6015	13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC
5015			VKGKGSLPLSAHGIVVAWLSRAEWDQVTVYLFCDDHKLQRYALN
1			RITYWRSRSGNELPLAVASTADLIRCKLLDVTGGLGTDELRLLY
1			
1			GMALVRFVNLISERKTKFAKVPLKCLAQEVNIPDWIVDLRHELT
1			HKKMPHINDCRRGCYFVLDWLQKTYWCRQLENSLRETWELEEFR
1			EGIEEEDQEEDKNIVVDDITEQKPBPQDDGKSTESDVKADGDSK
1			GSEEVDSHCKKALSHKELYERARELLVSYEEEQFTVLEKFRYLP
l			KAIKAWNNPSPRVECVLAELKGVTCENREAVLDAFLDDGFLVPT
i			FEOLAALQIEYEENVDLNDVLVPKPFSQFWQPLLRGLHSQNFTQ
			ALLERMLSELPALGISGIRPTYILRWTVELIVANTKTGRNARRF
1			
1		{	SAGQWEARRGWRLFNCSASLDWPRMVESCLGSPCWASPQLLRII
-1			F\KAMGQGLQDE\EQEKLLRICSIYTQSGENSLVQEGSEASPIG
1		1	KSPYTLDSLYWSVKPASSSFGSEAKAQQQEEQGSVNDVKBEEKE
1			EKEVLPDQVEEEEENDDQBEEEEDEDDEDDEEBDRMEVGPFSTG
1	İ	1	QESPTAENARLLAQKRGALQGSAWQVSSEDVRWDTFP\LGRMPR
	1		SRPRTPAELMLENYDTHVIFWTKPVL\EQRLEPSTCK\TDTLGL
,		Ī	
			\SCGVGS\GNCSNSSSSNFRGAFLLRARGSLH\GL\KTGLQLF
6016	. 13	2237	AEGCAERRGTEPVVELSMSWESGAGPGLGSQGMDLVWSAWYGKC

SEQ Predicted Predicted end Amino acid segment contains in the predicted end predicted end predicted end predicted end (A=Alanine, C=Cysteine, Glutamic Acid, F=Phenyla location corresponding corresponding to first L=Leucine, M=Methionine,	D=Aspartic Acid, E=
NO: nucleotide location Glutamic Acid, F=Phenyla location corresponding H=Histidine, I=Isoleucin	
location corresponding H=Histidine, I=Isoleucin	didnine, GaGlyCine,
	na V.T.
to first amino acid P=Proline, Q=Glutamine,	
amino acid residue of S=Serine, T=Threonine, V	
residue of amino acid W=Tryptophan, Y=Tyrosine	
amino acid sequence Codon, /=possible nucleo	otide deletion,
sequence \=possible nucleotide in	nsertion)
VKGKGSLPLSAHGIVVAWLSRAEV	WDQVTVYLFCDDHKLQRYALN
RITVWRSRSGNELPLAVASTADLI	IRCKLLDVTGGLGTDELRLLY
GMALVRFVNLISERKTKFAKVPL	KCLAQEVNIPDWIVDLRHELT
HKKMPHINDCRRGCYFVLDWLQK	-
EGIEEEDQEEDKNIVVDDITEQK	·-
GSEEVDSHCKKALSHKELYERARE	
KAI KAWNNPSPRVECVLAELKGV	-
1	
FEQLAALQI EYEENVOLNOVLVP	
ALLERMLSELPALGISGIRPTYII	
SAGQWEARRGWRLFNCSASLDWPF	_
F\KAMGQGLQDE\EQEKLLRICSI	
KSPYTLDSLYWSVKPASSSFGSEA	
EKEVLPDQVEEEERNDDQEEBEEI	
QESPTAENARLLAQKRGALQGSAV	WQVSSEDVRWDTFP\LGRMPR
SRPRTPAELMLENYDTHVIFWTK	PVL\EQRLEPSTCK\TDTLGL
\SCGVGS\GNCSNSSSSNFRGAFI	LLEARGSLH\GL\KTGLQLF
6017 203 3469 SHQEIEQNSAMAPRKRGGRGISF3	
NFALQTMEPALPMPPVEELDVMFS	
AEKKWQIYCSKKKDQEENKGATSW	WPEFYIDOLNSMAARKSLLAL
EKEEEEERSKTIESLKTALRTKPM	_
TMDYETSESRIHTSLIGCIKALMN	
SLSTENIKTKVAVLEILGAVCLVI	_
TRFQTLINDLDKSTGRYRDEVSLI	
DFRLHLRYK\FLMLGIHPVMDKLF	
DELEFAKRFELVHIDTKSATQMFE	
HCLQMPYKRSGNTVQYWLLLDRI	
FNIKNVVRMLVNENEVKQWKEQAE	
DAKTQEKEEMMQTLNKMKEKLEKE	
LSRRAVCASIPGGPSPGAPGGPFF	
LPPPPPPLPPGGPPPPGPPPLGA	AIMPPPGAPMGLALKKKSIPQ
PTNALKSFNWSKLPENKLEGTVWT	reiddtkvfkildledlertf
SAYQRQQDFFVNSNSKQKEADAII	DDTLSSKLKVKELSVIDGRRA
QNCNILLSRLKLSNDEIKRAILTN	MDEQEDLPKDMLEQLLKFVPE
KSDIDLLEEHKHELDRMAKADRFI	LFEMSRINHYQQRLQSLYFKK
KFAERVAEVKPKVEAIRSGSEEVE	FRSGALKOLLEVVLAFGNYMN
KGORGNAYGFKISSLNKIADTKSS	SIDKNITLLHYLITIVENKYP
SVLNLNEELRDIPQAAKVNMTELL	
KSQPPQPGDKFVSVVSQFITVASE	
KHFGEEAGKIQPDEFFGIFDQFLC	
RRARMEAQLKEQRERERKMRKAKE	
FDKDLSKLKRNRKRITNOMTDSSF	
6018 13 2510 TISOSGGIRRREAVWFEVVNMDE	
ALSSSYSSDALDFETEHKLDPVFI	-
; ; ;	
GEAVGADSGTSSAVSLKNRAARTI	
TSSGVSYGGTVSLQDAVTRRPPVI	
GDLKGGNKAAIQGNGDVGAGAATG	
AHPAAPGPVSRVYSRDRNQKCDDC	
ACAGYFLLQILRRIGAVGQAVSRI	
WWLGIGWYQFVTLISWLNVFLLTR	
LSLRGQG\NFFSFLPVLNWASMHR	
PLQGDSEAFPWHWMSGVEQQVASI	LSGQCHHHGENLRELTTLLQK
LQARVDQMEGGAAGPSASVRDAVG	GQPPRETDFMAFHQEHEVRMS
HLEDILGKLREKSEAIQKELEQTK	KQKTISAVGEQLLPTVEHLQL
ELDQLKSELSSWRHVKTGCETVDA	AVQERVDVQVREMVKLLFSED
QQGGSLEQLLQRFSSQFVSKGDLQ	
TKQLPTSEAVVSAVSEAGASGITE	
MVDFALESGGGSILSTRCSETYET	
VVIQPDIYPGNCWAFKGSQGYLVV	
SPTGNISSAPKDFAVYGLENEYQE	
QALKRPDDTAFQIVELRIFSNWGH	
6019 2 1066 TPNDREPPPQRPPSSRRASHLAQE	TTSAASLGDQTQTLGSLTTA

SEQ Predicted predicted end beginning nucleotide location corresponding to first amino acid residue of residue of amino acid segment containing signal pep (A=Alanine, C=Cysteine, D=Aspartic Acid, Glutamic Acid, F=Phenylalanine, G=Glycin H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=S	E=
NO: nucleotide location corresponding to first amino acid residue of residue of amino acid residue of amino acid residue of residue	E= 2,
location corresponding to first amino acid residue of amino acid residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unknown, *=S	2,
corresponding to first L-Leucine, M=Methionine, N=Asparagine, to first amino acid residue of residue of amino acid residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unknown, *=S	
to first amino acid residue of residue of amino acid residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unknown, *=S	
amino acid residue of S=Serine, T=Threonine, V=Valine, residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown, *=S	
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unknown, *=S	
" "" "" " " " " " " " " " " " " " " "	
	top
amino acid sequence Codon, /=possible nucleotide deletion,	
sequence \=possible nucleotide insertion)	
PVITSAIRSMPGISSQILTNAQGQVIGTLPWVVNSASVAA	PAPA
QSLQVQAVTPQLLLNAQGQVIATLASSPLPPPVAVRK\PS	PPES
LLKSEVQPIKPTPTVPQPAVVIASPAPAAKPSASAPIPIT	
PTVSQLVSKPHTPSLDEDGINLEEIREFAKNFKIRRLSLG	COUL
QVGQALTATEGPAYSQSAICRFEKLDITPKSAQKLKPVLE	TIVI
EAELRNQEGQQNLMEFVGGEPSKKRKTSFTPQAIEALN	
KNPLPTGQEITEIAKELNYDREVVRVWFCNRRQTLKNTSKI	AYPE
	NVF
QIP 6020 4953 549 EATOFEVSTGNYGNKEDTTCKPLASTTOVSPAVEDGNYVV	
MINISTER DESCRIPTION OF THE PROPERTY OF THE PR	
AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALI	
QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLI	
RKLRSRSLSQIHEAAVRMRSBATDVKSTLAEIEDWLDKLM(LTE
EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASC	
GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNS	
GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLI	REF
FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNES	DVD
GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYI	TND
AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKE	
LTQTASSTAGAMEBLQDQEGWBYASLIGWKFHWKQRSSDTE	
RWRRKMAPSETHGAAAI FKLEGALGADTTEDGDEKSLEKQI	
TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSH	SDP
YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQT	
NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITP:	
HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLY	
QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGO	
ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVII	HRQ
FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAF	PCR
DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEE	EIV
DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVABFE	GLT
DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVF	ADD
RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKI	TOT C
KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEXDLKISVY	DAD
TFTRDEKVGETIIDLENPF\LSRPG\SHCG\IPEEYCVSGV	עזע
RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYS	NIW
COLUMN (FIQ (DEQUARACIÓN EQPILA ELOGRATA GORDAS	LDE
FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHST	FQP
NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPG	NEE
NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKE	
SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCR	
HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMK	
PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPN	MNP
KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLL	ILL
LFVAVLLYSLPNYLSMKIVKPNV	
6021 4953 549 EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYY	LPW
AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIEALK	SGT
QGKIPANQLAELWLKLIDBVIEDTRYTLPLTEGKANVTVLD	rot
RKLRSRSLSQIHEAAVRMRSEATDVKSTLAEIEDWLDKLMQ	יעטט. אאר
EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASG	210
GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNS	.10
GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLK	(EF
FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYQNES	4Xb
GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYD	INR
AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKR	KKD
LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTF	RRR
RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKOK	ISA
TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSF:	SDP
YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQT	/LO
NPPKVIMELFDNDQVGKDEFLGRS1FSPVVKLNSEMD1TPKI	.Lw
HPVMNGDKACGDVLVTAELILRGKDGSNLPILPPQRAPNLY	
QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGG	
BSVVIKNLKKTPNPPSSVLFMKVFLPKEBLYMPPLVIKVID:	DC PACE
BOAVAIGHT THE POST THE WAS THE POST TO THE POST THE POST TO THE POST THE PO	IKŲ
FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPI	CR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			DIVIEMBDTKPLLASKCLSSMSTALSKMASPATVHLTEKEEEIV
			DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
			DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
1	1		RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG
			KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPQEKDLKISVYDYD
1			TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
İ			RDSLR/PTQ/LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
			FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFQP
		Į	NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
			NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEQLCIVAKKEHFW
			SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
	1		HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
			PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
			KLDLPNRPBTSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL LFVAVLLYSLPNYLSMKIVKPNV
6022	4953	549	
0022	1,233	347	EAIQFEVSIGNYGNKFDTTCKPLASTTQYSRAVFDGNYYYYLPW AHTKPVVTLTSYWEDISHRLDAVNTLLAMAERLQTNIBALKSGI
.			QGKIPANQLAELWLKLIDEVIEDTRYTLPLTEGKANVTVLDTQI
			RKLRSRSLSQIHEAAVRMRSEATDVKSTLABIEDWLDKLMOLTE
1			EPQNSMPDIIIWMIRGEKRLAYARIPAHQVLYSTSGENASGKYC
1		İ	GKTQTIFLKYPQEKNNGPKVPVELRVNIWLGLSAVEKKFNSFAE
1 i			GTFTVFAEMYENQALMFGKWGTSGLVGRHKFSDVTGKIKLKREF
			FLPPKGWEWEGEWIVDPERSLLTEADAGHTEFTDEVYONESRYP
		1	GGDWKPAEDTYTDANGDKAASPSELTCPPGWEWEDDAWSYDINR
			AVDEKGWEYGITIPPDHKPKSWVAAEKMYHTHRRRRLVRKRKKD
			LTQTASSTAGAMEELQDQEGWEYASLIGWKFHWKQRSSDTFRRR
			RWRRKMAPSETHGAAAIFKLEGALGADTTEDGDEKSLEKQKHSA
1			TTVFGANTPIVSCNFDRDYIYHLRCYVYQARNLLALDKDSFSDP
			YAHICFLHRSKTTEIIHSTLNPTWDQTIIFDEVEIYGEPQTVLQ
1			NPPKVIMELFDNDQVGKDEFLGRSIFSPVVKLNSEMDITPKLLW
			HPVMNGDKACGDVLVTABLILRGKDGSNLPILPPQRAPNLYMVP
1			QGIRPVVQLTAIEILAWGLRNMKNFQMASITSPSLVVECGGERV
1			ESVVIKNLKKTPNFPSSVLFMKVFLPKEELYMPPLVIKVIDHRQ
			FGRKPVVGQCTIERLDRFRCDPYAGKEDIVPQLKASLLSAPPCR
1			DIVIEMEDTKPLLASKCLSSMSTALSKMASPATVHLTEKEBEIV
		}	DWWSKFYASSGEHEKCGQYIQKGYSKLKIYNCELENVAEFEGLT
1			DFSDTFKLYRGKSDENEDPSVVGEFKGSFRIYPLPDDPSVPAPP
1			RQFRELPDSVPQECTVRIYIVRGLELQPQDNNGLCDPYIKITLG KKVIE\DRDHYIPNTLNPVFGRMYELSCYLPOEKDLKISVYDYD
			TFTRDEKVGETIIDLENPF\LSRFG\SHCG\IPEEYCVSGVNTW
1		}	RDSLR\PTQ\LLQNVARFKGFPQPILSEDGSRIRYGGRDYSLDE
	j		FEANKILHQHLGAPEERLALHILRTQGLVPEHVETRTLHSTFOP
	į	Ì	NIS\RYYLRVIIWNTKDVILDEKSITGEEMSDIYVKGWIPGNEE
		,	NKQKTDVHYRSLDGEGNFNWRFVFPFDYLPAEOLCIVAKKEHFW
			SIDQTEFRIPPR\LIIQIW\DNDKFS\LDDYLGFPRTLTCRHTI
,			HFLQKSPGGNC/RGLDMIPDLKAMNPLKAKTASLFEQKSMKGWW
	1		PCYAEKDGARVMAGKVEMTLEILNEKEADERPAGKGRDEPNMNP
			KLDLPNRPETSFLWFTNPCKTMKFIVWRRFKWVIIGLLFLLILL
			LFVAVLLYSLPNYLSMKIVKPNV
6023	102	916	SQELGMFVELNNLLNTTPDRAEQGKLTLLCDAKTDGSFLVHHFL
			SFYLKANCKVCFVALIQSFSHYSIVGQKLGVSLTMARERGOLVF
		1	LEGL/IVCSGR\VFQAQKEPHPLQFLREANAGNLKPLFEFVREA
1			LKPVDSGEARWTYPVLLVDDLSVLLSLGMGAVAVLDFIHYCRAT
	1		VCWELKGNMVVLVHDSGDAEDEENDILLNGLSHQSHLILRAEGL
		}	ATGFCRDVHGQLRILWRRPSQPAVHRDQSFTYQYKIQDKSVSFF
			AKGMSPAVL
6024	3	3260	FLSFLCYPRFRCLFCLQFAIPASRMEQLNELELLMEKSFWEEAB
		1	1
1		i	LPAELFQKKVVASFPRTVLSTGMDNRYLVLAVNTVQNKEGNCEK
1			RLVITASQSLENKELCILRNDWCSVPVEPGDIIHLEGDCTSDTW
	-		RLVITASQSLENKELCILRNDWCSVPVEPGDIIHLEGDCTSDTW

SEQ Predicted Predicted end Amino acid segment containing	
ID beginning nucleotide (A=Alanine, C=Cysteine, D=As	nartic Acid F-
NO: nucleotide location Glutamic Acid, F=Phenylalani	partite Acid, E-
location corresponding H=Histidine, I=Isoleucine, K	Tradma
corresponding to first L=Leucine, M=Methionine, N=A	=bysine,
to first amino acid P=Proline, Q=Glutamine, R=Ar	sparagine,
amino acid residue of S=Serine, T=Threonine, V=Val	
residue of amino acid W=Tryptophan, Y=Tyrosine, X=	me,
	Unknown, =stop
YRLNLSQDEIKQEVEDYLPSFCKWAGDF	
PSDNSKDNSTCNIEVVKPMDIEESIWSP	
HRGYKTKYKIMPLELKTGKESNSIEHRS	
EAGLLLYLKTGQMYPVPANHLDKRELLX	LRNOMAFSLFHRISKS
ATRQKTQLASLPQIIEEEKTCKYCSQIG	NCALYSRAVEQQMDCS
SVPIVMLPKIEEETQHLKQTHLEYFSLW	
HQNIWLMPASEMEKSGSCIGNLIRMEHV	KIVCDGQYLHNFQCKH
GAIPVTNLMAGDRVIVSGEERSLFALSRO	
RNLSVLPESTLFRLDQEEKNCDIDTPLGI	
DLIIDFREPQFISYLSSVLPHDAKDTVAG	
VLLSKDYTLIVGMPGTGKTTTICTLVRI	LYACGFSVLLTSYTHS
AVDNILLKLAKFKIGFLRSR\QIQKVHP	
KS\LALLEBLYTSQLIDATTCMGINHPII	PSRKIFDFCIVDEASQ
ISQPICLGPLFFSRRFVLVGDHQQLPPL	VLNREARALGMSESLF
KRLEQNKSAVVQLTVQYRMNSKIMSLSNI	
NAVINLRHFKDVKLELEFYADYSDNPWLi	MGVFEPNNPVCFLNTD
KVPAPEQVEKGGVSNVTEAKLIVFLTSI	
YRQQLKIINDLLARSIGMVEVNTVDKYQI	
KDGTVGELLKDWRRLNVAITRAKHKLILI	LGCVPSLNCYPPLEKL
LNHLNSEKLIIDLPSREHESLCHILGDFC	
6025 3977 89 GGFPAQSDHLPPVFPLRSDLLITMSTLYN	VSPHPDAFPSLRALIA
ARYGEAGEGPGWGGAHPRICLQPPPTSRT	
GLWVWGATAVAQLLWPAGLGGPGGSRAAN	VLVQQWVSYADTELIP
AACGATLPALGLRSSAQDPQAVLGALGRA	ALSPLEEWLRLHTYLA
GEAPTLADLAAVTALLLPFRYVLDPPARF	
PEFRAVLGEVVLYSGARPLSHQPGPEAPA	ALPKTAAQLKKEAKKR
EKLEKFQQKQKIQQQQPPPGEKKPKPEKF	
PGEKKDVSGPMPDSYSPRYVEAAWYPWWE	
AANPRGVFMMCIPPPNVTGSLHLGHALTN	NAIODSLTRWHRMRGE
TTLWNPGCDHAGIATQVVVEKKLWREQGI	SRHQLGREAFLQEVW
KWKEEKGDRIYHQLKKLGSSLDWDRACFT	MDPKLSAAVTEAFVR
LHEEGIIYRSTRLVNWSCTLNSAISDIEV	/DKKELTGRTLLSVPG
YKEKVEFGVLVSFAYKVQGSDSDEEVVVA	
HPKDTRYQHLKGKNVIHPFLSRSLPIVFD	
PAHDQNDYEVGQRHGLEAISIMDSRGALI	NVPPPFLGLPRFEAR
KAVLVALKERGLFRGIEDNPMVVPLCNRS	KDVVEPLLRPOWYVR
CGEMAQAASAAVTRGDLRILPERHQRTWH	LAWMDNIRE\WCMFPG
KLWWG\HR\IPAYFVTVSDPAVPPGEDPD	GRYWVSGRNEABARE
KAAKEFGVSPDKISLQQDEDVLDTWFSSG	LFPLSILGWPNQSED
LSVFYPGTLLETGHDILFFWVARMVMLGL	
IVRDAHGRKMSKSLGNVIDPLDVIYGISL	
EVEKAKEGQKADFPAGIPECGTDALRFGL	CAYMSOGRDINLDVN
RILGYRHFCNKLWNATKFALRGLGKGFVP	SPTSQPGGHESLVDR
WIRSRLTEAVRLSNQGFQAYDFPAVTTAQ	YSFWLYELCDVYLEC
LKPVLNGVDQVAAECARQTLYTCLDVGLR	LLSPFMPFVTEELFQ
RLPRRMPQAPPSLCVTPYPEPSECSWKDP	EAEAALELALSITRA
VRP\LRADYNLHPESGPTCFLEVAD\EAT	
QAQVVVAVAEPWGLPAP\QGCAVALASDR	
ARELG\KLQ\AKRVEAQ\RQAQ\RLR\ER	
VQEADEAKLQQTEAELRKVDBAIALFQKM	
6026 2674 514 GPITFLKKKAKMKDMPLRIHVLLGLAITT	
TCEIRPWFTPRSIYMEASTVDCNDLGLLT	
TNNIAKIEYSTDFPVNLTGLDLSQNNLSS	
YLEENKLTELPEKCLSELSNLQELYINHN	
LLRLHLNSNRLQMINSKWFDALPNLEILM	
PLINLRSLVIAGINLTEIPDNALVGLENL	
VALQKVVNLKFLDLNKNPINRIRRGDFSN	
ISIDSLAVDNLPDLRKIEATNNPRLSYIH	
NSNALSALYHGTIESLPNLKEISIHSNPI	
IRFMEPDSLFCVDppEFQGQNVRQVHFRD	
SNLNVEAGSYVSFHCRATA\EPQPEIYWI	

SEO	Predicted	Predicted end	Amino acid cognont cort-
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
ł		}	KFYVHSEGTLDINGVTPKEGGLYTCIATNLVGADLKSVMIKVDG
		-	SFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFVK
i			TENSHAAQSARIPSDVKVYNLTHLNPSTEYKICIDIPTIYQKNR
1			KKCVNVTTKGLHPDQKEYEKNNTTTLMACLGGLLGIIGVICLIS
		·	CLSPEMNCDGGHSYVRNYLQKPTFALGELYPPLINLWEAGKEKS TSLKVKATVIGLPTNMS
6027	5254	4148	GGRRAPGRPGRSIKDEEEBTVFREVVSFSPDPLPVRYYDKDTTK
	, , ,	1210	PISFYLSSLEELLAWKPRLEDGFNVALEPLACROPPLSSORPRT
İ		ĺ	LLCHDMMGGYLDDRFIQGSVVQTPYAFYHWQCIDVFVYFSHHTV
-			TIPPVGWTNTAHRHGVCVLGTFITEWNEGGRLCEAFLAGDERSY
1			QAVADRLVQIT\RFFRFDGWLINIENSLSLAAVGNMPPFLRYLT
1			TQLHRQVPGGLVLWYDSVVQSGQLKWQDELNQHNRVFFDSCDGF
Į.			FTNYNWREEHLERMLGQAGERRADVYVGVDVFARGNVVGGRFDT
	i		DKVGGGFRPRASGPVPPLGPHFLMDLPFPSAPQRNDSSCSSQSG
			DPVALRNRCPAPAKLCPH
6028	120	3432	NCLLLQAKGFHGEIEDLQQWLTDTERHLLASKPLGGLPETAKEQ
			LNVHMEVCAAFEAKEETYKSLMQKGQQMLARCPKSAETNIDODI
			NNLKEKWESVETKLNER\KT\KLEEALNLA\MEFHNSL\QDFIN
			WLTQAEQTLNVASRPSLILDTVLFQIDEHKVFANEVNSHREQII
			ELDKTGTHLKYFSQKQDVVLIKNLLISVQSRWEKVVQRLVERGR
j	j		SLDDARKRAKQFHEAWSKLMEWLEESEKSLDSELEIANDPDKIK
			TQLAQHKEFQKSLGAKHSVYDTTNRTGRSLKEKTSLADDNLKLD
			DMLSELRDKWDTICGKSVERQNKLEEA\LLFSGQFTDALQALID WLYRVEPQLAEDQPVHGDIDLVMNLIDNHKAFQKELGKRTSSVQ
1			ALKRSARELIEGSRDDSSWVKVQMQELSTRWETVCALSISKQTR
1			LEAALRQAEEFHSVVHALLEWLAEAEQTLRFHGVLPDDEDALRT
			LIDQHKEFMKKLEEKRAELNKATTMGDTVLAICHPDSITTIKHW
İ			ITIIRARFEEVLAWAKQHQQRLASALAGLIAKQELLEALLAWLQ
1			WAETTLTDKDKEVIPQEIEEVKALIAEHQTFMEEMTRKQPDVDK
			VTKTYKRRAADPSSLQSHIPVLDKGRAGRKRFPASSLYPSGSOT
1			QIETKNPRVNLLVSKWQQVWLLALERRRKLNDALDRLEELREFA
			NFDFDIWRKKYMRWMNHKKSRVMDFFRRIDKDQDGKITRQEFID
i			GILSSKFPTSRLEMSAVADIFDRDGDGYIDYYEFVAALHPNKDA
			YKPITDADKIEDEVTRQVAKCKCAKRFQVEQIGDNKYRFFLGNQ
			FGDSQQLRLVRILRSTVMVRVGGGWMALDEFLVKNDPCRAKGRT
1			NMELREKFILADGASQGMAAFRPRGRRSRPSSRGASPNRSTSVS
			SQAAQAASPQVPATTTPKILHPLTRNYGKPWLTNSKMSTPCKAA ECSDFPVPSABGTPIQGSKLRLPGYLSGKGPHSGEDSGLITTAA
			ARVRTQFADSKKTPSRPGSRAGSKAGSRASSRRGSDASDFDISE
			IQSVCSDVETVPQTHRPTPRAGSRPSTAKPSKIPTPQRKSPASK
			LDKSSKR
6029	1	3533	IMPCGSSRLLRGCWTHPNEPVSDLSYFDCIESVMENSKVLGESM
			AGISQNAKTGDLPAFGECVGIASKALCGLTEAAAOAAYLVGIFD
			PNSQAGHQGLVDPIQFARANQAIQMACQNLVDPGSSPSOVLSAA
]		TIVAKHTSALCNACRIASSKTANPVAKRHFVQSAKEVANSTANL
			VKTIKALDGDFSEDNRNKCRIATAPLIEAVENLTAFASNPEFVS
	1		IPAQISSEGSQAQEPILVSAKPMLESSSYLIRTARSLAINPKDP
		I	PTWSVLAGHSHTVSDSIKSLITSIRDKAPGQRECDYSIDGINRC
			IRDIEQASLAAVSQSLATRDDISVEALQEQLTSVVQEIGHLIDP
			IATAARGEAAQLGHKGTQLASYFEPLILAAVGVASKILDHQQQM
			TVLDQTKTLAESALQMLYAAKEGGGNPKAQHTHDAITEAAQLMK
1			EAVDDIMVTLNEAASEVGLVGGMVDAIAEAMSKLDEGTPPEPKG
			TFVDYQTTVVKYSKAIAVTAQEMMTKSVTNPEELGGLASQMTSD
			YGHLAFQGQMAAATAEPEEIGFQIRTRVQDLGHGCIFLVQKAG\
			ALQVCPTDSYTKRELIECARAVTEKVSLVLSALQAGNKGTQACI TAATAVSGIIADLDTTIMFATAGTLNAENSETFADHRENILKTA
		ĺ	KALVEDTKLLVSGAASTPDKLAQAAQSSAATITQLAEVVKLGAA
			SLGSDDPETQVVLINAIKDVAKALSDLISATKGAASKPVDDPSM
			YQLKGAAKVMVTNVTSLLKTVKAVEDEATRGTRALEATIECIKQ
			BLTVFQSKDVPEKTSSPEESIRMTKGITMATAKAVAAGNSCRQE
			DVIATANLSRKAVSDMLTACKQASFHPDVSDEVRTRALRFGTEC

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
]	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
l	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	
		4	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		}	TLGYLDLLEHVLVILQKPTPELKQQLAAFSKRVAGAVTELIQAA
ľ			EAMKGTEWVDPEDPTVIAETELLGAAASIEAAAKKLEQLKPRAK
1		1	PKQADETLDFEEQILEAAKSIAAATSALVKSASAAQRELVAQGK
			VGSIPANAADDGQWSQGLISAARMVAAATSSLCEAANASVQGHA
			SEEKLISSAKQVAASTAQLLVACKVKADQDSEAMRRLQAAGNAV
			KRASDNLVRAAQKAAFGKADDDDVVVKTKFVGGIAQIIAAQEEM
1			LKKERELEEARKKLAQIRQQQYKFLPTELREDEG
6030	3	1777	FPGRGSPALQLEVLICLGLMGLERALNVLAPIFYRNIVNLLTEN
			APWNSLAWTVTSYVFLKFLQGGGTGSTGFVSNLRTFLWIRVOOF
			TSRRVELLIFSHLHELSLRWHLGRRTGEVLRIADRGTSSVTGLL
		}	SYLVFNVIPTLADIIIGIIYFSMFFNAWFGLIVFLCMSLYLTLT
		1 .	IVVTEWRTKFRRAMNTQENATRARAVDSLLNFETVKYYNAESYE
			VERYREALIKYQGLEWKSSASLVLLNQTQNLVIGLGLLAGSLLC
			AYFVTEQKLQVGDYVLFGTYIIQLYMPLNWFGTYYRMIQTNFID
1			MENMFDLLKK\ETEVKDLPGAGPFRFQKGRIEFENVHFSYADGR
			ETLQDVSFTVMPGQTLALVGPSGAGKSTILRLLFRFYDISSGCI
			RIDGQDISQVTQALFRFSHWELCPKDTVLFNDTIADNIRYGRVT
1	1		AGNDEVEAAAQAAGIHDAIMAFPEGYRTQVGERGLKLSGGEKOR
1	1	l .	VAIARTILKAPGIILLDEATSALDTSNERAIQASLAKVCANRTT
			IVVAHRLSTVVNADQILVIKDGCIVERGRHEALLSRGGVYADMW
6031	160	1004	QLQQQQEETSEDTKPQTMER
8031	190	1694	LRMSENLDKSNVNEAGKSKSNDSEEGLEDAVEGADEALQKAIKS
1			DSSSPQRVQRPHSSPPRFVTVEELLETARGVTNMALAHEIVVNG
Į			DFQIKPVELPENSLKKRVKEIVHKAFWDCLSVQLSEDPPAYDHA
			IKLVGEIKETLLSFLLPGHTRLRNQITEVLDLDLIKQEAENGAL
			DISKLAEFIIGMMGTLCAPARDEBVKKLKDIKEIVPLFREIFSV
			LDLMKVDMANFAISSIRPHLMQQSVEYERKKFQEILERQPNSLD
			FVTQWLEEASEDLMTQKYKHALPVGGMAAGSGDMPRLSPVAVQN
			YAYLKLLKWDHLQRPFPETVLMDQSRFHELQLQ\REQLTILGAV
1			LLVTFSMAAPGISSQADFAEKLKMIVKILLTDMHLPSFHLKDVL
			TTIGEKVCLEVSSCLSLCGSSPFTTDKETVLKGQIQAVASPDDP
Į.		Į	IRRIMESRILTFLETYLASGHQKPLPTVPGGLSPVQRELEEVAI
	<u>L</u>		KFARLVNYNKMVFCPYYDAILSKILVRS
6032	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
			SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
	1		YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
		1	QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
			PIGSSAGLLALSSALGGQSHLPIKDBKKHHDNDHQRDRDSIKSS
	}		SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK
1			SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
		ļ	ASIASSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
			NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
1			MNGELTSPGAAYAGLHNISPQMSAAAAAAAAAAAYGRSPVVGFD
	1		PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
			IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
1			DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
	1		SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
1	1	Ī	AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
			W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
			EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
1	1		W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
6033	39	2416	RATVYEVIY
6600	39	2415	AARLCRAQPTKSAWMIRDLSKMYPQTRHPAPHQPAQPFKFTISE
			SCDRIKEEFQFLQAQYHSLKLECEKLASEKTEMQRHYVMYYEMS
1	1		YGLNIEMHKQAEIVKRLNAICAQVIPFLSQEHQQQVVQAVERAK
		1	QVTMAELNAIIGQQQLQAQHLSHGHGLPVPLTPHPSGLQPPAIP
	1		PIGSSAGLLALSSALGGQSHLPIKDEKKHHDNDHQRDRDSIKSS
1	1		SVSPSASFRGAEKHRNSADYSSESKKQKTEEKEIAARYDSDGEK
1	}	i	SDDNLVVDVSNEDPSSPRGSPAHSPRENGLDKTRLLKKDAPISP
	1		ASIASSSSTPSSKSKELSLNEKSTTPVSKSNTPTPRTDAPTPGS
	<u></u>	L	NSTPGLRPVPGKPPGVDPLASSLRTPMAVPCPYPTPFGIVPHAG
			· · · · · · · · · · · · · · · · · · ·

	7	1 B 47 - 4 - 3 T 1	
SEQ ID	Predicted	Predicted end nucleotide	Amino acid segment containing signal peptide
NO:	beginning nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
IVO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding to first	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of		S=Serine, T=Threonine, V=Valine,
1		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			MNGELTSPGAAYAGLHNISPOMSAAAAAAAAAAAYGRSPVVGFD
1			PHHHMRVPAIPPNLTGIPGGKPAYSFHVSADGQMQPVPFPPDAL
			IGPGIPRHARQINTLNHGEVVCAVTISNPTRHVYTGGKGCVKVW
			DISHPGNKSPVSQLDCLNRDNYIRSCRLLPDGRTLIVGGEASTL
	1		SIWDLAAPTPRIKAELTSSAPACYALAISPDSKVCFSCCSDGNI
1			AVWDLHNQTLVRQFQGHTDGASCIDISNDGTKLWTGGLDNTVRS
1			W\DLREGRQLQQHD/FFTSPVFSLGYCP\TEEWLAVGMENSN\V
į.			EVLHVTKPDKYQLHLHESCVLSLKFAHCGKWF\VSTGKDNLLNA
	ľ		W\RTPYG\ASIF\QSKESSS\VLSCDI\SVDDKYIVTGS\GDK\
			RATVYEVIY
6034	2683	714	ESGRRRLKRRRSPCPGTAGGPGETNPGPGACPRGPREEAAAAM
1			EIAPQEAPPVPGADGDIEEAPAEAGSPSPASPPADGRLKAAAKR
1		Í	VTFPSDEDIVSGAVEPKDPWRHAQNVTVDEVIGAYKQACQKLNC
			RQIPKLLRQLQEFTDLGHRLDCLDLKGEKLDYKTCEALEEVFKR
			LQFKVVDLEQTNLDEDGASALFDMIEYYESATHLNISFNKHIGT
ł			RGWQAAAHMMRKTSCLQYL\DARNTPLLDHSAPFVARALRIRSS
			LAVLHLENASLSGRPLMLLATALKMNMNLRELYL\ADNKLNGLQ
			DSAQLGNLLKFNCSLQILDLRNNHVLDSGLAYICEGLKEQRKGL
1			VTL\VLWNNQLTHTGMAFLGMTLPHTQSLETLNLGHNPIGNEGV
1		J	RHLKNGLISNRSVLRLGLASTKLTCEGAVAVAEFIAESPRLLRL
		•	DLRENEIKTGGLMALSLALKVNHSLLRLDLDREPKKEAVKSFIE
			TQKALLAEIQNGCKRNLVLAREREEKEQPPQLSASMPETTATEP
1			QPDDEPAAGVQNGAPSPAPSPDSDSDSDSDGEEEEEEEGERDET
1			PSGAIDTRDTGSSEPQPPPEPPRSGPPLPNGLKPEFALALPPEP
			PPGPEVKGGSCGLEHELSCSKNEKELEELLLEASQESGQETL
6035	19	404	SVTYLGIILHKNTGALPADPVQLISQTPTPSTKQQLLSFLGMVG
1			YFYLWIPGFAILTKPLCKLTKENLADAIDPKSFSHSSFRSLKTA
			LENASTLALPDSSQPF\SLHTAEVQGCVVEILTQGLGPLPV
6036	1745	356	LPDVEKLGRRRGRKMDSVEKGAATSVSNPRGRPSRGRPPKLQRN
1		l .	SRGGQGRGVEKPPHLAALILARGGSKGIPLKNIKHLAGVPLIGW
1			VLRAALDSGAFQSVWVSTDHDEIENVAKQFGAQVHRRSSEVSKD
			SSTSLDAIIEFLNYHNEVDIVGNIQATSPCLHPTDLQKVAEMIR
1			EBGYDSVFSVVRRHQFRWSEIQKGVREVTEPLNLNPAKRPRRQD
			WDGELYENGSFYFAKRHLIEMGYLQGGKMAYYEMRAEHSVDIDV
ļ			DIDWPIAEQRVLRYGYFGKEKLKEIKLLVCNIDGCLTNGHIYVS
			GDQKEIISYDVKDAIGISLLKKSGIEVRLISERACSKQTLSSLK
			LDCKMEVSVSDKLAVVDEWRKEMGLCWKEVAYLGNEVSDEECLK
			RVGLSGAPADACSTAQKAVGYICKCNGGRGA\IREFAEHIC\LL
	i .	I	MEKGLINFMPKNRNLAVNIGEKK
	·		
6037	2936	1919	WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA
6037	2936	1919	WTSWWMSSVLTILLFSLOGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAFALSSRDSRFRDR
6037	2936	1919	WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAFALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG
6037	2936	1919	WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAFALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI
6037	2936	1919	WTSWWMSSVLTILLFSLOGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAFALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL
6037	2936	1919	WTSWWMSSVLTILLFSLOGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA
6037	2936	1919	WTSWWMSSVLTILLFSLOGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS
			WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLPFRMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD
6037	2936 1450	1919 426	WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH
			WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAFALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS
			WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAFALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG
			WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAFALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERALAGARDLSADRPRLDHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTPTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK
			WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSHGGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTPTSITTNTINTS SDKTDGTAGTPAISTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCBICD
			WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTPTSITTNTINTS SDKTDGTAGTPAISTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEEKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTOLQNKTFHCBICD VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL
			WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSHGGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTPTSITTNTINTS SDKTDGTAGTPAISTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCBICD
6038	1450		WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTPTSITTNTINTS SDKTDGTAGTPAISTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEEKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTOLQNKTFHCBICD VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL
			WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLPFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEEKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCEICD VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAVAVSSPFSLRTAP
6038	1450	426	WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCBICD VHVNSETQLKQHISSRHKDRAAGKPPKPKYSPYNKLQKTAHPL GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAVAVSSPFSLRTAP AATLFQTSALPPALLRPAPGPIRTAHTPVLFAPY
6038	1450	426	WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAFALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCBICD VHVNSETQLKQHISSRHKDRAAGKPPKPKYSPYNKLQKTAHPL GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAVAVSSPFSLRTAP AATLFQTSALPPALLRPAPGPIRTAHTPVLFAPY LDEYEARLTLANLDDFEEDNEDDDENRVNQEEKAAKITELINKL
6038	1450	426	WTSWWMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAFALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSHSGSDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPHRRKQIISCNICQLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGPVNKGDYLONKTFHCBICD VHVNSETQLKQHISSRHKDRAAGKPPKPKYSPYNKLQKTAHPL GVKLVFSKEPSKPLAPRILPNPLAAAAAAAVAVSSPFSLRTAP AATLFQTSALPPALLRPAPGPIRTAHTPVLFAPY LDEYEARLTLANLDDFEEDNEDDDENRVNQEEKAAKITELINKL NFLDEAEKDLATVNSNPFDDPDAAELNPFGDPDSEEPITETASP
6038	1450	426	WTSWMMSSVLTILLFSLQGNKMLNYSAPSAGGYLLPRKPVGTPA GGGFPRRHSVTLPSSKFRQNQLLSSLKGEPAPALSSRDSRFRDR SFSEGGERLLPTQKQPGGGQVNSSRYKT\ELCRPFEENGACKYG DKCQFAHGIHELRSLTRHPKYKTELCRTFHTIGFCPYGPRCHFI HNAEERRALAGARDLSADRPRLQHSFSFAGFPSAAATAAATGLL DSPTSITPPPILSADDLLGSPTLPDGTNNPF\AFSSQELASLFA PSMGLPGGGSPTTFLFRPMSESPHMFDSPPSPQDSLSDQEGYLS SSSSSHGGDSPTLDNSRRLPIFSRLSISDD SSALQEFGTRNHTFGVPLPPHRRRQIISCNICOLRFNSDSQAAAH YKGTKHAKKLKALEAMKNKQKSVTAKDSAKTTFTSITTNTINTS SDKTDGTAGTPAISTTTTVEIRKSSVMTTEITSKVEKSPTTATG NSSCPSTETEEBKAKRLL\YCSLCKVAVNSASQLEAHNSGTKHK TMLEARNGSGTIKAFPRAGVKGKGPVNKGNTGLQNKTFHCBICD VHVNSETQLKQHISSRRHKDRAAGKPPKPKYSPYNKLQKTAHPL GVKLVFSKEPSKPLAPRILPNPLAAAAAAAAVSSPFSLRTAP AATLFQTSALPPALLRPAPGPIRTAHTPVLFAPY LDEYEARLTLANLDDFEEDNEDDDENRVNQEEKAAKITELINKL NFLDEAEKDLATVNSNPFDDPDAAELNPFGDPDSEEPITETASP RKTEDSFYNNSYNPFKEVQTPQYLNPFDEPEAFVTIKDSPPQST

SEO	Predicted	Predicted end	Amino agid coment control
ID	beginning	nucleotide	Amino acid segment containing signal peptide (A-Alanine, C-Cysteine, D-Aspartic Acid, E-
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
"""	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
			PKPSPIPSPVLGRKPNASQSLLVWCKEVTKNYRGVKITNFTTSW
			RNGLSFCAILHHFRPDLIDYKSLNPQDIKENNKKAYDGFASIGI
ł			SRLLEPSDMVLLAIPDKLTVMTYLYQIRAHFSGQELNVVQIEEN
		-	SSKSTYKVGNYETDTNSSVDQEKFYAELSDLKREPELQQPISGA
ļ			VDFLSQDDSVFVNDSGVGESESEHQTPDDHLSPSTASPYCRRTK
			SDTEPQKSQQSSGRTSGSDDPGICSNTDSTQAQVLLGKKRLLKA
			ETLELSDLYVSDKKKDMSPPFICEETDEOKLOTLDIGSNLEKEK
			LENSRSLECRSDPESPIKKTSLSPTSKLGYSYSRDLDLAKKKHA
İ		İ	SLRQTESDPDADRTTLNHADHSSKIVOHRLLSROEELKERARVI.
			LEQARRDAALKAGNKHNTNTAAPFCNRQLSDQQDEERRROLRER
	1	1	ARQLIAEARSGGKMSBLPSYGERAAEKLKERSKASGDENDNIEI
1		1	DTNEEIPEGFVVGGGDELTNLENDLDTPEQNSKLVDLKLKKLLB
	1	1	VQPQVANSPSSAAQKAVTESSEQDMKSGTEDLRTERLQKTTERF
		1	RNPVVFSKDSTVRKTQLQSFSQYIENRPEMKRQRSIQEDTKKGN
	1		EEKAAITETQRKPSEDEVLNKGFKDS\SQYVVGELAALENEQKQ
			IDTRAALVEKRLRYLMDTGRNTEEEEAMMQEWFMLVNKKNALIR
			RMNQLSLLEKEHDLERRYELLNRELRAMLAIEDWQKTEAQKRRE
ì		ĺ	QLLLDELVALVNKRDALVRDLDAQEKQAEEEDEHLERTLEQNKG KMAKKEEKCVLO
6040	475	1052	· · · · · · · · · · · · · · · · · · ·
1	1,3	1052	PTALMTAPSCAFPVQFRQPSVSGLSQITKSLYISNGVAANNKLM
1			LSSNQITMVINVSVEVVNTLYEDIQYMQVPVADSPNSRLCDFFD PIADHIHSVEMKQGR\TLLHCAAGVSRSAALCLAYLMKYHAMSL
		Ì	LDAHTWTKSCRPIIRPNSGFWEQLIHYEFQLFGKNTVHMVSSPV
1			GMIPDIYEKEVRLMIPL
6041	2	3886	TEKDEKTAHNLENVLIHFWERLSEICVAKISEPEADVESVLGVS
	_		NLLQVLQKPKGSLKSSKKKNGKVRFADEILESNKENEKCVSSEG
			EKIECWELTTEPSLTHNSSGLLSPLRKKPLEDLVCKLADISINY
İ			VNERKSEQHLRFLSTLLDSFSSSRVFKMLLGDEKQSIVQAKPLE
			IAKLVQKNPAVQFLYQKLIGWLNEDQRKDFGFLVDILYSALRCC
}			DNDMERKKVLDDLTKVDLKWNSLLKIIEKACPSSDKHALVTPWL
:	i		KGDILGEKLVNLADCLCNEDLESRVSSESHFSERWTLLSLVLSQ
Į.			HVKNDYLIGDVYVERIIVRLHETLFKTKKLSEAESSDSSVSFIC
			DVAYNYFSSAKGCLLMPSSEDLLLTLFQLCAQSKEKTHLPDFLI
			CKLKNTWLSGVNLLVHQTDSSYKESTFLHLSALWLKNOVOASSI
1			DINSLQVLLSAVDDLLNTLLESEDSYLMGVYIGSVMPNDSEWEK
			MRQSLPMQWLHRPLLEGRLSLNYECFKTDFKEQDIKTLPSHLCT
l			SALLSKMVLIALRKETVLENNELEKIIAELLYSLQWCEELDNPP
			IFLIGFCEILQKMNITYDNLRVLGNMSGLLQLLFNRSREHGTLW
1			SLIIAKLILSRSISSDEVKPHYKRKESFFPLTEGNLHTIQSLCP
1 .			FLSKEEKKEFSAQCIPALLGWTKKDLCSTNGGFGHLAIFNSCLQ
			TKSIDDGELLHGILKIIISWKKEHEDIFLFSCNLSEASPEVLGV NIEIIRFLSLFLKYCSSPLAESEWDFIMCSMLAWLETTSENQAL
			YSIPLVQLFACVSCDLACDLSAFFDSTTLDTIGNLPVNLISEWK
			EFFSQGIHSLLLPILVTVTGENKDVSETSFQNAMLKPMCETLTY
	+		ISKEQLLSHKLPARLVADQKTNLPEYLQTLLNTLAPLLLFRARP
			VQIAVYHMLYKLMPELPQYDQDNLKSYGDEEEEPALSPPAALMS
	İ		LLSIQEDLLENVLGCIPVGQIVTIKPLSEDFCYVLGYLLTWKLI
1	[LTFFKAASSQLRALYSMYLRKTKSLNKLLYHLFRLMPENPTYAE
			TAVEVPNKDPKTFFTEELQLSIRETTMLPYHIPHLACSVYHMTL
			KDLPAMVRLWWNSSEKRVFNIVDRFTSKYVSSVLSFQEISSVQT
			STQLFNGMTVKARATTREVMATYTIEDIVIELIIQLPSNYPLGS
			IIVESGKRVGVAVQQWRNWMLQLSTYLTHQNGSIMEGLALWKNN
			VDKRFEGVEDCMICFSVIHGFNYSLPKKACRTCKKKFHSA\CLY
			KWFTSSNKSTCSLCRETFF
6042	1306	253	MAELAPASPSDIKASVSNGDTTLLCSRRQSCGMNEVRQVSLTYP
			GSPAPSHSLPLQPRSGGSLCPSRAW/PDPHOLFDDTSSAOSRGY
]			GAQRAPGGLSYPAASPTPHAAFLADPVSNMAMAYGSSLAAQGKE
			LVDKNIDRFIPITKLKYYFAVDTMYVGRKLGLLFFPYLHODWEV
			QYQQDTPVAPRFDVNAPDLYIPAMAFITYVLVAGLALGTQDRFS
			PDLLGLQASSALAWLTLEVLAILLSLYLVTVNTDLTTIDLVAFL
			GYKYVGMIGGVLMGLLFGKIGYYLVLGWCCVAIFVFMIRTLRLK

CEC	Predicted	Predicted end	Amino agid segment containing signal mentide
SEQ	•		Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ì	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1			
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
į.	sequence	<u> </u>	\=possible nucleotide insertion)
			ILADAAAEGVPVRGARNQLRMYLTMAVAAAQPMLMYWLTFHLVR
<u> </u>			
6043	403	599	LCLFFPFPCATPVLPLPSLISAL/CLSHLSVSSWFCPCQPPLPC
		ì	PLPPLQNKTAKGSLSTEQSERG
6044	793	412	KLEMWNFTLISKVKISREVTMIASKFGIGQOVRHSLLGYLGVVV
i		Į	DIDPVYSLSEPSPDELAVNDELRAAPWYHVVMEDDNGLPVHTYL
1		1	AEAQLSSELQDEHP\EQPSMDELAQTIRKQLQAPRLRN
6045	155	2299	SPLPQVAAMNYLRRRLSDSNFMANLPNGYMTDLQRPQPPPPPPG
			AHSPGATPGPGTATAERSSGVAPAASPAAPSPGSSGGGGFFSSL
			SNAVKQTTAAAAATFSEQVGGGSGGAGRGGAASRVLLVIDEPHT
			DWAKYFKGKKIHGBIDIKVEQAEFSDLNLVAHANGGFSVDMEVL
1	l		
			RNGVKVVRSLKPDFVLIRQHAFSMARNGDYRSLVIGLQYAGIPS
		!	VNSLHSVYNFCDKPWVFAQMVRLHKKLGTEEFPLIDQTFYPNHK
			BMLSS\TTYPVVVKMGHGTLWGWGKVKVDNQHDFQDIASVVALT
		.]	KTYATAEPFIDAKYDVRVQKIGQNYKAYMRTSVSGNWKTNTGSA
1			MLEQIAMSDRYKLWVDTCSEIFGGLDICAVEALHGKDGRDHIIE
			l ·
}			VVGSSMPLIGDHQDEDKQLIVELVVNKMAQALPRQRQRDASPGR
		1	GSHGQTPSPGALPLGRQTSQQPAGPPAQQRPPPQGGPPQPGPGP
			QRQGPPLQQRPPPQGQQHLSGLGPPAGSPLPQRLPSPTSAPQQP
1			ASQAAPPTOGOGROSRPVAGGPGAPPAARPPASPSPORQAGPPQ
1	1	1	ATROTSVSGPAPPKASGAPPGGQQRQGPPQKPPGPAGPTRQASQ
1	1	l	AGPVPRTGPPTTQQPRPSGPGPAGRPKPQLAQKPSQDVPPPATA
	1	İ	AAGGPPHPQLNKSQSLTNAFNLPEPAPPRPSLSQDEVKAETIRS
1		1	LRKSFASLFSD
6046	212	1075	EGLTGPCERVPFLLGRGPPHGATRAGHRRAVRWAGPESLPPLPR
****			SLIMDSPRAGTHQGPLDAETEVGADRCTSTAYQEQRPQVEQVGK
1		ļ	
		i	QAPLSPGLPAMGGPGPGPCEDPAGAGGAGGSEPLVTVTVQCA
			FTVALRARRGADLSSLRALLGQALPHQ\AQLGQLSYLAPGEDGH
1	1	1	WVPIPEEESLQRAWQDAAACPRGLQLQCRGAGGRPVLYQVVAQH
1	1	l	SYSAQGPEDLGFRQGDTVDVLCEVDQAWLEGHCDGRIGIFPKCF
			VVPAGPRMSGAPGRLPRSQQGDQP
		1.05	
6047	49	1405	PVLVTSLRMREADTLRPPQLMEVSADIISTVEFNHTGELLATGD
)	KGGRVVIFQREPESKNAPHSQGEYDVYSTFQSHEPEFDYLKSLE
	1 .	ì	IEEKINKIKWLPQQNAAHSLLSTNDKTIKLWKITERDKRPEGYN
1	1	i .	LKDEEGKLKDLSTVTSLQVPVLKPMDLMVEVSPRRIFANGHTYH
		1	INSISVNSDCETYMSADDLRINLWHLAITDRSFTP\NIVDIKPA
	f		•
			NMEDLTEVITASEFHPHHCNLFVYSSSKGSLRLCDMRAAALCDK
i		1	HSKLFEEPEDPSNRSFFSEIIS\SVSDVKFSHSDRYMLTR\DYL
		,	TVKVWDL\NMBARPIETYQVHDYLRSKLCSLYENDCIFDKFECA
1	1	1	WNGSDSVIMTGA\YNNFFRMFDRNTKRDVTL\EASRESSKPRAV
1		1	LKPRRVCVGGKRRRDDISVDSLDFTKKILHTAWHPAENIIAIAA
1		l .	TNNLYIFODKVNSDMH
66.5	<u> </u>	25.04	
6048	1	3194	GIRTPKFCDSPTSDLEMRNGRGRGKRMRPNSNTPVNETATASDS
			KGTSNSSKTRAGANSKGRRGSQNSSEHRPPASSTSEDVKASPSS
1			ANKRKNKPLSDMELNSSSEDSKGSKRVRTNSMGSATGPLPGTKV
	1		EPTVLDRNCPSPVLIDCPHPNCNKKYKHINGLKYHQAHAHTDDD
1		1	SKPEADGDSEYGEEPILHADLGSCNG\ASVSOK\GSLSPARSAT
			PKVRLVEPHSPSPSSKFSTKGLCKKKLSGEGDTDLGALSNDGSD
1			1 -
1			DGPSVMDETSNDAFDSLERKCMEKEKCKKPSSLKPEKIPSKSLK
i		1	SARPI/APLAIPPQQIYTFQTATFTAASPGSSSGLTATVAQAMP
			NSPQLKPIQPKPTVMGEPFTVNPALTPAKDKKKKDKKKKESSKE
1		1	LESPLTPGKVCRAEEGKSPFRESSGNGMKMEGLLNGSSDPHQSR
ŀ			_ · · · · · · · · · · · · · · · · · · ·
1			LASIKAEADKIYSFTDNAPSPSIGGSSRLENTTPTQPLTPLHVV
I			TQNGAEASSVKTNSPAYSDISDAGEDGEGKVDSVKSKDAEQLVK
	1	1	EGAKKTLFPPQPQSKDSPYYQGFESYYSPSYAQSSPGALNPSSQ
ì	1		
		1	AGVESQALKTKRDEEPESIEGKVKNDICEEKKPELSSSSCOPSV
			AGVESQALKTKRDEEPESIBGKVKNDICEEKKPELSSSSQQPSV
			IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ
			IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ YEEQQKRQSLEQQQRGVDKKAEMGLKEREAALKEEMKQKPSIPP
			IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ
			IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ YEEQQKRQSLEQQQRGVDKKAEMGLKEREAALKEEMKQKPSIPP
			IQQRPNMYMQSLYYNQYAYVPPYGYSDQSYHTHLLSTNTAYRQQ YEEQQKRQSLEQQQRGVDKKAEMGLKEREAALKEEMKQKPSIPP TLTKAPSLTDLVKSGPGKAKEPGADPAKSVIIPKLDDSSKLPGQ

Deginning muclectide	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Not nuclectide	_			
location corresponding to first amino acid maino acid maino acid maino acid amino acid amino acid amino acid sequence s	1			
to first amino acid amino acid amino acid amino acid sequence Sequence Sequence Sequence Sequence Sequence Sequence Serine, T-Threonine, W-Valine, N-Trytophan, Y-Tyrosine, X-Unknown, *-stop Codon, /-spossible nucleotide deletion, V-possible nucleotide insertion) FORKESTSDCLLPTEESSELGSKERPRSYNFYSSPITORGSY IFYMHOVSYSGYDYDHAYSYSGYDYHAYSYSSPITORGSY SYSTISMYSYSGYDYHAYSYSGYDYHAYSYSGYDYHAYSYSSPITORGSY SYSTISMYSYSGYDYHAASYSYGYDYHASYSGYDYHAYSYSGYDYHAYSYSGYDYHAYSYSGYDYHAYSYSGYDYHAYSYSGYDYHAYSYSGYDYHAYSYSGYDYHAYSYSGYDYHAYSYSGYDYHAYSYSGYDYHAYSYSGYDYHAASYSYGYDYHASYSGYDYHAASYSYGYDYHASYSGYDYHASYSGYDYHAASYSYSGYDYHAASYSYSGYDHAANASYSYGYDHAASYSYGYDHAASYSYGYDHAASYSYGYDHAASYSYGYDHAASYSYTAANASYSYGYDHAASYSGYDHAASYSYGYDHAASYSYGYDHAASYSYTAANASYSYGYDHAASYSYTAANASYSYGYDHAASYSYTAANASYSYAYSAANASYSAHAYSAANASYSAHAYSAANASYSHAANASYSHAANASYSHAANASYSHAANASYSHAANASAANAS	1,0.			
to first smino acid residue of amino acid sequence sequen		1		
### ### ### ### ### ### ### ### ### ##				
maino acid sequence sequence codon, /=possible nuclectice deletion, /=possible nuclectice deletion, /=possible nuclectice deletion, /=possible nuclectice deletion, /=possible nuclectice insertion regularists regula			1 .	
amino acid sequence Coden, /=possible nucleotide deletion, Lopessible nucleotide forestion PEGGESTSSDCKLPTSEESRIGSKEPRSSWHPVSSFITCHOSY PIYMHOYSYSGCSPONNESYSEMPANMONYPOSTIPSYSSTSD YCSKNSGGERADKARASPSVTCKSSSESKALDLIQOHASHYKSK SPITISKTSGREDRGGGTVWGGGSGSSVGGKSGGGSGSVGNSGGSGSVGNSGGSGSVGNSGGSSSSVGNSGGGSGSVGNSGGSGSVGNSGGSSSSVGNSGGSGSSVGNSGGSSSSVGNSGGSGSSVGNSGGSGSSVGNSGGSSSSSVGNSGGSGSSSVGNSGGSGSSVGNSGGSGSSVGNSGGSGSSVGNSGGSGSSVGNSGGSSSSVGNSGGSGSSVGNSGGSGSSVGNSGGSGSSVGNSGGSGSSVGNSGNSGSSVGNSGGSSSVGNSGGSSSVGNSGGSSSSVGNSGGSSSSVGNSGGSSSSVGNSGGSSSSVGNSGGSSSSVGNSGGSSSSVGNSGGSSSSVGNSGGSSSSVGNSGGSSSSVGNSGGSSSSVGNSGGSSSSVGNSGGSSSVGNSGGSSSVGNSGGSSSVGNSGGSSSVGNSGGSSSVGNSGSSSVGNSGSSSVGNSGGSSVGNSGSSVGNSGSSSVGNSGSVGNSGSS				
Sequence N_possible and ectide insertion				
ECKRET-SSUCKLPTBEESRLGSKEPRSSWHPVSSPLTUHOGS. 1 PYMHOVSYSGGUPHUS YSRIGH WINNONYDGSTLPSSYSTSP YGSKVGGGEGADKARAS PEVTCKSSSESKALDILOGHASHYSKS SPITISKTSCRENGGTVAGGGGGSSVGGGGGSSGSVGANGAGGSSPSVDR PT SPSGRIMSTHHHHHLGYSLLPAQYNLDYAAGLSSTAI VASQQG STREILY PPPRR 6049 215 1089 ANTGVPDREVESTREGOPGAPFGTSAAMHRSGSSPTLPESSAT. BDDYVS PPGGAPROVGSPTSSYSVGALALDRYGVGVGGAGGS VPAAVADYSYASSYHOYGGAYNRVERATHOPEREVTE PEVERW WORKKYKERTIT ISS STOLALDRREGKTOVLALPERALASIL GLTOTOVLINEONKESKIKK INKNEWP PENB PSSGDPALCASD GSPAWARDVEGASSRSLSHBHAHP PENGSTROKTOVLALPERALASIL GLTOTOVLINEONKESKIKK INKNEWP PENB PSSGDPALCASD GSPAWARDVEGASSRSLSHBHAHP PENGSTROKTOVLALPERALASIL GLTOTOVLINEONKESKIKK INKNEWP PENB PSSGDPALCASD GSPAWARDVEGASSRSLSHBHAHP PENGSTROKTOVLALPERALASIL GLTOTOVLINEONKESKIKK INKNEWP PENB PSSGDPALCASD GSPAWARDVEGASSRSLSHBHAHP PENGSTROKTOVLALPERALASIL GLTOTOVLINEONKESKIKK INKNEWP PENB PSSGDPALCASD GSPAWARDVEGASSRSLSHBHAHP PENGSTROKTOVLAND ASSINSILLPROSLOPELASINDE PENGSTROKTOVLAND ASSINSILLPROSLOPELASINDE PENGSTROKTOVLAND PRIMAKIVILLAMSSGGGTENSI I PANY I ARBITALILATIL LIBIDINISSI PSORVENSINE PENGSTROW PENGSTROKTOVLAND PRIMAKIVILLAMSSGGGTENSI I PANY I ARBITALILATIL LIBIDINISSI PSORVENSINE PENGSTROKTOVLAND PROGLEMENTA PARI I ELEBEPLLE PENGSTROKTOVLAND PSORVENSINE PENGSTROKTOVLAND PRIMAKIVILLI PENGSTROKTOVLAND PSORVENSINE PENGSTROKTOVLAND PRIMAKIVILLAMS PSORVENSINE PAN I TANY I ARBITALILATIL RIBIDINISSI PSORVENSINE PAN I TANY I ARBITALILATIL RIBIDINISSI PSORVENSINE PAN I TANY I ARBITALILATIL RIBIDINISSI PSORVENSINE PAN I TANY I ARBITALILATIL RIBIDINISSI PSORVENSINE PAN I TANY I ARBITALILATIL RIBIDINISSI PSORVENSINE PAN I TANY I ARBITALILATIL RIBIDINISSI PSORVENSINE PAN I TANY I ARBITALILATIL RIBIDINISSI PSORVENSINA PAN I TANY I ARBITALILATIL RIBIDINISSI PSORVENSINA PAN I TANY I ARBITALILATIL RIBIDINISSI PSORVENSINA PAN I TANY I ARBITALILATILAT			sequence	
IPYMHOTSYSGSTOPNINESYRSMPANMONYDGSTLPSSYSTS YGSKNGGGGDADKARAPSPYTCKSSSSKALDILOQHASIYTSK SPITISKTSGGERDRGGGTWGGGGSCSSVCGASGGRSVDRPRT SPSGRLWSTHHHHHLGYSLIPAQVLYAGGGSTSTAVIASQGG STPSLYPPPR AMTGUVPDREVEETBGGFQAPFGTSAAMHHESGGSSTIPESSAT DEDYYSPTGGAPHGYGFASAWHHESGGSSTIPESSAT DEDYYSPTGGAPHGYGFASAWHHESGGSTTIPESSAT DEDYYSPTGGAPHGYGFASAWHHESGGSSTIPESSAT DEDYYSPTGGAPHGYGFASAWHHESGGSSTIPESSAT DEDYYSPTGGAPHGYGFASAWHHESGGSSTIPESSAT DEDYYSPTGGAPHGYGFASAWHHESGGSSTIPESSAT DEDYYSPTGGAPHGYGFASAWHHESGGSSTIPESSAT DEDYYSPTGGAPHGYGFASAWHHESGGSSTIPESSAT DEDYYSPTGGAPHGYGFASAWHHESGGSSTIPESSAT DEDYYSPTGGAPHGYGFASAWHTESGAPHTERELAGASIL GYPAWER/GSSRSLSHHHALBYPTSGAPASAWTTS GATTATULAGASGTAV DESTAWARH GATTATULAGASGTAV PARAMEKKYLLMSGSGGTTSHMS I FANYIARDTRELGASTLIV DEGGGDTTMSNYFTSGRUTHFRVSVLITYFFVESKELEKOMHY YOSCLEALLONSDGAKTHGLWHMHGUGEGGGLIFKREBELEKOMHY YOSCLEALLONSDGAKTHGLWHMHGUGEGGGLIFKREBELEKOMHY YOSCLEALLONSDGAKTHGLWSGAGGTAMSSITPHQGLGMNIGHNIGHNIGHNIGHNIGHNIGHNIGHNIGHNIGHNIGH		sequence		
YGSKVSGGEDADKARASPEVTCKSSSESKALDLIQQHASHYKSK SPITISKTSGERRORGGTVWGGGGSCSSVGAGNGGGSPVTDRET				EDGKESTSSDCKLPTSEESRLGSKEPRPSVHVPVSSPLTQHQSY
SPITISINTSQUENGGGGCSCSSVGGASGGERSVERPS SPSGRIMSTHHHHHILGYSLLPAQYNLPYAGLSTAIVASQOG STPSLYPPPRR ANTOVPDRIVED STREGOPPOAPPOTSAMHHESGGSPTLPSSSAT DSDYYSPTOGAPHIGYCSPTSAYGVAKALMPYQVCYHGUNGSASIG YPARAYADYSYASYHQYGGAYNKPPATNOPKEKTTE PEVERN NGKPKKVRKPRTIYSS GLAALQREPGKTOVIALDERAELASL GLTOTOVKIHRGKNESKIKTUNDENPEATNOPKEKTTE PEVERN NGKPKKVRKPRTIYSS GLAALGREPGKTOVIALDERAELASL GLTOTOVKIHRGKNESKIKTUNDENPEATNOPKEKTTE PEVERN NGKPKKVRKPRTIYSS GLAALGREPGKTOVIALDERAELASL GLTOTOVKIHRGKNESKIKTUNDEN PEPEPSSDDHACHSP QSASINSILPPGSLOUPHALASCTIV AASSINSILPPGSLOUPHALASCTIV ROSOO 566 1718 KILERTCCAMEESBDSEKTTEKRIGPRHOPPLGEFGGSLGWVL PNTAMKKKVLLMKGSGGKTSKRSI IFANYIARDTRILGATILD RIHGLINSLSSTISLDDSVGRTHTEPVEHSHVRTLEGINLVIAHLM DCGGGOTTMENYFTSQRDHIFRNVEVLIYVPDVESRELEKDHIV YQSCLEALIANSPORAKIFCLWKHOVCKORDAHERFKISNIIKQ FKLSCSKLAASFGSNEVWRNSPAAFIDIFTSNTTYWVVWMSDPSI PSAATLIHINNARKIFEKKERTODOPKQCLLMR ROSOO 6051 566 1718 KOLERTCCAMEESBDSEKTTEKRNIGFRHOPPLGEFGGGSLGWUL PNTAMKKVLLMKSGSGKTSKRSI IFANYIARDTRILGATILD DCGGQOTTMENYFTSQRDHIFRNVEVLITVVGDUESRLEEKDHIV YQSCLEALIONSPDAKIFCLWKRDLVQCEGRDAHERFKISNIIKQ FKLSCSKLAASFGGMEVRNSNAFAFIDIFTSNTYWMVWMSDPSI PSAATLIHINNARKIFEKKERTODOPKQCLLMR RLSSPLECSCFRTSIWDETLYKANSIIVQLIFWQGLEBNLRN FABIIFADEVLLFERATFLVISHYQCKEGRDAHERFKLSNIIKQ FKLSCSKLAASFGGMEVRNSNAFAFIDIFTSNTYWMVWMSDPSI PSAATLIHINNARKIFEKKERVODPKQCLLMR PTAMKKVLLMKSGGSKTSWRSIIFANYIARDTRILGATILD RIHSLQINSLSSTYSLUDSVGRTTFDVEHSHVRTLONDLUMLM DCGGGOTTMENYFTSQRDHIFRNUFLTYVDVENGERELEKDHIV YQSCLSALIONSPDAKIFCLVIKRMDIVOGCEGRDLIFKEREELDHIV YQSCLSALIONSPDAKIFCLVIKRMDIVOGCEGRDLIFKEREELDHIV YQSCLSALIANSFDAKIFCHUNGFRHOPPGCCLLMR RASHLESCGFRTSIWDETLYKANSIIVQLIFWGDEFGGGSIGWVL PTAMKKVLLMKGSGSKTSWRSIIFANYIARDTRILGATILD RHSLQINSLSSTYSLUDSVGRTTFDVEHSHVRTLVANDLUMLM DCGGGOTTMENYFTSQRDHIFRNUFYNDEHDREFGGASIGNIK PFLESCSFRTSIWDETLYKANSIIVQLIFWGDEFGGASIGNIK PFLESCSFRTSIWDETLYKANSIIVQLIFWGDEFGGASIGNIK PFLESCSFRTSIWDETLYKANSIIVQLIFWGDEFGGASIGNIK PFLESCSFRTSIWDETLYKANSIIVQLIFWGDEFGGASIGNIK PFLESCSFRTSIWDETLYKANSIIVTOPHEGFRTSGRTSSBRSSRAAD RRHLIILADINSDRLFTVNOVTUGGSKYGI INLOSLKRYPTKYWOL RHS	1			IPYMHGYSYSQSYDPNHPSYRSMPAVMMQNYPGSYLPSSYSFSP
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PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD RIHSLQINSSLSTYSLVDSVGNTKTFDVEWBHVRRLGAULVILLA RIHSLQINSSLSTYSLVDSVGNTKTFDVEWBHVRRLGAULVILLA DCGGGDTFMENY FTSORDNIFRNVEVLIVVFDVESRELLEKDMHY YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREEDLR RLSRPLECSCFRTSINDETLYKAWSSIVQLIFNVQLEMVLRIN FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ FKLSCSKLAASFOSMEVRNSNFAAFIDIFTSNTYWWVMSDPSI PSAATLINIRNARKHFEKLERVDGPKQCLLMR 6052 566 1718 KGLERTCCAMEESDSEKTTEKENLGFRMDPPJGEFG\GSIGWVL PNTAMKKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGANILDL RHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGATILD RHSLQINSPASTIVDTYSQRDIFFRVEVLIYVPDVESRELEKDMHY YQSCLEAILQNSPDAKIFCLVHKMDLVQEDQRDLIFKEREDDLR RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQLLEMNLRN PAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ FKLSCSKLAASFQSMEWRNSNFAAFIDIFTSNTYWWVMSDPSI PSAATLINIRNARKHFEKLERVUSPKQCLLMR FKLSCSKLAASFQSMEWRNSNFAAFIDIFTSNTYWWVMSDPSI PSAATLINIRNARKHFEKLERVUSPKQCLLMR HDSGHGDDESSTSSGTAGTSSVPELPGFYDPKKRYFFILLPG HNNCNPLTKESIRQKEMESKRIRLLGEDRRKKLARMGFNASSM LRKSQLGFILNVTNYCHLAHELKLSCMERKKVQIRSMDPSALASD RFNLILADTNSDRLFFTVNDVTVGSKYGIINLGSLKTPTLKVFM HENLYFTNRKV\NSVCWASLINHLDSEUTSLAPDFATLKVFM HENLYFTNRKV\NSVCWASLINHLDSAVTSVRILQBQYIMASD MAGKIKLWDLRTTKCVRQVEGRINDSAVTSVRILQBQYIMASD MAGKIKLWDLRTTKCVRQVEGRINDSAVTSVRILQBQYIMASD MAGKIKLWDLRTTKCVRQVEGRINDSAVTSVRILQBQYIMASD MAGKIKLWDLRTTKCVRQVEGRINDSAVTSVRILQBQYIMASD MAGKIKLWDLRTTKCVRQVEGRINDSAVTSVRILQBQYIMASD MAGKIKLWDLRTTKCVRQVEGRINDSAVTSVRILQBQYIMASD MAGKIKLWDLRTTKCVRQVEGRINDSAVSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIOGLHAQCQLARHVLLLAKSLKV UTTGIVPDWGDSIEVKNEDQIOGLHAQCQLARHVLLLAKSLKV DMTTEEIDALVHREIISHNAYPSPLAYGGPFKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYNGYHGDTSTFLVGNVDEGKK LVEVARGRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHANDBDLPMEEGMAFTIEPIITEGSPE	6051	522	1710	7
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DCGGQDTFMENYFTSQRDNIFRNVEVLIYVFDVESRELEKDMHY YQSCLEAILQMSPDAKIFCLUHKMDLQEQORDLIFKEREEDLIR RLSRPLECSCFRTSINDETLYKAMSSIVYQLIPNVQQLEMNLRN FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ FKLSCSKLAASFQSMEVYENSNFAAFIDIFTSNTYVMVMSDPSI PSAATLINIRNARKHFEKLERVDGPKQCLLIMR 6052 566 1718 KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSIGWVL PNTAMKKVLLMGKSGSGKTSMRSIIFANYIARDTRRLGATILD RIHSLQINSSISTISLUDSVONTKTFDVEHSHVPFLGNLVLNLM DCGGQDTFMENYFTSQRDNIFRNVEVLIYVPDVESRELEKDMHY YQSCLEAILQNSPDAKIPCLVHKMDLVQEDQRDLIFKEREEDLR RLSRPLECSCFRTSINDETLYAMSSIVYQLIPNVQQLEMNLRN PAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ FKLSCSKLAASFQSMEVMISNFAAFIDIFTSNTYWVMSDPSI PSAATLINIRNARKHFEKLERVDGPKQCLLMR 6053 201 1704 KGTEMNKSRWQSRRRHGRSHQQNPWFRLRDSEDRSDRAAQPA HDSGHGDDESPSTSSGTATSSVPELDFYFTDEKKRYFFLLPG HNNCNPLTKESIRQKEMESKRLRLLQEEDRRKKIARMFPALSM LRKSQLGFLNVTNYCHLAHELRLSCMERKKVQIRSMDPSALASD RFNLILADTNSDRLFTVNDVTVGGSKYGIINLSSLKTPTLKVFM HENNLYFTNRKVNSVCMSLANDLSHILLGMLAFTPTLKVFM HENNLYFTNRKVNSVCMSLANDLSHILLGMLAFTPTLKVFM HENNLYFTNRKVNSVCMSLANDLSHILLGMLAFTPTLKVFM HENNLYFTNRKVNSVCMSLANDLSHILLGMLAFTPTLKVFM HENNLYFTNRKVNSVCMSLANDLSHILLGMLAFTPTLKVFM MAGKIKLWDLRTTKCVRQYEGHVNEYAYLLDVHGGCATLL PASLFVNSHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQANNCFS GEIFAIDLRCGNOGKGMKATRLFIDSAVTSKTILLODEQLYMASD MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGILVAVG QDCYTRIMSLINDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG APGILMAVGQOLYCYSYS 6054 1 1054 PPIARLQEFGTSRRHMAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSSQGRNFFFRRQRDISHSIVLPAAVSSAHEVPKHIKKPDY VTTGIVPDWGDSIEVKMEDQIQGLHQACQLARHVLLLAGKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFYKSVCTSVNNVLCH GIPDSRPLQDGIINIDVTYYNGYHDTSETFLVGNVDECGKK LVEVARRCDBEALAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHANDDSDLPMEGMAFTIEFIITTGSSFE	1			
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FAEIIEADEVLLFERATFLVISHYQCKEQRDAHRFEKISNIIKQ FKLSCSKLAASFQSMEVRNSNFAAFIDITTSMTYMVVMSDPSI PSAATLINIRNARKHFEKLERVDGPKQCLLMR 6052 566 1718 KGLERTCCAMEESDSEKTTEKENLGPRMDPPLGEPG\GSLGWVL PNTAMKKKVLLMGKSGSGKTSMRSIIFANYJARDTRRLGATILD RIHSLQINSSLSTYSLVDSVGNTKTFDVEHSHVRFLGNLVLNLW DCGGQDTFMENYFTSQRDNIFRNVEVLTYVPDVESRELEKDMHY YQSCLEAILQNSPDAKIPCLVHKMDLVQEDQRDLIFKEREEDLR RLSRPLECSCFRTSIWDETLYKAWSSIVYQLIPNVQQLEMNIRN FAEIIEADEVLLFERATFLVISHYQCKSQRDAHRFEKISNIIKQ FKLSCSKLAASFQSMEVRNSNFAAFIDIFTSNTYVMVVMSDPSI PSAATLINIRNARKHFEKLERVLGPKQCLLMR KGTEMNKSRWGSRRFRSHGQRSHQQMFWPRLRDSEDRSDRRAQPA HDSGHGDDESPSTSSGTAGTSSVPELPGFYFDPEKKRYFRLLPG HNNCNPLTTESIRQKEMESKRLRLLQEEDRRKKIARMGFNASSM LRKSQLGFLNVTNYCHLAHELRLSCMERKKVQIRSMDPSALASD RFNILLADTNSDRLFTVNDVTVGGSKYGIINLGSLKTPTLKVPM HENLYFTRKV\NSVCWASLNHLDSHILLCLMGLAETPGCATLL PASLFVNSHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQANNCFS GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEQYLMASD MAGKIKLMDLRTTKCVRQYSGHVNEYAYLPLHVHEEGGILVAVG QDCTYTRIWSHLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG APGLIMAVQQDLYCYSYS 6054 1 1054 PPIARLOSFGTSRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV DMTTEEIDALVHREISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPPSRPLQDGDIINIDVTVYYNGYHGDTSSTFLVGNVDECCKK LVEVARRGRCRDEAIAACRAGAPFSVIGNTISHITHQNFQVCPHF VGHGIGSYFHGHPEIWHANDSDLPMEEGMAFTIEPIITESSPB	1			
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LRKSQLGFLNVTNYCHLAHELRLSCMERKKVQIRSMDPSALASD RFNLILADTNSDRLFTVNDVTVGGSKYGIINLQSLKTPTLKVFM HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLAETPGCATLL PASLFVNSHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQANNCFS TGLSRRVLLTNVVTGHRQSFGTNSDVLAQQFALMAPLLFNGCRS GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEQYLMASD MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEGILVAVG QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG APGLLMAVGQDLYCYSYS 6054 1 1054 PPIARLOEFGTSRRMMAAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVVLLLAKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHANDSDLPMEEGMAFTIEPIITEGSPB]		l	1
RFNLILADTNSDRLFTVNDVTVGGSKYGIINLQSLKTPTLKVFM HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLAETPGCATLL PASLFVNSHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQANNCFS TGLSRRVLLTNVVTGHRQSFGTNSDVLAQQFALMAPLLFNGCRS GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEQYLMASD MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEGILVAVG QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG APGLLMAVGQDLYCYSYS 6054 1 1054 PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARVLLLAGKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHANDSDLPMEEGMAFTIEPIITEGSPB			1	The state of the s
HENLYFTNRKV\NSVCWASLNHLDSHILLCLMGLAETPGCATLL PASLFVNSHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQANNCFS TGLSRRVILITNVVTGHRQSFGTTNSDVLAQQFALMAPLLFNGCRS GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEQYLMASD MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEGILVAVG QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG APGLLMAVGQDLYCYSYS 6054 1 1054 PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGPPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHANDSDLPMEEGMAFTIEPIITEGSPB			1	· · · · · · · · · · · · · · · · · · ·
PASLFVNSHPAGIDRPG\MLCSFRIPGAWSCAWSLNIQANNCFS TGLSRRVLLTNVVTGHRQSFGTNSDVLAQQFALMAPLLFNGCRS GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEQYLMASD MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGILVAVG QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG APGLLMAVGQDLYCYSYS PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSSQQRRNFFFRRQDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPB			1	
TGLSRRVLLTNVVTGHRQSFGTNSDVLAQQFALMAPLLFNGCRS GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEQYLMASD MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGILVAVG QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG APGLLMAVGQDLYCYSYS FPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSQQRRNFFFRRQDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNYDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPB	1			
GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEQYIMASD MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGILVAVG QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG APGLLMAVGQDLYCTSYS 6054 1 1054 PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNYDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPB			1	1
MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGILVAVG QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG APGLLMAVGQDLYCYSYS 6054 1 1054 PPIARLQEFGTSRRIMAAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSSQQRRNFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNYDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPB	1		1	
QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG APGLLMAVGQDLYCYSYS 6054 1 1054 PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLAHVLLLAGKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPB	1		1	GEIFAIDLRCGNQGKGWKATRLFHDSAVTSVRILQDEQYLMASD
APGLIMAVGQDLYCYSYS 6054 1 1054 PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPB				MAGKIKLWDLRTTKCVRQYEGHVNEYAYLPLHVHEEEGILVAVG
6054 1 1054 PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHIYLH KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPB				QDCYTRIWSLHDARLLRTIPSPYPASKADIPSVAFSSRLGGSRG
KQSSSQQRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPE			1	APGLLMAVGQDLYCYSYS
KQSSSQQRRNFFFRRQRDISHSIVLPAAVSSAHPVPKHIKKPDY VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPB	6054	1	1054	PPIARLQEFGTSRRHMAAPSGVHLLVRRGSHRIFSSPLNHTYLH
VTTGIVPDWGDSIEVKNEDQIQGLHQACQLARHVLLLAGKSLKV DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPB		_	1	
DMTTEEIDALVHREIISHNAYPSPLGYGGFPKSVCTSVNNVLCH GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPB			1	
GIPDSRPLQDGDIINIDVTVYYNGYHGDTSETFLVGNVDECGKK LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPB			1	
LVEVARRCRDEAIAACRAGAPFSVIGNTISHITHQNGFQVCPHF VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPB				1
VGHGIGSYFHGHPEIWHHANDSDLPMEEGMAFTIEPIITEGSPB			1	
			I	
FKVLEDAWTVVSLD/TSKVSAQFEHTVLITSRGAQILTKLPHEA			1	
	L	<u> </u>	<u></u>	FKVLEDAWTVVSLD/TSKVSAQFEHTVLITSRGAQILTKLPHEA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P-Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
6055	421	2364	PPYFLLSFLAWWLYGQSDRTETDISQSAGPPPGTLOCSALHHDP
			GCANCSRFCRDCSPPACQCHTHVFPGNALNGVQPPBLSRTLALI
			SSREPPRKKKKSQTETGKERERTSFLTQGGKRFELQHGLAGICM
1			TLLITGDSIVSAEAVWDHVTMANRELAFKAGDVIKVLDASNKDW
			WWGQIDDEEGWFPASFVRLWVNHEDEVEEGPSDVQNGHLDPNSD
			CLCLGRPLQNRDQMRANVINEIMSTERHYIKHLKDICEGYLKQC
			RKRRDMFSDEQLKVIFGNIEDIYRFQMGFVRDLEKQYNNDDPHL
ļ			SEIGPCFLEHQDGFWIYSEYCNNHLDACMELSKLMKDSRYQHFF
Ì			EACRLLQQMIDIA\IDGFLLTPVQKICKYPLQLAELLKYTAQDH
ĺ			SDYRYVAAALAVMRNVTQQINERKRRLENIDKIAQWQASVLDWB
ļ			GEDILDRSSELIYTGEMAWIYOP\YGRNQQRVFFLFDHQMVLCK
			KDLIRRDILYYKGRIDMDKYEVVDIEDGRDDDFNVSMKNAFKLH
		ŀ	NKETEEIHLFFAKKLBEKIRWLRAFREERKMVQEDEKIGFEISE
			NOKRQAAMTVRKVPKQKGVNSARSVPPSYPPPQDPLNHGQYLVP
ļ			\DGIAQSQVFEFTEPKRSQSPFWQNFSRLTPFKK
6056	43	3358	SGGRGPVRVRSEQLSPSAEQVSQISQISLGRRPLSSLPPPPSRA
			LAPTRAPDTALTIMEVAEVESPLNPSCKIMTFRPSMEEFREFNK
l.			YLAYMESKGAHRAGLAKVIPPKEWKPRQCYDDIDNLLIPAPIQQ
			MVTGQSGLFTQYNIQKKAMTVKEFRQLANSGKYCTPRYLDYEDL
ĺ			ERKYWKNLTFVAPIYGADINGSIYDEGVDEWNIARLNTVLDVVE
			EECGISIEGVNTPYLYFGMWKTTFAWHTEDMDLYSINYLHFGEP
			KSWYAIPPEHGKRLERLAQGFFPSSSQGCDAFLRHKMTLISPSV
1			LKKYGIPFDKITQEAGEFMITFPYGYHAGFNHGFNCAESTNFAT
İ		İ	VRWIDYGKVAKLCTCRKDMVKISMDIFVRKFQPDRYQLWKQGKD
			IYTIDHTKPTPASTPEVKAWLQRRRKVRKASRSFQCARSTSKRP
		ļ	KADEEEEVSDEVDGAEVPNPDSVTDDLKVSEKSEAAVKLRNTEA
			SSEEESSASRMQVEQNLSDHIKLSGNSCLSTSVTEDIKTEDDKA
			YAYRSVPSISSEADDSIPLSTGYEKPEKSDPSELSWPKSPESCS
		•	SVAESNGVLTEGEESDVESHGNGLEPGEIPAVPSGERNSFKVPS
1			IAEGENKTSKSWRHPLSRPPARSPMTLVKQQAPSDEELPEVLSI
1		}	EEEVEETESWAKPLIHLWQTKPPNFAAEQEYNATVARMKPHCAI
			CTLLMPYHKPDSSNEENDARWETKLDEVVTSEGKTKPLIPEMCF
			IYSEENIEYSPPNAFLEEDGTSLLISCAKCCVRVHASCYGIPSH
		ĺ	EICDGWLCARCKRNAWTAECCLCNLRGGALKQTKNNKWAHVMCA
			VAVPEVRFTNVPERTQIDVGRIPLQRLKLKCIFCRHRVKRVSGA
1			CIQCSYGRCPASFHVTCAHAAGVL\MEPDDWPYVVNITCFRHKV
1			NPNVKSKACEKVISVGQTVITKHRNTRYYSCRVMAVTSQTFYEV
1			MFDDGSFSRDTFPEDIVSRDCLKLGPPAEGEVVQVKWPDGKLYG
1	1		AKYFGSNIAHMYQVEFEDGSQIAMKREDIYTLDEELPKRVKARF
			VSAGRCHLGTCQVNSLSSPHVSQAQQETYLGFWINSKKSQCNIF
6057	1	953	LSGTY EVAND VEGECCI CONVEYCHARCEPER MOLTER CONVEY
003/	1 *	853	FVÄRLKEQEGEGGLGPRKEKGRARGRERRKMQLTRCCFVFLVQ GSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKS
			RPMANSTLLGLLAPPGEAWGILGOPPNRPNHSPPPSAKVKKIFG
			WGDFYSNIKTVALNLLVTGKIVDHGNGTFSVHFOHNATGOGNIS
1			ISLVPPSKAVEFHQEQQIFIEAKASKIFNC\RMEWEKVE\RGRR
1		1	TSLFTHDPAKICSRDHAQSSATWSCSQPFKVVCVYIAFYSTDYR
	1		LVQKVCPDYNYHSDTPYYPSG
6058	1	986	HPLPSASLGLPSVSLGVSLCVRSALLEAVVPMLPKRRRARVGSP
5555		700	SGDAASSTPPSTRFPGVAIYLVEPRMGRSRRAFLTGLARSKGFR
			VLDACSSEATHVVMEETSAEEAVSWQERRMAAAPPGCTPPALLD
		1	ISWLTESLGAGOPVPVECRHRLEVAGPSKGPLSPAWMPAYACOR
			PTPLTHHNTGLSEALE ILAEAAGFEGSEGRLLTFCRAASVLKAL
1	1		PSPVTTLSQLQGLPHFGEHSSRVVQELLEHGVCEEVERVRRSE/
			,
1			RLFTQIFGVGVKTADRWYREGLRTLDDLREQPQKLTQQQKAGEP SREAGPWASLNCTLDPSASTP
6059	2	3650	
5033	4	3050	QQDFESLADLTDHRAHRCPGDGDDDPQLSWVASSPSSKDVASPT
1		1	QMIGDGCDLGLGEEEGGTGLPYPCQFCDKSFIRLSYLKRHEQIH
		1	SDKLPFKCTYCSRLFKHKRSRDRHIKLHTGDKKYHCHECEAAFS BEDHIKTULKTUCCCVDBYCTUCVBCFCCTCGLOCHMOAUKVNIK
	1	[RSDHLKIHLKTHSSSKPFKCTVCKRGFSSTSSLQSHMQAHKKNK EHLAKSEKEAKKDDFMCDYCEDTFSQTEBLEKHVLTRHPQLSEK
	<u> </u>	L	ENDANSEARANDEMODICEDIFSCIEDERAVUTARIFQUSER

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1			
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
j	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
]	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ADLQCIHCPEVFVDENTLLAHIHQAHANQKHKCPMCPE\QFSSV
	1		\EGVYCHLDSHRQPDSSNHSVSPDPVLGSVASMSSATPDSSASV
1		1	BRGSTPDSTLKPLRGQKKMRDDGQGWTKVVYSCPYCSKRDFNSL
1			AVLEIHLKTIHADKPQQSHTCQICLDSMPTLYNLNEHVRKLHKN
			HAYPVMQFGNISAFHCNYCPEMFADINSLQEHIRVSHCGPNANP
			SDGNNAFFCNQCSMGFLTESSLTEHIQ\Q\AHCSVGSAKLESPV
1			VQPTQSFMEVYSCPYCTNSPIFGSILKLTKHIKENHKNIPLAHS
	1		KKSKAEQSPVSSDVEVSSPKRQRLSASANSISNGEYPCNOCDLK
		1	
			PSNFESFQTHLKLHLELLLRKQACPQCKEDFDSQESLLQHLTVH
1		1	YMTTSTHYVCESCDKQPSSVDD\LQKH\LLDMPHPLCCTHCT\L
			CQEVFDS\KVSI\QVHLAVKHSNEKKMYRCTACNWDFRKEADLQ
Į.			VHVKHSHLGNPAKAHKCIFCGETFSTEVELQCHITTHSKKYNCK
			FCSKAFHAIILLEKHLREKHCVFDAATENGTANGVPPMATKKAE
1	1	1	PADLQGMLLKNPEAPNSHEASEDDVDASEPMYGCDICGAAYTME
}	1		VLLQNHRLRDHNIRPGEDDGSRKKAEFIKGSHKCNVCSRTFFSE
1			NGLREHLQTHRGPAKHYMCPICGERFPSLLTLTEHKVTHSKSLD
		i	TGTCRICKMPLQSEEEFIEHCQMHPDLRNSLTGFRCVVCMQTVT
			STLELKIHGTFHMQKLAGSSAASSPNGQGLQKLYKCALCLKEFR
			SKQDLVKLDVNGLPYGLCAGCMARSANGOVGGLAPPEPADRPCA
			GLRCPECSVKFESAEDLESHMQVDHRDLTPETSGPRKGTOTSPV
		1	PRKKTYQCIKCQMTFENEREIQIHVANHMIEEGINHECKLCNQM
			FDSPAKLLCHLIEHSFEGMGGTFKCPVCFTVFVQANKLQQHIFA
]	!		VHGQEDKIYDCSQCPQKFFFQTELQNHTMSQHAQ
6060	2145	202	
0000	2145	202	SYBIVGKNKLEVNHSQLKALCKCSLPSRLLPLGENLPLLDRGFR
			KEPRSRGSRERDNMLHLHHSCLCFRSWLPAMLAVLLSLAPSASS
		1	DISASRPNILLLMADDLGIGDIGCYGNNTMRTPNIDRLAEDGVK
	1		LTQHISAASLCTPSRAAFLTGRYPVRSGMVSSIGYRVLQWTGAS
		1	GGLPTNETTFAKILEEKGYATGLIGKWHLGLNCESASDHCHHPL
			HHGFDHFYGMPFSLMGDCARWELSEKRVNLEQKLNFLFQVLALV
			ALTLVAGKLTHLIPVSWMPVIWSALSAVLLLASSYFVGALIVHA
			DCFLMRNHTITEQPMCFQRTTPLILQEVASFLKRNKHGPFLLFV
		1	SFLHVHIPLITMENFLGKSLHGLYGDNVKEMDWMVGRILDTLDV
1			EGLSNSTLIYFTSDHGGSLENQLGNTQYGGWNGIYKGGKGMGGW
			EGGIRVPGIFRWPGVLPAGRVIGEPTSLMDVFPTVVRLAGSEVP
1		1	QDRVIDGQDLLPLLLGTAQHSDHEFLMHYCERFLHAARWHORDR
1			GTMWKVHFVTPVFQPEGAGACYGRKVCPCFGEKVVHHDPPLLFD
1			LSRDPSETHILTPASEPVFYQVMER\VQQAVWEHQRTLSPVPLQ
		1	LDRLGNIWRPWLQPCCGPFPLCWCLREDDPQ
6061	110	1330	MNIHMKRKTIKNINTFENRMLMLDGMPAVRVKTELLESEQGSPN
"""	"""	1330	
1		!	VHNYPDMEAVPLLLNNVKGEPPEDSLSVDHFQTQTEPVDLSINK
		1	ARTSPTAVSSSPVSMTASASSPSSTSTSSSSSSRLASSPTVITS
		}	VSSASSSTVLTPGPLVASASGVGGQQFLHIIHPVPPSSPMNLQ
			SNKLSHVHRIPVVVQSVPVVYTAVRSPGNVNNTIVVPLLEDGRG
1			HGKAQMDPRGLSPRQSKSDSDDDDLPNVTLDSVNETGSTALSIA
		1	RAVQEVHPSPVSRVRGNRMNNQKFPCSISPFSIESTRRQRTVLN
		1	PPDSRKTAYSTDCDF\EGLQQKLYTKSSSPGRVHRRTHTGEKPY
			KCTWEGCTWKFARSDELTRHYRKHTGVKPFKCADCDRSFSRSDH
L_		1	LALHRRHMLV
6062	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
1	1		LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
1			TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
1			EFSEPEEEIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
		1	LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELODFE
			BEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEELP
			INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP
60.5	I		YPYCYQGGRVICRVIMPCNWWVARMLGRV
6063	71	1079	ETMAKNGPENCEDCHILNAEAFKSKKICKSLKICGLVFGILALT
1			LIVLFWGSKHFWPEVPKKAYDMEHTFYSNGEKKKIYMEIDPVTR
1	1		TEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKTQIKVIP
	j		EFSEPEEBIDENEEITTTFFEQSVIWVPAEKPIENRDFLKNSKI
			LEICDNVTMYW\INPTL\ISGTFAKQLHHNFAFIILVSELQDFE
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
		 	EEGEDLHFPANEKKGIEQNEQWVVPQVKVEKTRHARQASEEBLP
			TNDVTPNCTEEDDMI DEBCYCCTYCD CANARDASEEELD
			INDYTENGIEFDPMLDERGYCCIYCRRGNRYCRRVCEPLLGYYP
6064	913	311	YPYCYQGGRVICRVIMPCNWWVARMLGRV
]) 113	311	NLPQSLPRPTEHSPPYSLEKMTDLVAVWDVALSDGVHKIEFEHG
}			TTSGKRVVYVDGKEEIRKEWMFKLVGKETFYVGAAKTKATINID
1			AISGFAYEYTLEINGKSLKKYMEDRSKTTNTWVLHMDGENFRIV
1			LEKDAMDVWCNGKKLETAGEFVDDGTETHFSIGTH\ACYIKAV\
6065	1153	C41	SSG\KRKEGIIHTLIVDNREIPEIAS
0003	1133	641	MSVRVARVAWVRGLGASYRRGASSFPVPPPGAQGVAELLRDATG
1	ļ	}	AEEEAPWAATERRMPGQCSVLLFPGQGSQVVGMGRGLLNYPRVR
1			BLYAAARRVLGYDLLELSLHGPQETLDRTVHCQPAIFVASLAAV
			EKLHHLQPSVIENCVAAAGFSVGEFAALVFAGAMEFAEG
6066	68	3470	VKENMPATRKPMRYGHTEGHTEVCFDDSGSFIVTCGSDGDVRIW
			EDLDDDDPKFINVGEKAYSCALKSGKLVTAVSNNTIQVHTFPEG
			VPDGILTRFTTNANHVVFNGDGTKIAAGSSD\FLVKIVDVMDSS
			QQKTFRGHDAPVLSLSFDPKDIFLASASCDGSVRVWQISDQTCA
			ISWPLLQKCNDVINAKSICRLAWQPKSGKLLAIPVEKSVKLYRR
1			ESWSHQFDLSDNFISQTLNIVTWSPCGQYLAAGSINGLIIVWNV
			ETKDCMERVKHEKGYAICGLAWHPTCGRISYTDAEGNLGLLENV
			CDPSGKTSSSKVSSRVEKDYNDLFDGDDMSNAGDFLNDNAVEIP
i			SFSKGIINDDEDDEDLMMASGRPRQRSHILEDDENSVDISMLKT
1			GSSLLKEEEEDGQEGSIHNLPLVTSQRPFYDGPMPTPROKPFOS
			GSTPLHLTHRFMVWNSIGIIRCYNDEQDNAIDVEFHDTSIHHAT
1		·	HLSNTLNYTIADLSHEAILLACESTDELASKLHCLHFSSWDSSK
			EWIIDLPQNBDIEAICLGQGWAAAATSALLLRLFTIGGVOKEVF
1	}		SLAGPVVSMAGHGEQLFIVYHRGTGFDGDQCLGVOLLELGKKKK
			QILHGDPLPLTRKSYLAWIGFSAEGTPCYVDSEGIVRMLNRGLG
ļ			NTWTPICNTREHCKGKSDHYWVVGIHENPQQLRCIPCKGSRFPP
			TLPRPAVAILSFKLPYCQIATEKGQMEEQFWRSVIFHNHLDYLA
			KNGYEYEESTKNOATKEQQELLMKMLALSCKLEREFRCVELADL
			MTQNAVNLAIKYASRSRKLILAQKLSELAVEKAAELTATQVEEE
1			EEEEDFRKKLNAGYSNTATEWSQPRFRNQVEEDAEDSGEADDEE
ļ			KPEIHKPGQNSFSKSTNSSDVSAKSGAVTFSSQGRVNPFKVSAS
			SKEPAMSMNSARSTNILDNMGKSSKKSTALSRTTNNEKSPIIKP
			LIPKPKPKQASAASYFQKRNSQTNKTEEVKEENLKNVLSETPAI
			CPPQNTENQRPKTGFQMWLEENRSNILSDNPDFSDEADIIKEGM
			IRFRVLSTEERKVWANKAKGETASEGTEAKKRKRVVDESDETEN
		İ	QEEKAKENLNLSKKQKPLDFSTNQKLSAFAFKQE
6067	858	321	LPWQRLGVLLSRGKMAVTGWLESLRTAQKTALLQDGRRKVHYLF
1		1	PDGKEMAEEYDEKTSELLVRKWRVKSALGAMGQWQLEVGDPAPL
			GAGNLGPELIKESNANPIFMRKDTKMSFQWRIRNLPYPKDVYSV
		ŀ	SVDQKERCIIVRTTNKKYYKKFSIPDLDRHQLPLDDALLSFA\T
			PTAP
6068	13	1730	GSKMADLANEEKPAIAPPVFVFQKDKGQKSPAEQKNLSDSGEEP
]			RGEAEAPHHGTGHPESAGEHALEPPAPAGASASTPPPPAPEAQL
<u> </u>			PPFPRELAGRSAGGSSPEGGEDSDREDGNYCPPVKRERTSSLTQ
]			FPPSQSEERSSGFRLKPPTLIHGQAPSAGLPSQKPKEQQRSVLR
	1		PAVLQAPQPKALSQTVPSSGTNGVSLPADCTGAVPAASPDTAAW
	l		RSPSEAADEVCALEEKEPQKNESSNASEEEACEKKDPATQQAFV
	Ì		FGONLEDBY CHEEKEPANESSNASEKEACEKKUPATQQAFV
	!		FGQNLRDRVKLINESVDEADMENAGHPSADTPTATNYFLQYISS
			SLENSTNSADASSNKFVFGQNMSERVLSPPKLNEVSSDANRENA
			AAESGSESSSQEATPEKESLAESAAAYTKATARKCLLEKVEVIT
	ļ	Ì	GEEAESNVLQMQCKLFVFDKTSQSWVERGRGLLRLNDMASTDDG
		İ	TLQSRLSDAGPRGSLR\LILNTKLWAQMQIDKASEK\SIRITAM
[ĺ	İ	DNEDQGVKVFLISASSKDTGQVYAALHHRILALRSRVEQEQEAK
			MPAPEPGAAPSNEEDDSDDDDVLAPSGATAAGAGDEGDGQTTGS
6069			T
6005	583	27	PTRPGQAGSSSAMAAQRLGKRVLSKLQSPSRARGPGGSPGGLQK
			RHARVTVKYDRRELORRLDVEKWIDGRLEELYRGMEADMPDEIN
			IDELLELESEEERSRKIQGLLKSCGKPVEDFIQELLAKLQGLHR

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ŀ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
<u> </u>	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			Q\PGLRQPSPSP\DGQPSAPFQGPGARTASPLTLLALFPGPPER
			RPALLCVLSCI
6070	478	858	IRVTVDGEFLHYIFPLQFLDSPEW/RFTETHRGRHF\QVTLTAE
1			TDCRYVSWRRKKLYLLFAQHRYISRLFSVLIGSDIADKLYALND
			RVYIGKRYHYDIRLPNFYQMSTPEIRRSPLTQHFQNSRRYW
6071	2	1654	HEARTKGNMALARP\VRLFSLVTRLLLAPRRGLTVRSPDEPLPV
1 00/1	-		VRIPVALQRQLEQRQSRRRNLPRPVLVRPGPLLVSARRPELNQP
]			ARLTLGRWERAPLASOGWKSRRARRDHFSIERAOOEAPAVRKLS
		1	SKGSFADLGAWKPRVLHALQE\AAPEVVQ\PTTVQSSTIPSLLR
	1		GRHVVCAAETGSGKTLSYLLPLLQRLLG\HPSLDSLPIPAPRGL
ł			VLVPSRELAQQVRAVAQPLGRSLGLLVRDLEGGHGMRRIRLQLS
1			ROPSADVLVATPGALWKALKSRLISLEQLSFLVLDEADTLLDES
			FLELVDYILEKSHIAEGPADLEDPFNPKAQLVLVGATFPEGVGO
ļ			LLNKVASPDAVTTITSSKLHCIMPHVKQTFLRLKGADKVAELVH
1			ILKHRDRAERTGPSGTVLVFCNSSSTVNWLGYILDDHKIQHLRL
}			-
i			QGQMPALMRVGIFQSFQKSSRDILLCTDIASRGLDSTGVELVVN
1			YDFPPTLQDYIHRAGRVGRVGSEVPGTVISFVTHPWDVSLVQKI
	ļ		ELAARRRSLPGLASSVKEPLPQAT
6072	1	742	KMERTEMMPTINSQLEFKSKPFPLVSSSRWLVKRGELTAYVEDT VLFSRRTSKOOVYFFLFNDVLIITKKKSEESYNVNDYSLRDOLL
			VESCONEELNSSPGKNSSTMLYSRQSSASHLFTLTVLSNHANEK
			VEMLLGAETQSERARWITALGHSSGKPPADRTSLTQVEIVRSFT
Į			AKQPDELSLQVADVVLI\YQRVSDGWYEGER\LRDGERGWFPME
			CAKEITCQATIDKNVERMGRLLGLETNV
6073	620	B60	PCRRGLARPLSRRPG/SILVHCAVGVSRSATLVLAYLMLYHHLT
			LVEAIKKVKDHRGIIPNRGFLRQLLALDRRLRQGLEA
6074	168	1110	PGARCMATELQCPDSMPCHNQQVNSASTPSPEQLRPGDLILDHA
l	1		GGNRASRAKVILLTGYAHSSLPAELDSGACGGSSLNSEGNSGSG
			DSSSYDAPAGNSFLEDCELSRQIGAQLKLLPMNDQIRELQTIIR
1			DKTASRGDFMFSADRLIRLVVEEGLNQLPYKECMVTTPTGYKYE
i			GVKFEKGNCGVSIMRSGEAMEQGLRDCCRSIRIGKILIQSDEET
ì			QRAKVYYAKFPPDIYRRKVLLMYPILQTG\NTVIEAVKVLIEHG
			VQPSVIILLSLFSTPHGAKSIIQEFPEITILTTEVHPVAPTHFG
<u>.</u>	<u> </u>		QKYFGTD
6075	320	1091	PPTCQPQEVEHH\YGYVPILGNKTLPSRCHQCVIVSSSSHLLGT
		İ	KLGPEIERAECTIRMNDAPTTGYSADVGNKTTYRVVAHSSVFRV
1	1		LRRPQEFVNRTFBTVFIFWGPPSKMQKPQGSLVRVIQRAGLVFP
1			NMEAYAVSPGRMRQFDDLFRGETGKDREKSHSWLSTGWFTMVIA
		1	VELCDHVHVYGMVPPNYCSQRPRLQRMPYHYYEPKGPDECVTYI
<u></u>	<u> </u>	<u> </u>	QNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT
6076	1721	107	HPSPTEAPRVQHLTMDCTWRILFLVAAATGTHAQVQLVQSGAEV
			KKPGASVKVSCKVSGYTLTELSMHWVRQAPGKGLEWMGAFDPED
[1		GETIYAQKFQGRVTMTEDTSTDTAYMELSSLRSEDTAVYYCATD
			HGDYAFDIWGQGTMVTVSSAPTKAPDVFPIISGCRHPKDNSPVV
1			LACLITGYHPTSV\TVTWYMGTQSQA\QRTFPEIQRRDSYYMTS
			SQLSTPLQQWRQGEYKCVVQHTASKSKKEIFRWPESPKAQASSV
			PTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEEQEERE
1		1	TKTPECPSHTQPLGVYLLTPAVQDLWLRDKATFTCFVVGSDLKD
1			AHLTWEVAGKVPTGGVEEGLLERHSNGSQSQHSRLTLPRSLWNA
1	1		GTSVTCTLNHPSLPPQRLMALREPAAQAPVKLSLNLLASSDPPE
			A\ASWLLCEVSGFSPPNILLMWLEDHGEVNTSGFAPARPLPKP\
1			RSTTFWA\WSVLRVPAPPSPQPATYTCVVSHEDSRTLLNASRSL
1			EVSYVTDHGPMK
6077	3687	1268	LLPDMNLQPIFWIGLISSVCCVFAQTDENRCLKANAKSCGECIQ
			AGPNCGWCTNSTFLQEGMPTSARCDDLEALKKKGCPPDDIENPR
			GSKDIKKNKNVTNRSKGTAEKLKPEDITQIQPQQLVLRLRSGEP
1			QTFTLKFKRAEDYPIDLYYLM\DLSYSMKDDLENVKSLGTDLMN
			EMRRITSDFRIGFGSFVEKTVMPYISTTPAKLRNPCTSEQNCTS
		1	PFSYKNVLSLTNKGEVFNELVGKQRISGNLDSPEGGFDAIMQVA
		1	VCGSLIGWRNVTRLLVFSTDAGFHFAGDGKLGGIVLPNDGQCHL
L	1		ACCOST CALLES TO THE LA LONG LA LA LA LA

650	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ	j	1	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	L.		
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			ENNMYTMSHYYDYPSIAHLVQKLSENNIQTIFAVTEEFOPVYKE
1			LKNLIPKSAVGTLSANSSNVIQLIIDAYNSLSSEVILENGKLSE
	1		
<i>\</i>	1	İ	GVTISYQSY\CKNGVNGTGBNGRKCSNISIGDEVQFEISITSNK
j			CPKKDSDSFKIRPLGFTEEVEVILQYICECECQSEGIPESPKCH
			EGNGTFECGACRCNEGRVGRHCECSTDEVNSEDIGCFTARKENQ
	1		FQKSASNHGRVPSAGQCVCRKRDNTNEIYSGKFCECDNFNCDRS
ł	1		NGLICGGNGVCKCRVCECNPNYTGSACDCSLDTSTCEASNGQIC
			NGRGICECGVCKCTDPKFQGQTCEMCQTCLGVCAEHKECVQCRA
			FNKGEKKDTCTQECSYFNITKVESRDKLPQPVQPDPVSHCKEKD
	1		· -
ŀ			VDDCWFYFTYSVNGNNEVMVHVVENPECPTGPDIIPIVAGVVAG
1			IVLIGLALLLIWKLLMIIHDRREFAKFEKEKMNAKWDTGENPIY
	İ		KSAVTTVVNPKYEGK
6078	1426	180	ETEDVMELLEEDLTCPICCSLFDDPRVLPCSHNFCKKCLEGILE
1			GSVRNSLWRPVPFKCPTCRKKTFSYWELIPLQVNYSLKGIVEKY
1			· -
1			NKIKISPKMPVCKGH\LGQPLNIF\CL\TDMQLDL/CGIC\ATR
			GEHTKHVFCSIEDAYAQERDAFESLFQSFETWRRGDALSRLDTL
I			ETSKRKSLQLLTKDSDKVKEFFEKLQHTLDQKKNEILSDFETMK
Ì			LAVMQAYDPEINKLNTILQEQRMAFNIAEAFKDVSEPIVFLQQM
		Į.	QEFREKIKVIKETPLPPSNLPASPLMKNFDTSQWEDIKLVDVDK
1	1		LSLPQDTGTFISKIPWSFYKLFLLILLLGLVIVFGPTMFLEWSL
	1		FDDLATWKGCLSNFSSYLTKTADFIEQSVFYWEQVTDGFFIFNE
		}	
		<u> </u>	RFKNFTLVVLNNVAEFVCKYKLL
6079	1586	141	ATARDLGCARRIDRVVMESTPSRGLNRVHLQCRNLQEFLGGLSP
		ļ.	GVLDRLYGHPATCLAVFRELPSLAKNWVMRMLFLEQPLPQAAVA
	1	}	LWVKKEFSKAQEESTGLLSGLRIWHTQLLPGGLQGLILNPIFRQ
			NLRIALLGGGKAWSDDTSQLGPDKHARDVPSLDKYAEERWEVVL
}	j]	HFMVGSPSAAVSQDLAQLLSQAGLMKSTEPGEPPCITSAGFOFL
1	1	1	
1	1	1	LLDTPAQLWYFMLQYLQTAQSRGMDLVEILSFLFQLSFSTLGKD
	1	Į.	YSVEGMSDSLLNFLQHLREFGLVFQRKRKSRRYYPT/RALAINL
	Į.		SSGVSGAGGTVHQPGFIV\VETNYRLYAYTESELQIALIALFSE
1			MLYPFP\NMVV\ARVTR\ESVQQAIASGITAQOIIHFLRTRAHP
1	ł	}	VMLKQTPVLPPTITDQIRLWELERDRLRFTEGVLYNQFLSQVDF
1			ELL\LAHAPKLGVLVFE/NTPAKRLMVVTPAGHSDVKRFWKROK
i		[HSS
-6000	 		
6080	1	1199	IETIDHVGEFAMAAQAAGVSRQRAATQGLGSNQNALKYLGQDFK
ļ		}	TLRQQCLDSGVLFKDPBFPACPSALGYKDLGPGSPQTQGIIWKR
1		}	PTELCPSPQFIVGGATRTDICQGGLGDCWLLAAIASLTLNEELL
1		1	YRVVPRDQDFQENYAGIFHFQPLCPPSP\FWQYGEWVEVVIDDR
ì		1	LPTKNGQLLFLHSEQGNEFWSALLEKAYAKLNGCYEALAGGSTV
[EGFEDFTGGISEFYDLKKPPANLYOIIRKALCAGSLLGCSIDVY
ľ	1	İ	- · · · · · · · · · · · · · · · · · · ·
		[SAAEAEAITSQKLVKSHAYSVTGVBEVNFQGHPEKLIRLRNPWG
1	1		EVEWSGAWSDDAPEWNHIDPRRKEELDKKVEDGEFWMSLSDFVR
1	1	1	QFSRLEICNLSPDSLSSEEVHKWNLVLFNGHWTRGSTAGGCQNY
1.	1 .	1	PGSS
6081	3	865	EMLPLLLPLPLLWA/GALAQDARFRLEMPESVTVQEGLCIFVHC
1	1	1	
1		1	SVFYLEYGWKDSTPAYGHWFREGVSVDQETPVATNNSTQKVQKE
1		1	TOGRFHLLGDPSRNNCSLSIRDARRRDNGSYFFWVARGRTKFSY
		1	KYSPLSVYVTALTHRPDILIPEFLKSGHPSNLTCSVPWVCEQGT
		1	PPIFSWMSAAPTSLGPRTLHSSVLTIIPRPQDHGTNLICQVTFP
1			GAGVTTERTIQLSVSWKSGTVEEVVVLAVGVVAVKILLLCLCLI
	}		ILSFHKKKAVRAVEVEENVYAVMG
6082	283	1000	+
0002	283	1288	EARSPGPTQTRTAPGLAAPGLAQPAALRLLLSRPPSAAMDGDGD
1			PESVGQPEEASPEEQPEEASAEEERPEDQQEEEAAAAA\Y\LDE
		1	LPEPLLA/LRVLAALPRHE\LVQACR\LVCLRWKELVDGAPLWL
!		j	LKCQQEGLVPEGGVEEERDHWQQFYFLSKRRRNLLRNPCGEEDL
1	1		EGWCDVEHGGDGWRVEELPGDSGVEFTHDESVKKYFASSFEWCR
	1		1
1		1	KAQVIDLQAEGYWEELLDTTQPAIVVKDWYSGRSDAGCLYELTV
		ł	KLLSEHENVLAEFSSGQVAVPQDSDGGGWMEISHTFTDYGPGVR
L			FVRFEHGGQDSVYWKGWFGARVTNSSVWVEP
6083	1865	309	KOWCAERRGLGMSLADELLADLEEAABEEEGGSYGEEEEEPAIE
			

Predicted Predicted Predicted on Incleotide Inc	C-050	1 Dunal area	1 5 11 1	
No. nuclectice corresponding to first amino acid residue of amino acid residue of amino acid sequence	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
location cofirst amino acid residue of amino acid amino ac			3	
to first amino acid amino acid amino acid amino acid acquence PP-PICINE, O-Glutumine, R-Asgragine, PP-PICINE, O-Glutumine, R-Asgragine, PP-PICINE, O-Glutumine, R-Asgragine, PP-PICINE, O-Glutumine, R-Asgragine, PP-PICINE, O-Glutumine, R-Asgragine, PP-PICINE, O-Glutumine, R-Asgragine, PP-PICINE, O-Glutumine, R-Asgragine, PP-PICINE, O-Glutumine, R-Asgragine, PP-PICINE, O-Glutumine, R-Asgragine, PP-PICINE, O-Glutumine, R-Asgragine, PP-PICINE, O-Glutumine, R-Asgragine, PP-PICINE, O-Glutumine, R-Asgragine, PP-PICINE, PP-PICINE, O-Glutumine, R-Asgragine, PP-PICINE, PP-PIC	NO:	1)	
to first anino acid residue of anino acid an	1			
amino acid	l		1	
maino acid andio acid sequence Martyptophan, YaTyrosine, Xaunknown, ***stop Codon, 'possible nucleotide insertion) Vapossible nucleotide insertion Vapossible nucleotide insertion Vapossible nucleotide insertion V	1	to first		P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence	İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Sequence Naposible muclectide insertion:	ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence N=possible muclectide insertion	J	amino acid	sequence	Codon, /=possible nucleotide deletion.
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DVOETOLDLSGDSVKTIAKLMEDSKMPARIMKKIEEVISKQAKA SEVMGPVEAAPEYRVIVDANNLTVELENEINIIKKPIRKYSKA FPELESLYPNALDYIRTVERIGNSLOKKONMENLQQILTMATIM VVSVTASTTQQQLSEELERLEEACCMALELMASKKRIYEVVE SRMSFIAPNLSIIGASTAKIMOVAGGIKTYSEVUE SRMSFIAPNLSIIGASTAKIMOVAGGIKTYEVEE SRMSFIAPNLSIIGASTAKIMOVAGGIKTUSLMENDAGRIMLIG AQRKTISGPSSTSVLPHTGYYYHSDLVQSLPPIPPPSVAP\DL RRKAARLVAAKKTLAARVDSPHSSTSGKVGYEKLGDIERKFOKM QEPPPVKQVKPLPAPLDGGRKKRGGRYSKMKERLGLIEIR KKQ ANNMSGGELEBDAVGBLOFSIGHLIGKSGRVAQTOVMEATKA RISKTLORTLOKGSVVVGGKSTIEDRSSGTASSVAPTPLQGLEI VNPQAAEKKVABANQKYFSSMAEPLKVKGEKSGLMST 6085 2 1456 SGPRSFGGRRVGRISLGGKRNFEVTLLEGVSSERVERRRRARV GVARVKPGNPKKSPBATQVPK/VPAQVYLPGRGPPLREGELVM DEEXYVLYHRAQOTAPCLSFOIVEDHLIGHELPLTLYLCAGT QASSAQSNILMMLMRMINLHGTKPPPSEGSBEREEEBDEBEEER KPQLELAMPHYNGGINKVEVSNILGEBPVAGKEKGQVBVPALR RLLQVVEEPOALAAFLRDEQAGMKPIFSFAGHMEGGFALDMSPR VTGRLLIFGDCOKNHLHLYTTOGSWHVDGWSKKGQVBVPALR RLLQVVEEPOALAAFLRDEQAGMKPIFSFAGHMEGGFALDMSPR VTGRLLIFGDCOKNHLHLYTTOGSWHVDGWSKKGQVBVPALR RLLQVVEEPOALAAFLRDEQAGMKPIFSFAGHMEGGFALDMSPR VTGRLHIFGDCCOKNHLHATPTGGSWHVDGPVHTGTBLQGW SPTENTVFASCSADASIRIWDIRAPSKACMLTTATAHDGDVRV ISWSREPPFLLSGGDDGALKINDLRQFKSGGPVATFKRHAPPY SVEMHPQDGSVFAASSADHQITOMDLG/IVERDLQGGKKEPYPP NKWHIDDLKKKTVIEILEFSTEVKAVKLER\DKIVVLDSMIKK FTFTHRP\HQLHVEPKTVCVNPKGLCVLLGGGKKEPYPP NKWHIDDLKKKTVIEILEFSTEVKAVKLER\DKIVVLDSMIKK FTFTHRP\HQLHVEPKTVCVNPKGCCVLLGMSLLAPPOTHTG HVQLVDLASTEKPPVDIPAHBGVLSCIALNILQGRKKEPYPP NKWHIDDLKKKTVIEILEFSTEVKAVKLER\DKIVVVADPLCWM THARADFDFRKNQSSLASASFLPKYTFSKMFSKFOVPGGSS CICAPGTEPNAVIALCAGSSYKKLENPKGSCTRDVYAQPLCWM TVHIFAAEDPFRKNQSSLASASFLPKYTFSKMFSKFOVPGGSS CICAPGTEPNAVIALCAGSSYKLENPKGSCTRDVYAQPLCWM TVHIFAAEDPFRKNQSSLASASFLPKYTFSKMFSKFOVPGGSS CICAPGTEPNAVIALCAGSCYVTYSFRQAVVIALLVKXVVIELEFKTUK EUGTVSAVATGLODETICTENFLAAIA\HHTTSKYRFVILVILLEAKD QQKHFPPLCCCPPHAMGEVLLFRKLIGVTOVTVVRFPTTIVALL CELLGIYDEGGREEVSAVTIVIINMSQLESAGGTTF TTAKISBELLDDTICEKKERDALSS	ļ	Į.	1	VNPQAAEKKVAEANQKYFSSMAEFLKVKGEKSGLMST
DVORETQLDLGSDSVTITAKLMDSKMPARIMKLERYISKOAKA SEWGGVEARAPPRYVIVADANILTVETERDIYKYSKR PPELESLVPNALDVIRTVKELGNSLDKCKNNENLQQILTNATIM VVSVTASTTQQQISEELERLEBACDMALDINISKMPACHIMLIG AQRKTLSGFSSTSVLHTGYIYHSDTVQSLPPIPPPFSVAP\DL RRKAARILVAAKCTLAARVDSHFBSTEGKYEKYDKY QEPPPVKQVKPLPAPLDGQRKKRGGRYFKMKERLGLTERKPKW QEPPVKQVKPLPAPLDGGRKKRGGRYFKMKERLGLTERKPKW QEPPVKQVKPLPAPLDGGRKKRGGRYFKMKERLGLTEIR\KQ ANMMSFGEIEEDDAVGBLDGFSLGHLKKSKGUNGTVVEAPTKA RISKTLQRTLQKOGSVVYGGKSTIRDRSSGTASSVAPTPLQGLEI VNPQALEKKVARANQKYPSSMAEPLLVKGKSGLMST 6085 2 1456 SGPRSFQGRAVGRISLGGKRNPEVTLLPGVSSERVRRWRRARV GVARVKPGNPWKSPSPATQVPR/VPAQVYLPGRGPLRKGEELVM DERAYVLYHRAQTGAFCLSSFOLVENHLGHEPLTLLLCAGT QASSAQSNRLMMLRMINHIGTKPPPSEGSDEREEBEDEBEEER KPQLELAWPYHYGGINRVYSNILGEBPVAGSKKGQVSVPALR RLLQVVERFOALAAFLRDEQQMKPIFSFAGHMGEGFALDWSPR VTGRLLTGGCQKNHLWTTTOGSWHVDGWSKKGQVSVPALR RLLQVVERFOALAAFLRDEQQAMKPIFSFAGHMGEGFALDWSPR VTGRLTGGCCQKNHLWTTTOGSWHVDGWSKKGQVSVPALR RLLQVVERFOALAAFLRDEQQAMKPIFSFAGHMGEGFALDWSPR VTGRLTGGCCQKNHLWTTTOGSWHVDGWSKKGQVSVPALR RLLQVVERFOALAAFLRDEQQAMKPIFSFAGHMGEGFALDWSPR VTGRLTGGCCQKNHLWTTTOGSWHVDGWSKKGQVSVPALR RLLQVVERFOALAAFLRDEQQAMKPIFSGADMSPRV ISWSREPPLLGGCDOALKTHDLRQFKSGGSVATFKQHVAPVT SVEWHQDSGVFAASGADHQITGWBLG/TVERDEAGDVADPG LADLPQQLLFYHGGGETELKELHMHPQCFGLLVSTALSGFIFFRT ISV 6086 2419 1357 GAATORGGAMNLLPCNPHGMGLLYAGFNQDHGCFACGMEMGFRV YNTDPLKKEKQGFLESGGGGVWMLPFCRYLALUGGGKKPRYPP NKWHMDLKKKTVIEIEFSTEVKAVKLRR\DKIVVLDSHIKV FFTHNPH,RQLHVEPLTYVRKGCLULOPINSMSLLAFPGTHTG HVQLVDLASTEKPPVDIPAHBGVLSGIALNILQGTRIATASEKGT LIRIFDTSSGHLIQEIRRGSQANIYCINFNQGIKLCVSDHG TVHIFAADDPKRNKQSSLASASFLFFYFSSKMSFSKFQVFSGSS CICAFGTEFANAVIAICAGSSYTKLENPKGSCTRDVTAQPLEMT FORSTANDATAICAGSSYTKLENPKGSCTRDVTAQPLEMT GIATYVDTCGRECVEAVYU TWRMPGLTNYTHALLYKPU GIATYVDTCGRECVEAVYU TWRMPGLTNYTHANINJULLEKKYP GIATYVDTCGRECVEAVYU TWRMPGLTNYTHALLYKPULLIFYKVLK EELSPIOPVGFRECKSATVITAVI INMSQLFANYCLLIFYKVLK EELSPIOPVGFRECKENDYTHAAIAHHTTSSHPKNITJULLEKKPP DOMENSLLSSSSGOAISIASASPSPMHTYGGFGTTTPQTTT TTAKISBELIADTIGEKKERBDJSNDS 6086 1684 689 GASGLVRLLQQGBECLLAPVARKLVPFVGGVKKGFRAAFFFÖKE LERGRILDSTTISKKFREDDASO	6084	1865	309	KOWCAERRGLGMSLADELLADLEEAAEEEEGGSYGEEEEEPATE
SEWMEPURADPYNYUTUDANNILTUE IENELMI IHKPI IROXYSKIR PPELESLVPNALDYI RTVKELGNSLDKCKNNEHLQQILTNATIM VVSVTASTTQGQLISEELERLERACHMALEINASHER YEYVE SRMSFIAPNISI II GASTAAKIMOVAGGITNISKMRACNIMILG AQRKTISGSSTSVLPHTOYTYHSDIVQSIP IPPEPSVAPLQI RRKAARIVAAKCTLAARVDSHESTEGKVGYELKDEIERKPOKM QEPPPVKOVRLPAPLIGGGKKKGGGRYREPIPPPSVAPLQI RRKAARIVAAKCTLAARVDSHESTEGKVGYELKDEIERKPOKM QEPPPVKOVRLPAPLIGGGKKKGGGRYREPIPPSVAPLQILEI RRKAARIVAAKCTLAARVDSHESTEGKVGYELKDEIERKPOKM QEPPVKOVRLPAPLIGGGKKKGGGRYREPIPPSVAPLQILEI RISKTIORTIOKOGVVVGGKKKGGGRYRESVAPTPIQQILEI VNPQAAEKKVAEANQKYFSSMAEFIKVKGEKSGRWSQTOVMEATKA RISKTIORTIOKOGVVVGGKSTIRDRSSAVAPPIQGLEI VNPQAAEKKVAEANQKYFSSMAEFIKVKGEKSGLMST GVARVKREPHKSPSATQYFK,VAQOVYLDFGGEPURRGEELIVM DERAYVLYHRAQTGAFCLSFDIVXDHIGGNSTEEPITLLICAGT QASSAGSNICHMLEMMINIKTKPPSSEGBEEBEDEBEBEER KPQLELAMVPHYGGIRVEVSMICGEPVAGWSEKGQVEVPALR RLLQVVEEPOLAAPFIREDCAQMKPIFSDEEGEBEDEBEER KPQLELAMVPHYGGIRVEVSMICGEPVAGWSEKGQVEVPALR RLLQVVEEPOLAAPFIREDCAQMKPIFSOWEGGFALWSPV SYBHHPODSGVFAASGADHQITQMDLG/TVERDPEAGDVALDWS SPTENTVFASCSADASIRIWDIRAABSKACMLTTATAHGGVNV ISWSREPPELSGGDDGALKTWOLGGVAFTSVATKGWVAPVY SVBMHPODSGVFAASGADHQITQMDLG/TVERDPEAGDVALDWS SYBHNIVASCSADASIRIWDIRAABSKACMLTTATAHGGVNV ISWSREPPELSGGDDGALKTWOLGFACKTWAPVY SVBMHPODSGVFAASGADHQITQMDLG/TVERDPEAGDVALDWS SYBHNIVASCSADASIRIWDIRAABSKACMLTTATAHGGVNV ISWSREPPELSGGDDGALTYMDLG/TVERDRGAGDVALDWS SYBHNIVASCSADASIRIWDIRAABSKACMLTTATAHGGVNV ISWSREPPELSGGDDGALTVADLGCFACKMENGRFW PNTTDHPLKEKEKQEPLEGGVOHVEMLPRCNYLALVGGKKKPYPP NKWMINDLKKKTVI SIEPSTEVKAVKLRRIDKIVVULDSHIKV PTTTHRPLAQHAPEKTONKSGLLALSGANTALTARSKGT LIRIPTISSGBILIQELIRAGQAANIVCINDONSILLAFGGTHTG HVQLVUDLASTEKPPVIPAHGGCHALVAGGTSLASHGHT HVQLVUDLASTEKPPVIPAHGGCHALVAGTVAAGFTHTO HVQLVUDLASTEKPPVIPARGCLUAPCHONSILLAFGGTHTG HVQLVUSAVATLCOMPRECHALVATORUPACALLLEFKUL CCLAGTYDEGEVGAVVINTUNINGGLINTAKPRILVIJINGHAG GARTYMOTTGREVGAVVINTUNINGGLINTAKPRILVIJINGHAG GARTYMOTTGREVGAVVINTUNINGGLINTAKPRILVIJINGHAG GCCCPFFAMGEVALVATUVINTUNINGGLINTAKPRILVIJINGH GARTYVOLTARGUSSHERAVALVALUMLKSNGELSEGGTFF TTAKISBELISDTIGEKKERSPBJSVDG DAGHHTSLLSSSSGDAIGIBKAAVL				The state of the s
PPELESLVPNALDY IRTVKEIGNELDKCKYMENIGOLICMATIA VVSVTASTTOGQQLSEELERLERACMALEINASKHRIYEYVE SRMSFIAPNISIIIGASTAAKIMOVAGGITMISKMAACKIMILG AQRKTISGFSSTSVLHTTYTYHBDIVQSLPPIPPFSVAP\DL RRKAARILVAAKCTIAARVDSHFBSTSGKYEKENGENEKYDKW QEPPPVKQVKPLPAPLDGGRKKRGGRYSKKMERLGITEIR\KQ ANRMSFGEIEEDAVGBLOFSGLGHLGKSGKNOTQVIDEATIK RISKTLOPTLOKQSVVVGGKSTIRDRSGTASSVAPTPLQGLEI VNPQAAEKKVAENAQKYFSSMABFLKVKGEKSGLMST GOSSTSTGGRAVQGRISGERNEPVTILEGVSSERVRERKRRARV GVARVKPGNPWKPSPATQVPF\VPAQVYLPGRGPPLREGELIVM DEEXYVLVHRAQATGAPCLSFDIVADHLGHUSYSERVERKRRARV GVARVKPGNPWKPSPATQVPF\VPAQVYLPGRGPPLREGELIVM DEEXYVLVHRAQATGAPCLSFDIVADHLGHUSPSSERVERKRRARV GVARVKPGNPWKPSPATQVPF\VPAQVYLPGRGPPLREGELIVM RILGVVEEPQALAAFIRDEQAQMKPIFSFAGMEGFALDWSPR VTGRILTGDCQKNTHLWTPTDGGSWHVDQFPVGHVREVEDLQW SPTENTVPASCSADASIRIVMINGARASKACMITTATAHGGDVNV ISWSREPPFLISGGDDGALKIWDLRQFKSGSFVATFKQHVAPVT SVEMHPDDGSVPASAGADGITOMDIGITYATAHGGDVNV ISWSREPPFLISGGDDGALKIWDLRQFKSGSFVATFKQHVAPVT SVEMHPDDGSVPASAGADGITYOMDIGITYATAHGGDVNV ISWSREPPFLISGGDCALKIWDLRQFKSGSFVATFKQHVAPVT SVEMHPDDGSVPASAGADGITYOMDIGITYATAHGGDVNV ISWSREPPFLISGGDCALKIWDLRQFKSGSFVATFKQHVAPVT SVEMHPDDGSVPASAGADGITYOMDIGITYATAHGGDVNV ISWSREPPFLISGGDCALKIWDLRQFKSGSFVATFKQHVAPVT SVEMHPDDGSVPASAGADGITYOMDIGITYATAHGGDVNV ISWSREPPFLISGGDCALKIWDLRQFKSGSFVATFKQHVAPVT SVEMHPDDGSVPASAGADGITYOMDIGITYATAHGGDVNV ISWSREPPFLISGGDCALKIWDLRQFKSGSFRAFFTHT ISV 6086 2419 1357 GAATOHGGAMNLLPCNPHGMGLLYAGFNODHGCFACGMENGFRV YNTDPLKKKERQBFLEGGVGRVEMLFRCNYLALVGGKFRFAFTHT HVQLVDLASTEKPPVDIPAHGGVLLVCDLRFNCNISLLAFPGTHTG HVQLVDLASTEKPPVDIPAHGGVLLVCVLGTRIATASEKGT LIRIPTISSGHLIQELRRGSQAANIYCLINFKQDKSILCVSDHG TVHIFFAAEDPRRHKQSSLASASFLPKYFSKMSFSKFOVPGGSP CICAPGTERNAVIALCAGSSYYKELINF KRGSCREDVYAQFLEMT DDKL GOSOFFICHAMGVULTYTUPTTYTTYPTTPTTAKLGELICHTYSKYLVLINKAGGLSGCTAFTVAVLL EELSPIOPYGKFLCVKLVVFYSFMQAVIALLUKVGVISEHHTW EWQTVEAVATGLQFFIRGTSAASHATVLVININMSCIPAMYCLLLFKVULABLE GSCCDSFLAMMOVSDIRDDISEGVRHVCRTVRGHFRKLIFPEDQ DQMHTSLLSSSSQDAISIASSMPSPMGHVQGGGGTFAAFRFQKE ELEGRILRGPLARGPDSVNDS GAGGUWRLDDGIEGGLARAVLDFUKGKGGG	1	1		
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EWQTVEAVATGLQDFIICIEMFLAAIA\HHYTFSYKPYVQEAEE GSCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKKLFPEDQ DQNEHTSLLSSSGDAISIASSMPPSPMGHYQGFGHTVTPQTTP TTAKISDEILSDTIGEKKEPSDKSVDS 6088 1684 689 GASGLVRLLQQGHRCLLAPVAPKLVPPVRGVKKGFRAAFRFQKE LERQRLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLQENFSLDLL KTAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI	[
GSCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKKLFPEDQ DQNEHTSLLSSSSQDAISIASSMPPSPMGHYQGFGHTVTPQTTP TTAKISDEILSDTIGEKKEPSDKSVDS 6088 1684 689 GASGLVRLLQQGHRCLLAPVAPKLVPPVRGVKKGFRAAFRFQKE LERQRLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLQENFSLDLL KTAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI		İ		l .
DQNEHTSLLSSSSQDAISIASSMPPSPMGHYQGFGHTVTPQTTP TTAKISDEILSDTIGEKKEPSDKSVDS 6088 1684 689 GASGLVRLLQQGHRCLLAPVAPKLVPPVRGVKKGFRAAFRFQKE LERQRLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLQENFSLDLL KTAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI				EWQTVEAVATGLQDFIICIEMFLAAIA\HHYTFSYKPYVQEAEE
TTAKISDEILSDTIGEKKEPSDKSVDS 6088 1684 689 GASGLVRLLQQGHRCLLAFVAPKLVPFVRGVKKGFRAAFRFQKE LERQRLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLQENFSLDLL KTAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE QLTLSEEFFVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI	1		1	GSCFDSFLAMWDVSDIRDDISEQVRHVGRTVRGHPRKKLFPEDQ
TTAKISDEILSDTIGEKKEPSDKSVDS 6088 1684 689 GASGLVRLLQQGHRCLLAFVAPKLVPFVRGVKKGFRAAFRFQKE LERQRLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLQENFSLDLL KTAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE QLTLSEEFFVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI				
GASGLVRLLQQGHRCLLAPVAPKLVPPVRGVKKGFRAAFRFQKE LERQRLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLQENFSLDLL KTAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI		1		1
LERORLLRCPPPPVRRSEKPNWDYHAEIQAFGHRLOENFSLDLL KTAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI	6088	1684	689	
KTAFVNSCYIKSEEAKRQQLGIEKEAVLLNLKSNQELSEQGTSF SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI				-
SQTCLTQFLEDEYPDMPTEGIKNLVDFLTGEEVVCHVARNLAVE QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI	1			
QLTLSEEFPVPPAVLQQTFFAVIGALLQSSGPERTALFIRDFLI		1		
	1		1	
TQMTGKELFEMWKIINPMGLLVBELKKRNVSAPESRLTRQSG\A				
	1	1	1_	TQMTGKELFEMWKIINPMGLLVBELKKRNVSAPESRLTRQSG\A

SEQ	Predicted	Predicted end	Drive and compat containing
	1		Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į.	residue of	amino acid	
		1	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence]	\=possible nucleotide insertion)
			PTALPLYFVGLYCDKKLIAEGPGETVLVAEEEAARVALRKLYGF
1		1	TENRRPWNYSKPKETLRAEKSITAS
6089	3	3054	TRLGIPGSTISSRPRLCALAAEGHFLGHSWTGSRAGAHTGAPAW
0005		3037	
		1	PSRRLRDLPAGGMWRLRRAAVACEVCQSLVKHSSGIKGSLPLQK
Į.		ì	LHLVSRSIYHSHHPTLKLQRPQLRTSFQQFSSLTNLPLRKLKFS
ļ			PIKYGYQPRRNFWPARLATRLLKLRYLILGSAVGGGYTAKKTFD
ł		1	QWKDMIPDLSEYKWIVPDIVWEIDEYIDFEKIRKALPSSEDLVK
ł		1	LAPDFDKIVESLSLLKDFFTSGSPEETAFRATDRGSESDKHFRK
Ì		1	VSDKEKIDQLQEELLHTQLKYQRILERLEKENKELRKLVLOKDD
		1	
	1	1	KGIPFIESLRKSLIDMYSEVLDVLSDYDASYNTQDHLPRVVVVG
		1	DQSAGKTSVLEMIAQARIFPRGSGEMMTRSPVKVTLSEGPHHVA
			LFKDSSREFDLTKEEDLAALRHEIELRMRKNVKEGCTVSPETIS
1		[LNVKGPGLQRMVLVDLPGVINTVTSGMAPDTKETIFSISKAYMQ
		1	DPNAIILCIQDGSVDAERSIVTDLVSQMDPHGRRTIFVLTKVDL
		İ	AEKNVASPSRIQQIIEGKLFPMKALGYFAVVTGKGNSSESIEAI
		1	REYEEEFFQNSKLLKTSMLKAHQVTTRNLSLAVSDCFWKMVRES
ŀ	ļ		VEQQADSFKATRFNLETEWKNNYPRLRELDRNELFEKAKNEILD
	1	1	F.
j			EVISLSQVTPKHWEEILQQSLWERVSTHVIENIYLPAAQTMNSG
ŀ			TFNTTVDIKLKQWTDKQLPNKAVEVAWETLQEEFSRFMTEPKGK
ļ	İ]	EHDDIFDKLKEAVKEESIKRHKWNDFAEDSLRVIQHNALEDRSI
i	1	1	SDKQQWDAAIYFMEEALQARLKDTENAIENMVGPD\WKKRWLYW
			KNRTQEQCVHNETKNELEKMLKCNEEHPAYLASDEITTVRKNLE
			SRGVEVDPSLIKDTWHQVYRRHFLKTALNHCNLCRRGFYYYORH
1	ŀ		FVDSELECNDVVLFWRIQRMLAITANTLRQQLTNTEVRRLEKNV
	ļ	•	KEVLEDFAEDGEKKIKLLTGKRVQLAEDLKKVREIOEKLDAFIE
		1	
			ALHQEK
6090	194	1560	PVFVPAPGAVLEQAS/ASPPLATQTVVPLQHCKIPELPVQASIL
		l	FELQLFFCQLIALFVHYINIYKTVWWYPPSHPPSHTSLNFHLID
İ		1	FNLLMVTTIVLGRRFIGSIVKEASQRGKVSLFRSILLFLTRFTV
			LTATGWSLCRSLIHLFRTYSFLNLL/FPLLSVWDVHSVPAAELR
			P\RKTSLFNHMASMGPREAVSGLAKSRDYLLTLR\RRGSSTODS
1			CMARTPCP/PHACCLSPSLIRSEVEFLKMDFNWRMKEVLVSSML
			SAYYVAFVPVWFVKNTHYYDKRWSCELFLLVSISTSVILMOHLL
		{	· - ·
			PASYCDLLHKAAAHLGCWQKVDPALCSNVLQHPWTEECMWPQGV
			LVKHSKNVYKAVGHYNVAIPSDVSHFRFHFFFSKPLRILNILLL
}		!	LEGAVIVYQLYSLMSSEKWHQTISLALILFSNYYAFFKLLRDRL
1		i	VLGKAYSYSASPQRDLDHRFS
6091	3279	412	SSRTREMEEKEILRRQIRLLQGLIDDYKTLHGNAPAPGTPAASG
1			WQPPTYHSGRAFSARYPRPSRRGYSSHHGPSWRKKYSLVNRPPG
1	1		PSDFPADHAVRPLHGARGGQPPVPQQHVLERQVQLSQGQNVVIK
l			VKPPSKSGSASASGAQRGSLEEFEDTPWSDQRPREGEGEPPRGO
1			LQPSRPTRARGTCSVEDPLLVCQKEPGKPRMVKSVGSVGDSPRE
1	1		
	I		PRRTVSESVIAVKASFPSSALPPRTGVALGRKLGSHSVASCAPQ
	1		
			LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQAREASLVVTCR
			LLGDRRVDAGHTDQPVPSGSVGGPARPASGPRQARKASLVVTCR TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTPRIVKKTPASPLSAPPFPLSLPSWRA
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTPYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RFAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSXYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RROALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA RRLSLSRSLVLNRLRPVASGGKAQPGSPWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQREKRKEYCMYYNFFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLPPAGSCSRSLASRAVQ RSLAIIRQARQREKKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAFGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCOLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSSSPPASLDHEAPSLQBAALAAACSNRLCKLPSFISLQS
			TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL
6092	143	3190	TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATKSHLSLE RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTPYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSSPPASLDHEAPSLQEBALAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL AKAPPTGESSEPEAKVLHTKRLYRAVVEAVHRLDLILCNKTAYQ
6092	143	3190	TNKFRKNNYKWVAASSKSPRVARRALSPRVAAENVCKASAGMAN KVEKPQLIADPEPKPRKPATSSKPGSAPSKYKWKASSPSASSS SFRWQSEAGSKDHASQLSPVLSRSPSGD\RPAVGHSGLKPLSGE TPLSAYKVKSRTKIIRRGSTSLPGDKKSGTSPAATAKSHLSLR RRQALRGKSSPVLKKTPNKGLVQVTTHRLCRLPPSRAHLPTKEA SSLHAVRTAPTSKVIKTRYRIVKKTPASPLSAPPFPLSLPSWRA RRLSLSRSLVLNRLRPVASGGKAQPGSPWWRSKGYRCIGGVLY KVSANKLSKTSGQPSDAGSRPLLRTGRLDPAGSCSRSLASRAVQ RSLAIIRQARQRREKRKEYCMYYNRFGRCNRGERCPYIHDPEKV AVCTRFVRGTCKKTDGTCPFSHHVSKEKMPVCSYFLKGICSNSN CPYSHVYVSRKAEVCSDFLKGYCPLGAKCKKHTLLCPDFARRG ACPRGAQCQLLHRTQKRHSRRAATSPAPGPSDATARSRVSASHG PRKPSASQRPTRQTPSSAALTAAAVAAPPHCPGGSASPSSSKAS SSSSSSSSPPASLDHEAPSLQEAALAAACSNRLCKLPSFISLQS SPSPGAQPRVRAPRAPLTKDSGKPLHIKPRL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
į	J	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
{	residue of	1	Codon, /=possible nucleotide deletion,
Ì	amino acid	sequence	\=possible nucleotide insertion)
L	sequence		VIQLIKTNKKHIHSRSTLECAYRTHLVAGIGFYQHLLLYIQSHY
		1	QLELQCCIDWTHVTDPLIGCKKPVSASGKEMDWAQMACHRCLVY
}	}	}	OFRPOCCIOMINATORI I SEDENICO I CITA DO TOMBENOI CAL
(}	1	LGDLSRYQNELAGVDTELLAERFYYQALSVAPQIGMPFNQLGTL
1	}		AGSKYYNVEAMYCYLRCIQSEVSFEGAYGNLKRLYDKAAKMYHQ
ł			LKKCETRKLSPGKKRCKDIKRLLVNFMYLQSLLQPKSSSVDSEL
ļ			TSLCQSVLEDFNLCLFYLPSSPNLSLASEDEEEYESGYAFLPDL
1			LIFQMVIICLMCVHSLERAGSKQYSAAIAFTLALFSHLVNHVNI
Í			RLQAELEEGENPVPAFQSDGTDEPESKEPVEKEEEPDPEPPPVT
			PQVGEGRKSRKFSRLSCLRRRRHPPKVGDDSDLSEGFESDSSHD
1			SARASEGSDSGSDKSLEGGGTAFDAETDSEMNSQESRSDLEDME
1			EEEGTRSPTLEPPRGRSEAPDSLNGPLGPSEASIASNLQAMSTQ
			MFQTKRCFRLAPTFSNLLLQPTTNPHTSASHRPCVNGDVDKPSE
1	Ì	1	PASEEGSESEGSESSGRSCRNERSIQEKLQVLMAEGLLPAVKVF
1			LDWLRTNPDLIIVCAQSSQSLWNRLSVLLNLLPAAGELQESGLA
ł	}	1	LCPEVQDLLEGCELPDLPSSLLLPEDMALRNLPPLRAAHRRFNF
}			DTDRPLLSTLEESVVRICCIRSFGHFIARLQGSILQFNPEVGIF
ł	,		VSIAQSEQESLLQQAQAQFRMAQEEARRNRLMRDMAQLRLQLEV
		1	SQLEGSLQQPKAQSAMSPYLVPDTQALCHHLPVIRQLATSGRFI
}			VIIPRTVIDGLDLLKKEHPGARDGIRYLEAEFKKGNRYIRCQKE
1		1	VGKSFERHKLKRQDADAWTLYKILDSCKQLT\LAQGAGEEDPSG
ì			MYTIITGLPLDNPSLLSGPMQAALQAAAHASVDIKNVLDFYKQW
ł			KEIG
L		<u></u>	ACGRRAMLALRVART/SRWGAL\RGAVWAPGTRPSKRRACWALL
6093	76	1002	ACGRRAMLALKVARTY SRWGAL (RGAVWAPOTRESIGNACIAND)
j	1		PPVPCCLGCLAERWRLRPAALGLRLPGIGQRNHCSGAGKAAPR\
	}		PAAGAGAAAEAPGGQWGPASTPSLYENPWTIPNMLSMTRIGLAP
Ì			VLGYLIIEEDFNIALGVFALAGLTDLLDGFIARNWANQRSALGS
1			ALDPLADKILISILYVSLTYADLIPVPLTYMIISRDVMLIAAVF
}		}	YVRYRTLPTPRTLAKYFNPCYATARLKPTFISKVNTAVQLILVA
j	}		ASLAAPVFNYADSIYLQILWCFTAFTTAASAYSYYHYGRKTVQV
}		}	IKD
6094	23	1010	PFLRCLRGDQKAKMSERKVLNKYYPPDFDPSKIPKLKLPKDRQY
1		1	VVRLMAPFNMRCKTCGEYIYKGKKFNARKETVQNEVYLGLPIFR
1	1	}	FYIKCTRCLAEITFKTDPENTDYTMEHGATRNFQAEKLLEEEEK
1	1	1	RVOKEREDEELNNPMKVLENRTKDSKLEMEVLENLQELKDLNQR
1		}	OAHVDFEAMLROHRLSEEERRROOQEEDEQETAALLEEARKRRL
	1		LEDSDSEDEAAPSPLQPALRPNPTAILDEAPKPKRKVEVWEQSV
	į.		GSLGSRPPLSRLVVVKKAKADPDCSNGQPQA/APHPRSPAEQEG
1		}	GQPYTPDAWRVLPEPTGCIPGQ
6005		1599	TRGRAAERSRGRGHGFLGGGFA\SVVDYFPSEDFYRCGYCKNES
6095	1	1033	GSRSNGMWAHSMTVQDYQDLIDRGWRRSGKYVYKPVMNQTCCPQ
}	1	1	YTIRCRPLQFQPSKSHKKVLKKMLKFLAKGEVPKGSCE\DEPMD
	1	1	STMDDAVAGDFALINKLDIQCDLKTLSDDIKESLESEGKNSKKE
}	1	}	
1			EPQELLQSQDFVGEKLGSGEPSHS

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6100 2 713 FVEVSGYRSRADFEPRGRDTMTYAYLFKYIIIGDTGVGKSCIL QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQES RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTAC VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVG SASQRNSRDIGSNSGCC	}			
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RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSN VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTAC VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVG SASQRNSRDIGSNSGCC	6100	2	713	FVEVSGYRSRADPEPRGRDTMTYAYLFKYIIIGDTGVGKSCLLL
VIMLIGNKSDLESRRDVKREEGEAFARE\HGLIFMETSAKTAC VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVG SASQRNSRDIGSNSGCC	J	1		QFTDKRFQPVHDLTIGVEFGARMVNIDGKQIKLQIWDTAGQESF
VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVG SASQRNSRDIGSNSGCC	1			RSITRSYYRGAAGALLVYDITRRETFNHLTSWLEDARQHSSSNM
SASQRNSRDIGSNSGCC				
\				VEEAFINTAKEIYRKIQQGLFDVHNEANGIKIGPQQSISTSVGP
6101 1 1399 FRGRAWPI.REVSHWT.GCDDVCSWCASWGDT.DAT.CADT.CDT.TAE				
	6101	1	1399	FRGRAWPLREVSHWLGCRRVCSWSASWGRLPALSARLSPLLAFR
	1			GKMVFPLSCAVQQYAWGKMGSNSEVARLLASSDPLAQIAEDKPY
AELWMGTHPRGDAKILDNRISQKTLSQWIAENQDSLGSKVKDT		<u></u>		AELWMGTHPRGDAKILDNRISQKTLSQWIAENQDSLGSKVKDTF

SEQ	Predicted	Predicted end	lamino anid
ID	beginning	nucleotide	Amino acid segment containing signal peptide
			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
J	amino acid	sequence	Coden (
		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			NGNLPFLFKVLSVETPLSIQAHPNKELAEKLHLQAPQHYPDANH
			KPEMAIALTPFQGLCGFRPVEEIVTFLKKVPEFQFLIGDEAATH
1	Į	į.	LKQTMSHDSQAVASSLQSCFSHLMKSEKKVVVEQLNLLVKRISQ
			QAAAGNNMEDIFGELLLQLHQQYPGDIGCFAIYFLNLLTLKPGE
			AMFLEANVPHAYLKGDCVECMACSDNTVRAGLTPKFIDVPTLCE
	1	}	MICYTECCCADE BY DEDCOEDRY CAMPBRIDGE AND A TOP
İ			MLSYTPSSSKDRLFLPTRSQEDPYLSIYDPPVPDFTIMKA\EVP
1	1	j	G\SVTEYKDLALDSASILLMVQGTVIASTPTTQTPIPLQRGGVL
			FIGANESVSLKLTEPKDLLIFRACCLL
6102	70	2415	QTPQATLAANGAEDSRGGEMLPAGEIGASPAAPCCSESGDERKN
1			LEEKSDINVTVLIGSKQVSEGTDNGDLPSYVSAFIEKEVGNDLK
1			SLKKLDKLIEQRTVSKMQLEEQVLTISSEIPKRIRSALKNABES
1	1	}	KQFLNQFLEQETHLFSAINSHLLTAQPWMDDLGTMISQIEEIER
1	1		HLAYLKWISQIEELSDNIQQYLMTNNVPEAASTLVSMAELDIKL
1	1		QESSCTHLLGFMRATVKFWHKILKDKLTSDFEEILAQLHWPFIA
1			DDOCOTUCE CDDA CADELYON DESTROY AND CONTRACT
1	1		PPQSQTVGLSRPASAPEIYSYLETLFCQLLKLQTSHELLTEPK\
ļ	1		HSQKNTLFLPPLLSS/WPIQVMLTPLQKRFRYHFRGNRQTNVLS
ŀ	1		KPEWYLAQVLMWIGNHTEFLDEKIQPILDKVGSLVNARLEFSRG
	1		LMMLVLEKLATDIPCLLYDDNLFCHLVDEVLLFERELHSVHGYP
	ł		GTFASCMHILSEETCFQRWLTVERKFALQKMDSMLSSEAAWVSQ
	i		YKDITDVDEMKVPDCAETFMTLLLVITDRYKNLPTASRKLOFLE
ł	1		LQKDLVDDFRIRLTQVMKEETRASLGFRYCAILNAVNYISTVLA
			DWADNVFFLQLQQAALEVFAENNTLSKLQLGQLASMESSVFDDM
			INLLERLKHDMLTRQVDHVFREVKDAAKLYKKERWLSLPSQSEO
			AVMSLSSSACPLLLTLRDHLLQLEQQLCFSLFKIFWQMLVEKLD
			AVISUSSSACPEDITERDHELQLEQQLCFSEKTFWQMLVEKLD
1			VYIYQEIILANHFNEGGAAQLQFDMTRNLFPLFSHYCKRPENYF
			KHIKEACIVLNLNVGSALTAGKDVLPVQLQGSFPAT
6103	207	2523	ESNSTMTTYLEFIQQNEERDGVRFSWNVWPSSRLEATRMVVPVA
	•		ALFTPLKERPDLPPIQYEPVLCSRTTCRAVLNPLCQVDYRAKLW
	1		ACNFCYQRNQFPPSYAGISELNQPAELLPQFSSIEYVVLRGPQM
İ)		PLIFLYVVDTCMEDEDLQALKESMQMSLSLLPPTALVGLITFGR
j			MVQVHELGCEGISKSYVFRGTKDLSAKQLQEMLGLSKVPVTQAT
	i i		RGPQVQQPPPSNRFLQPVQKIDMNLTDLLGELQRDPWPVPQGKR
}			PLRSSGVALSIAVGLLECTFPNTGARIMMFIGGPATQGPGMVVG
1			DELETTE CHURCH TO TO THE TOTAL
1			DELKTPIRSWHDIDKDNAKYVKKGTKHFEALANRAATTGHVIDI
1			YACALDQTGLLEMKCCPNLTGGYMVMGDSFNTSLFKQTFQRVFT
1			KDMHGQFKMGFGGTLEIKTPR\EIKISGAIGPCVSLNSKGPCVS
1			ENEIGTGGTCQWKICGLSPTTTLAIYFEVVNQHNAPIPQGG\RG
1			A\IQFVTQY\QHSSGQRRIRVTTIARN\WADAQTQIQNIAASFD
1 .]		QEAAAILMARLAIYRAETEEGPDVLRWLDRQLIRLCQKFGEYHK
1			DDPSSFRFSETFSLYPQFMFHLRRSSFLQVFNNSPDESSYYRHH
			FMRQDLTQSLIMIQPILYAYSFSGPPEPVLLDSSSILADRILLM
			DTFFQILIYHGETIAQWRKSGYQDMPEYENFRHLLQAPVDDAQE ILHSRFPMPRYIDTEHGGSQARFLLSKVNFSQTHNNMYAWGQES
1]		
6104	124	730	GAPILTDDVSLQVFMDHLKKLAVSSAA
0.104	124	732	KVSEYIILSKDKILFHALAMLVLVVSPWSAARGVLRNYWERLLR
			KLPQSRPGFPSPPWGPALAVQ\AQPCLQSQQMIPVEVKRI/RSL
1			LDSIFWMAAPKNRRTIEVNRCRRRNPQKLIKVKNNIDVCPECGH
			LKQKHVLCAYCYEKVCKETAEIRRQIGKQEGGPFKAPTIETVVL
			YTGETPSEQDQGKRIIERDRKRPSWFTQN
6105	3	989	PLHGACTSLVLQRFCHRRPRPCAPARPEDMRRPAAVPLLLLLCF
		,,,	CSOBJENTACCED DEMINDMICCODE CONTROL CALACTER CAL
1			GSQRAKAATACGRPRMLNRMVGGQDTQEGEWPWQVSIQRNGSHF
1			CGGSLIAEQWVLTAAHCFRNTSETSLYQVLLGARQLVQPGPHAM
			YARVRQVESNPLYQGTASSADVALVELEAPVPFTNYILPVCLPD
			PSVIFETGMNCWVTGWGSPSEEDLLPEPRILQKLAVPIIDT\PR
			CNLLYSKDTEFGYQPKTIKNDMLCAGFEEGKKDACKGDSAGPLV
			CLVGQSWLQAGVISWGEGCARQNRPGVYIRVTAHHNWIHRIIPK
	<u> </u>		The state of the s

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
1 -	1	i e	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
}	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	l ·		
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 -	\=possible nucleotide insertion)
<u> </u>		-	LQVQPSEVGRPEVTPPGPGAP
L			1
6106	3	1302	GRPPTAPHTGRPPTANRGDPRLDLKRGCARLLTSIESRGRPAAS
ł	1		AGLRRDRCALRRWPLRRAPLARATRRRAGSPRRCAPRPRACPQG
			WSRARHOPGGLCLLLLLLCQFMEDRSAQAGNCWLRQAKNGRCOV
	Ļ		LYKTELSKEECCSTGRLSTSWTEEDVNDNTLFKWMIFNGGAPNC
1	1]	IPCKETCENVDCGPGKKCRMNKKNKPRCVCAPDCSNITWKGPVC
ì			· ·
	,	Ì	GLDGKTYRNECALLKARCKEQPELEVQYQGRCKKTCRDVFCPGS
	1		STCV\VDQTNNAYCVTCNRICPEPASSEQYLCGNDGVTYS\SAC
1	1		HLRKATCLLGRSIGLAYEGKCIKAKSCEDIQCTGGKKCLWDFKV
1			GRGRCSLCDELCPDSKSDEPVCASDNATYASECAMKEAACSSGV
1			
		<u> </u>	LLEVKHSGSCNSISEDTEEEEEDEDQDYSFPISSILEW
6107	623	168	SRCSSPRPBPGRGRGK/LSPSEHRKWVEVFKACDEDHKGYLSRE
			DFKTAVVMLFGYKPSKIEVDSVMSSINPNTSGILLEGFLNIVRK
1			KKEAQRYRNEVRHIFTAFDTYYRGFLTLEDFKKAFRQVAPKLPE
1	1	1	RTVLEVFREV\DRDS\DGHVSF
6108	3	1348	GGSLRFSPPRVPSCSRVFCPVPPGGCGLPSPMSASRPQSPTTPW
1 9108	3	1348	· · · · · · · · · · · · · · · · · · ·
1	1		CLPRRYMKHKRDDGPEKQEDEAVDVTPVMTCVFVVMCCSMLVLL
		1	YYFYDLLVYVVIGIFCLASATGLYSCLAPCVRRLP\SASAGESA
			LLAPTIPNNSLPYFHKRPQARMLLLALFCVAVSVVWGVFRNEDQ
1			WAWVLQDALGIAFCLYMLKTIRLPTFKACTLLLLVLFLYDIFFV
			FITPFLTKSGSSIMVEVATGPSDSATREKLPMVLKVPRLNSSPL
1	1		
]		ALCDRPFSLLGFGDILVPGLLVAYCHRFDIQVQSSRVYFVACTI
			AYGVGLLVTFVALALMQRGQPALLYLVPCTLVTSCAVALWRREL
ļ			GVFWTGSGFAKVLPPSPWAPAPADGPQPPKDSATPLSPQPPSEE
			PATSPWPAEQSPKSRTSEEMGAGAPMREPGSPAESEGRDQAQPS
			PVTQPGASA
6109	1	1381	CRSRAGAASGGAILEGTKLRRQRVDTNKPLDPLVPSALRAAMLY
6103	1	1381	1
			LEDYLEMIEQLPMDLRDRFTEMREMDLQVQNAMDQLEQRVSEFF
	ł.		MNAKKNKPEWREEQMASIKKDYYKALEDADEKVQLANQIYDLVD
}			RHLRKLDQELAKFKMELEADNAGITEILERRSLELDTPSQPVNN
			HHAHSHTPVEKRKYNPTSHHTTTDHIPEKKFKSEALLSTLTSDA
ľ	l		SKENTLGCRNNNSTASSNNAYNVNSSQPLGSYNIGSLSSGTGAG
į			
1		1	GI\TMAAAQAVQATAQMKEGRRTSSLKASYEAFKNNDFQLGKEF
1			SMARETVGYSSSSALMTTLTQNASSSAADSRSGRKSKNNNKSSS
1			QQSSSSSSSSSSSSSSSSTVVQEISQQTTVVPESDSNSQVDWT
			YDPNEPRYCICNQVSYGEMVGCDTQDCPIEWFHYGCVGLTEAPK
			GKWYCPQCT\AAMKRRGSRHK
6110	77	2464	ACPSAATMSDODHSMDEMTAVVKIEKGVGGNNGGNGNGGGAFSQ
9110	1 "	2707	1 -
1	}		ARSSSTGSSSSTGGGGGESQPSPLALLAATCSRIESPNENSNNS
			QGPSQSGGTGELDLTATQLSQGANGWQIISSSSGATPTSKEQSG
1			SSTNGSNGSESSKNRTVSGGQYVVAAAPNLQNQQVLTGLPGVMP
}			NIQYQVIPQFQTVDGQQLQFAATGAQVQQDGSGQIQIIPGANQQ
ł			IITNRGSGGNIIAAMPNLLQQAVPLQGLANNVLSGQTQYVTNVP
			VALNGNITLLPVNSVSAATLTPSSOAVTISSSGSOESGSOPVTS
}			GTTISSASLVSSQASSSSFFTNANSYSTTTTTSNMGIMNFTTSG
1			SSGTNSQGQTPQRVSGLQGSDALNIQQNQTSGGSLQAGQQKBGE
1			Q\NQQTQAAPKSLSRPQLVQGG\QALQ\AFQAAPLSGQTFTTQA
1			ISOETLONLOLOAVPNSGPIIIRTPTVGPNGQVSWOTLOLONLO
			VQNPQAQTITLAPMQGVSLGQTSSSNTTLTPIASAASIPAGTVT
1			
1	1	1	VNAAQLSSMPGLQTINLSALGTSGIQVHPIQGLPLAIANAPGDH
1	1		GAQLGLHGAGGDGIHDDTAGGEEGENSPDAQPQAGRRTREACT
			CPYCKDSEGRGSGDPGKKKQHICHIQGCGKVYGKTSHLRAHLRW
J)		HTGERPFMCTWSYCGKRFTRSDELQRHKRTHTGEKKFACPECPK
1	1		RFMRSDHLSKHIKTHONKKGGPGVALSVGTLPLDSGAGSEGSGT
1	1		_
1	1		ATPSALITTNMVAMEAICPEGIARLANSGINVKEGGQFCSPINT
1			SANGF
			<u> </u>

Deginning nuclectide location locati	SEO	Predicted	Predicted end	Thring agid gorment containing girms worlds
No. nucleotide corresponding to first maino acid residue of maino acid residue of maino acid sequence				Amino acid segment containing signal peptide
Cortisponding to first amino acid residue of amino acid residue of amino acid residue of amino acid amino acid sequence Sectine, T-MITHCOMINE, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, P-PTOINE, Q-GIULamine, R-Arginine, R-Arginine, R-Arginine, R-Arginine, R-Bright, R-Brig				
to first amino acid residue of amino acid residue of amino acid sequence sequence 6111 1637 737 879EVPCOPANA, V=TyPcoPana, Y=UTyPcoPana, Y	10.	1		
to first amino acid residue of amino acid amino acid sequence sequ	1			
amino acid residue of amino acid sequence with property and sequence with property acid sequence sequence with property acid sequence sequence with property acid sequence sequence with property acid sequence sequence with property acid sequence sequence with property acid sequences and sequence sequences sequences acid sequence sequences sequ	Į			
residue of amino acid sequence	l		i e	
amino acid sequence Codon, /-possible nucleotide insertion 6111 1637 797 RVDERVEGAMAPEGERLAGROVLIDISOUTYDSGAGGGTAIAC SVERVAPALKSRIAVERCTNESSYSRRALVOOLOGICAPDISOS VARAPARACOLIKEEGIRPYLLHINGVVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPARACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VANDALASVASITEROIDTS/STDE VANDALASVASITEROIDTS/STDE VANDALASVASITEROIDTS/STDE VANDALASVASITEROIDTS/STDE VANDALASVASITEROIDTS/STDE VATAPACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VATAPACOLIKEEGIRPYLLHINGVASEFDOIDTS/STDE VARAFORDA VANDALASVASITEROIDTS/STDE VARAFORDA VARAF		l .		
Sequence				
6111 1637 797 RVDRYRGAMAPRGRILAGRGVLYDISGAGGGTALAG SVERVANLKSRICHVECTNESGYRRELYOOLGHPISSOE VTARAPARACOLLKERGIREYLLIHUGU'ASSFDQIDTS/STPNC VVIADAGES FSTQNMNNAPQVLRELEKPVLISLGKGKYYKESS LIMLDVOPYMGALEYACGI RAEVGGRSSDEPFKSLAGAIGVERHO AVMIGDDIVGDVGSAGRCGMRALQVRTGKFRFSDEHIPEKVRAD VVINLABAVDLLIGHAK 6112 77 196 MSSHKSPFSKRFLAKKGKDNRFILOMIWLKTGNKIRIMK 6113 1779 567 MEGRSNAACOVILOGAMGERSGVYASSEASSFGKRADVSWSSQL ETWUDHLAMTEINSGRIAAVESCFGASGGPIALPGRVLLISGSVI TKSCKRKAKPRIPFLFFDILIVUSG IVLNKRKYKSADAVSWSSQL ETWUDHLAMTEINSGRIAAVESCFGASGGPIALPGRVLLISGSVI TKSCKRKAKPRIPFLFDILIVUSG IVLNKRKYKSADAVSWSSQL ETWUDHLAMTEINSGRIAAVESCFGASGGPIALPGRVLLISGSVI TKSCKRKAKPRIPFLFDILIVUSGIVISLAVATIONGCTGYSALITERH HCKKCKVVCAECSROSFILDRLS FKPVRVCSLCYRELAAQORK REAREGGAGVURASHLARPI CGRVENTHIONETSALITERH HCKKCKVVCAECSROSFILDRLS FKPVRVCSLCYRELAAQORK REAREGGAGVURASHLARPI CGRVENTHIONETSALATERH HCKKCRVVCAECSROSFILDRLS FKPVRVCSLCYRELAAQORK REAREGGAGVURASHLARPI CGRVENTHIONETSALATERH HCKKCRVVCAECSROSFILDRLS FKPVRVCSLCYRELAAQORK REAREGGAGVURASHLARPI CGRVENTHIONETSALATERH HCKKCRVVCAECSROSFILDRLS FKPVRVCSLCYRELAAQORK REAREGGAGVURASHLARPI CARRACTIC FY TARAHATIC PAMISTER THE PAMISTER T	1		sequence	
SVEAVABLIKKSRLKVYRCTINEGOKSRABLIOGLOGICALGPIDISS (VTAPAPAPACOLLKERGIR PYLLIHDUGV\ASSEDQITDTS/STPNC VVADAGESSISYOMMANAFQVIMELEKPVLISINGKSYYKETSG LMLDVSPYMRALEYACGI RAEVGGRSDEPFY KSALQAIGVERISGOUNGDIVOGVOGGAGGGGMAGVAVIORDIVERSKEPSKEBIPEVKADG AVMIGDDIVOGVOGGAGGGGGMAGVAVIORTKERRSDEBIPEVKADG AVMIGDDIVOGVOGGAGGGGGMAGVAVIORTKERRSDEBIPEVKADG AVMIGDDIVOGVOGGAGGGGSSOVASSEASSIGKERADUSWASSA 6112 77 196 MSSHKSFRSKEFLAKKKNINFILOMIKLKTONKIRHINK 6113 1779 567 MEGRSKARGOVILOGANGGESSOVASSEASSIGKERADUSWASSA EENSKERSPKSFELAKKONTOGIAVAGGESSOVASSEASSIGKERADUSWASSA LEEUPSTLQAKURMINITAKKSFYOKASSAATERGEVILGEVL TKECRKKAKRRIFFI.FPDTLUVGS IVLINKKYRSOHI IPLEEV LELLPSTLQAKURMINITAKKSFYOKASASTERGEVILGEVL TKECRKKAKRRIFFI.FPDTLUVGS IVLINKKYRSOHI IPLEEV RGLARATGRA STEHAAPHI IPUKATDI ONGCOTTRESALTERH HCRKCRVVVCAECSROFILIPRIS PKPVRVCSLCYETERAAGTATG PAMSSTTROWFGLISTADPREBEILS PSOLHCHOEDGSSSER EELEEGOAGV PRAASHAAPI IPUKATDI ONGCOTTRESALTERH HCRKCRVVVCAECSROFILIPRIS PKPVRVCSLCYETERAAGTATG PAMSSTTROWFGLISTADPREBEILS PSOLHCHOEDGSSSER FGURD FIRMOVORGVASUASIEDPY PCVTLCPY GETTAGRAFFER KROCS PROSILAAGEMCSOS PKNCTTVERACMFSPPP PV PABOVO GHLPPHADRRALFLEVAAPRAGEOFPHCHAGGAFTAGAGGSTAGATAGA FERNASSTAGATUR TO THE TOP TO	(111		707	
VTAPAPARACQILKERGIRPYLLIHIDAVASERDOIDTS/STENC VVIDAGESISTONINNAPQUIMELREVULISIGGRYYYETSG LIMIDVOPPWIKALEVACGIKAEVGGKSPUPYKSHIJQAIGVEHIQ AVMIGDDIVGOVGGQGCOMRALQVTTGKPPPSEHIPPXKAIQAIGVEHIQ VVDNLAEAVDLLLQHADK VVDNLAEAVDLLLQHADK VVDNLAEAVDLLLQHADK VVDNLAEAVDLLLQHADK VVDNLAEAVDLLLQHADK VVDNLAEAVDLLLQHADK VVDNLAEAVDLLLQHADK VVDNLAEAVDLLLQHADK VVDNLAEAVDLLLQHADK VVDNLAEAVDLLLQHADK VVDNLAEAVDLLAATEV VVDNLAEAVDLLAATEV VVDNLAEAVDLLAATEV VVDNLAEAVDLLAATEV VVDNLAEAVDLLAATEV VVDNLAEAVDLAAAAVDLAAA	9111	163/	797	
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AARPQTLNRPGQELFRQLRYHESSGPLETLSRLRELCRWW LRPDVLSKAQILELLULDGFLSILPGELRWWQLHNPESGES\L WPCWRSCRGTLMGHPGGTRALP\EPGRCALDGYRS\LRSAQIWSL ASPLRSSSALGHLLEPYPELEARDFLAGGSDTPAAQMPALFPRE GCPGDQVTPTRSLTAQLQETMTFKDVEVTFSQDEWGWLDSAQRN LYRDVMLENYRNMASLGK GLISLFPPAAMHPAAFPLPVVVAAVLWGAAPTRGLIRATSDHNA SMDFADLPALPGATLSQEGLQGFLVEAHPDNACSPIAPPPPAPV NGSVFIALLRRPDCNFDLKVLNAQKAGYGAAVVHNVNSNELLNM VWNSEBIQQQIWIPSVFIGERSSEYLRALFVYEKGARVLLVPDN TFPLGYYLIPFTGIVGLVLLAMGAVMIARCIGHRKRLQRNRLTK \EQLKQI\PTHDYQKGDQYDVCAICLDBYEDGDKLRVLPCAHAY HSRCVDFWLTDTRKTCFICKQPVERGPGDEDGEETQGEEGDB GEPRDHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL SPPSSPVILV 6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGEKGREEKVKREVDCKIKQEKQEKQERKKKK KEKEKETQKEKIGEKGREEKVKREVDCKIKQEKQEKGERKKK KEKEKETQKEKIGGKGFEKVKREVDCKIKQEKQEKGERKKK NKQILVIGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPPRSYWMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II 6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRWTSAPPQRFFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLPGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ			1100	<u> </u>
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LEQLKQI\PTHDYQKGDQYDVCAICLDBYEDGDKLRVIPCAHAY HSRCVDPWLTQTRKTCPICKQPVHRGPGDEDQEEETQGQEEGDB GEPRDHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL SPPSSPVILV				
HSRCVDPWLTQTRKTCPICKQPVHRGPGDEDQEEETQGQEEGDB GEPRDHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL SPPSSPVILV 6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQEKQERKGK EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPPRSYWEMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II 6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ				1.
GEPRDHPASERTPLLGSSPTLPTSFGSLAPAPLVFPGPSTDPPL SPPSSPVILV 6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQEKQERKGK EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II 6119 1217 462 DPRFVTENTTKAPAQBRTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIAFFTPDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ				1
SPPSSPVILV 6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGEKGKEEKVKRKEVEQKI KQEKQERGKGK EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLEIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II 6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALFTLLLNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIAFFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ	1			1
6118 1044 247 STISCRACTSGATPGAQSHRSARGHAAGGKETAALGMERGKVKK KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQERQKK EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II 6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ				
KEKEKETQKEKIGEKGREEKVKRKEVEQKIKQEKQERRKGK EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II 6119 1217 462 DPRFVTENTTKAPAQBRTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRFFRVCDHKRTIRKGLTAATR QELLAKALRTLLLNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ	6110	1044	242	
EKEEKRTKQGKETNKEKEQFKGQEEKGENKDSTLTRTPLEPLEK NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II DPRFVTENTTKAPAQBRTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALRTLLLNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ	9118	1044	44/	·-
NKQILVLGLDGAGKTSVLHSLASNRVQHSVAPTQGFHAVCINTE DSQMEFLEIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II 6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ]			
DSQMEFLBIGGSKPFRSYWEMYLSN/ADSLARSFSVGFKQDSQP ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II 6119 1217 462 DPRFVTENTTKAPAQBRTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIAFFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ				1 · · · · · · · · · · · · · · · · · · ·
ITWKAKKYLHQLIAANPVLPLVVFANKQDLEAAYHITDIHEALA II 6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIAFFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ		}		
II 6119 1217 462 DPRFVTENTTKAPAQERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ				·
6119 1217 462 DPRFVTENTTKAPAGERTTQPRSSREGTLRSTMEYLSALNPSDL LRSVSNISSEFGRRVWTSAPPPQRPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ				
LRSVSNISSEFGRRVWTSAPPPORPFRVCDHKRTIRKGLTAATR QELLAKALETLLLNGVLTLVLEEDGTAVDSEDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ	2330	1010		
QELLAKALETLLLNGVLTLVLEEDGTAVDSBDFFQLLEDDTCLM VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ	9113	1217	462	·- ·
VLQSGQSWSPTRSGVLSYGLGRERPKHSKDIARFTFDVYKQNPR DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ				·-
DLFGSLNVKATFYGLYSMSCDFQGL\GPKKVLRELLRWTSTLLQ		1		
GLGHMLLGISSTLRHAVEGAEQWQQKGRLHSY				
— — — — — — — — — — — — — — — — — — —		<u> </u>	<u> </u>	GLGHMLLGISSTLRHAVEGAEQWQQKGRLHSY

	1 S	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	1	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first		S=Serine, T=Threonine, V=Valine,
1	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	residue of	amino acid	Codon, /=possible nucleotide deletion,
1	amino acid	sequence	\=possible nucleotide insertion)
	sequence	179	LERAGGGGLSSRALVGSGACLSLVARANGKGLPRGRKEFVEAVR
6120	785	1/9	
1			VRYVAPRYRTPRAVCLRLWSCRREVIMSGRGKQGGKVRAKAKSR
			SSRAGLQFPVGRVHRLLRKGNYAERVGAGAPVYLAAVLEYLTAE
İ			ILELAGNAARDNKKTRIIPRHLQLAIRNDEELNKLLGKVTIAQG
		ļ	G\VLPNIQAVLLPKKTESQKDEGANDP
6121	1612	107	FVRAQARGSROPVRRPLLGAGSRLRCRSCGRMEPLKVEKFATAN
			RGNGLRAVTPLRPGELLFRSDPLAYTVCKGSRGVVCDRCLLGKE
			KLMRCSQCRVAKYCSAKCQKKAWPDHKRECKCLKSCKPRYPPDS
	j		VRLLGRVVFKLMDGAPSESEKLYSFYDLESNINKLTEDKKEGLR
i			QLVMTFQHFMREEIQDASQLPPAFDLFEAFAKVICNSFTICNAE
			MQEVGVGLYPSISLLNHSCDPNCSIVFNGPHLLLRAVRDIEVGE
			ELTICYLDMLMTSEERRKQLRDQYCFECD\CFRCQTQDKDADML
ļ			TGDEQVWKEVQESLKKIEELKAHWKWEQVLAMCQAIISSNSERL
		}	PDINIYQLKVLDCAMDACINLGLLEEALFYGTRTMBPYRIFFPG
			SHPVRGVQVMKVGKLQLHQGMFPQAMKNLRLAFDIMRVTHGREH
İ		†	SLIEDLILLE/AMRRQHQSILRERSQREIRRVSLLNALLRSHT
			LCFVSCVNLSYWKFCSVFV
6122	2	2324	RFRKMADGGAASQDESSAAAAAAADSRMNPSETSKPSMESGDG
1		İ	NTGTQTNGLDFQKQPVPVGGAISTAQAQAFLGHLHQVQLAGTSL
			QAAAQSLNVQSKSNEESGDSQQPSQPSQQPSVQAAIPQTQLMLA GGOITGLTLTPAOOOLLLOOAQAQAQLLAAAVQQHSAAQQHSAA
			GATISASAATPMTQIPLSQPIQIAQDLQQLQQLQQQNLNLQQFV
j			LVHPTTNLQPA\QFIISQTPQGQQGLLQA\QNLLTQLPRQSQAN
ŀ			LLQSQPRI\TLTSQPATPTCTIAATPIQTLPQSQSTPKRIDTPS
1			LERP\SDLEELEQFAKTFKQRRIKLGFT\QGDAGLAMVKLYGND
ļ			FSPTTIFRFEALNLSFKNMCKLKPLLEKWLNDAENLSSDSSLSS
			PSALNSPGIEGLSRRRKKRTSIEA\NIRVALEKSFLEN\QKPTS
			EEITMIADQLNMEKGVIRVWFCNRRQKEKRINPPSSGG\TSSSP
	1		IKAIFPSPTSLVATTPSLVTSSAATTLTVSPVLPLTSAAVTNLS VTGTSDTTSNNTATVISTAPPASSAVTSPSLSPSPSASASTSEA
1			SSASETSTTQTTSTPLSSPLGTSQVMVTASGLQTA/AQLLPFKG
	i		AAQLPANASLAAMAAAAGLNPSLMAPSQFAAGGALLSLNPGTLS
			1 =
			GALSPALMSNSTLATIQALASGGSLPITSLDATGNLVFANAGGA PNIVTAPLFLNPONLSLLTSNPVSLVSAAAASAGNSAPVASLHA
			TSTSAESIQNSLFTVASASGAASTTTTASKAQ
6123		2944	HLLHRWFGTDMOMINFTTGEFQLTEACPYLGTHSEESRFGILHL
6123	3	2344	HLOPLEMKRVGVVFTPADYGKVTSLILIRNNLTVIDMIGVEGFG
	1		ARELLKVGGRLPGAGGSLRFKVPESTLMDCRRQLKDSKQILSIT
			KNFKVENIGPLPITVSSLKINGYNCQGYGFEVLDCHQFSLDPNT
1	1		SRDISIVFTPDFTSSWVIRDLSLVTAADLEFRFTLNVTLPHHLL
1	1		PLCADVVPGPSWEESFWRLTVFFVSLSLLGVILIAFQQAQYILM
ļ			EFMKTRQRQNASSSSQQNNGPMDVISPHSYKSNCKNFLDTYGPS
			DKGRGKNCLPVNTPQSRIQNAAKRSPATYGHSQKKHKCSVYYSK
	1		HKTSTAAASSTSTTTEEKOTSPLGSSLPAAKEDICTDAMRENWI
			SLRYASGINVNLOKNLTLPKNLLNKEENTLKNTIVFSNPSSECS
1			MKEGIQTCMFPKETDIKTSENTAEFKERELCPLKTSKKLPENHL
			PRNSPQYHQPDLPEISRKNNGNNQQVPVKNEVDHCENLKKVDTK
			PSSEKKIHKTSREDMFSEKQDIPFVEQEDPYRKKKLQEKREGNL
			ONLNWSKSRTCRKNKKRGVAPVSRPPEQSDLKLVCSDFERSELS
ì			
1			SDINVRSWCIQESTREVCKADAEIASSLPAAQREAEGYYQKPEK
			KCVDKFCSDSSSDCGSSSGSVRASRGSWGSWSSTSSSDGDKKPM
1			VDAQHFLPAGDSVSQNDFPSEAPISLNLSHNICNPMTGNSLPQY
1	1		AEPSCPSLPAGPTGVEEDKGLYSPGDLWPTPPVCVTSSLNCTLE
			NGVPCVIQESAPVHNSFIDWSATCEGQFSSAYCPLELNDYNAFP
			EENMYANGFPCPADVQTDFIDHNSQSTWNTPP\NMPAS\WGNA
L	<u>L</u>	<u> </u>	QFPSSSRPYLKSTPKACLPMSGLFGPI\WAP\QSDVYENCCPIN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P-Proline O-Clutomine P America
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
ł	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ŀ			W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence		\=possible nucleotide insertion)
			PTTEHSD/THMENQA\VVCKEYYPGF\NPFRAYMNLDIWTTT\A
			NRNANFPLSRDSSYCGNV
6124	1573	236	SDEALRLAGERGMGRVQLFEISLSHGRVVYSPGEPLAGTVRVRL
			GAPLPFRAIRVTCIGSCGVSNKANDTAWVVEEGYFNSSLSLADK
		j	GSLPAGEHSFPFQFLLPATAPTSFEGPFGKIVHQVRAAIHTPRF
ł			SKDHKCSLVFYILSPLNLNSIPDIEQPNVASATKKFSYKLVKTG
			SVVLTASTDLRGYVVGQALQLHADVENQSGKDTSPVVASLLQKV
		j	SYKAKRWIHDVRTIAEVEGAGVKAWRRAQWHEQILVPALPQSAL
1			PGCSLIHIDYYLQVSLKAPEATVTLPVFIGNIAV/NPCPSEPPA
			RPGAASWGPTPGG\PSAPPQEEAEARAAAGGPHFLDPVFLSTKS
			HSQRQPLLATLSSVPGAPEPCPQDGSPASHPLHPPLCISTGATV
	İ	'	PYFAEGSGGPVPTTSTLILPPEYSSWGYPYEAPPSYEQSCGGVE
			PSLTPES
6125	1	904	L
	1		KTCPKLTCAFTVSVPDSCCRVCRGDGELSWEHSDGDIFRQPANR
J	1	j	EARHSYHRSHYDPPPSRQAGGLSRFFGARSHRGALMDSQQASGT
			IVQIVINNKHKHGQVCVSNGKTYSHGESWHPNLRAFGIVECVLC
			TCNVTKQECKKIHCPNRYPCKYPQKIDGKCCKVCPG/KKAKEBL
1			PGQSFDNKGYFCGEETMPVYESVFMEDGETTRKIALETERPPQV
			EVHVWTIRKGILQHFHIEKISKRMFEELPHFKLVTRTTLSQWKI
5.05			FTEGEAQISQMCSSRVCRTELEDLVKVLYLERSEKGHC
6126	1224	389	RLLSEAPCPRSRRRFQMNPEWGQAFVHVAVAGGLCAVAVFTGIF
			DSVSVQVGYEHYAEAPVAGLPAFLAMPFNSLVNMAYTLLGLSWL
ļ			HRGGAMGLGPRYLKDVFAAMALLYGPVQWLRLWTQWRRAAVLDQ
1			WLTLPIFAWPVAWCLYLDRGWRP\WLFLSLECVSLASYGLALLH
1	İ		PQGFEVALGAHVVPAVGQALRT\HRHYG/SATPSATYLALGVLS
			CLGFVVLKLCDHQLARWRLFQCLTGHFWSKVCDVLQFHFAFLFL
l			THFNTHPRFHPSGGKTR
6127	1335	463	VLPRRCLVFVVNTMDSSREPTLGRLDAAGFWQVWQRFDADEKGY
		1	IEEKELDAFFLHMLMKLGTDDTVMKANLHKVKQQFMTTQDASKD
			GRIRMKELAGMFLSEDENFLLLFRRENPLDSSVEFMQIWRKYDA
l			DSSGFISAAELRNFLRDLFLHHKKAISEAKLEEYTGTMMKIFDR
ŀ			NKDGRLDLNDLARILALQENFLLQFKMDACSTEKRKGDFEKIFA
			YYDVSKTGALEGP\EVDGFVKDMMELVQPSISGVDLDKFREILL
			RHCDVNKDGKIQKSELALCLGLKINP
6128	2511	843	TCRMSRRQLERWVWSSQQVQARGRNVRAPRLGKIAMGLEMSSKD
	1	0.15	
			SPGSLDGRAWEDAQKPQSAWCGGRKTRVYATSSRRAPPSEGTRR
			GGAARPEKTAEEGPPAAPGSLRHSGPLGPHACPTALPEPQVTSA
			MSSQVVGIEPLYIKAEPASPDSPKGSSETETEPPVALAPG\PAP
	i		TRCLPGHKEEEDGEGAGPGEQGGGKLVLSSLPKRLCLVCGDVAS
1			GYHYGVASCEACKAFFKRTIQGSIEYSCPASNECEITKRRRKAC
l	l i		QACRFTKCLRVGMLKEGVRLDRVRGGRQKYKRRPEVDPLPFPGP
			FPAGPLAVAGGPRKTAAPVNALVSHLLVVEPEKLYAMPDPAGPD
			GHLPAVATLCDLFDREIVVTISWAKSIPGFSSLSLSDQMSVLQS
	Į į		VWMEVLVLGVAQRSLTLQDELAFAEYLVLDEEGARPAGLGELG\
1		ľ	AALLQLVRRLQALRLEREEYVLLKALALANSDSVHIEDEPRLWS
			SCEKLLHEALLEYEAGRAGPGGGAERRRAGRLLLTLPLLRQTAG
			KVLAHFYGVKLEGKVPMHKLFLEMLEAMMD
6129	1764	771	ARFARSAHEGKMPKKKTGARKKAENRREREKQLRASRSTIDLAK
			HPCNASMECDKCQRRQKNRAFCYFCNSVQKLPICAQCGKTKCMM
			KSSDCVIKHAGVYSTGLAMVGAICDFCEAWVCHGRKCLSTHACA
]		CPLTDAEC\VECERGVWDHGGRIFSCSFCHNFLCEDDQFEHQAS
1			CQVLEAETFKCVSCNRLGQHSCLRCKACFCDDHTRSKVFKQEKG
1			KQPPCPKCGHETQETKDLSMSTRSLKFGRQTGGEEGDGASGYDA
			VWWI.CCDVVCDTCVUDEEDDEVEX EDDEEDDECKS CO
ļ			YWKNLSSDKYGDTSYHDEEEDEYEAEDDEEEEDEGRKDSDTESS
6130	3	577	DLFTNLNLGRTYASGYAHYEBQEN
U-230	L	577	GRGGTMREYKVVVLGSG\GVGKSALTV\QFVTCTF1EKYDPT1E

SEQ Predicted predicted end nucleotide (A=Alanine, C=Cysteine, D=Aspartic Ac Glutamic Acid, F=Phenylalanine, G=Gly location corresponding to first amino acid residue of amino acid sequence Predicted end nucleotide (A=Alanine, C=Cysteine, D=Aspartic Ac Glutamic Acid, F=Phenylalanine, G=Gly H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, Codon, /=possible nucleotide deletion \ possible nucleotide insertion) DFYRKEIEV\DSSPSVAGISWTQQGTEQF\ASMRDLY	id, E= cine, , *=Stop , IKKGOGC
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence sequence location corresponding to first amino acid residue of amino acid sequence sequence location corresponding to first amino acid residue of amino acid sequence location corresponding to first amino acid w=Tryptophan, Y=Tyrosine, X=Unknown, Codon, /=possible nucleotide deletion loffyrkEIEV\DSSPSVAGISWTQQGTEQF\ASMRDLY	cine, , *=Stop ,
location corresponding to first to first amino acid residue of amino acid sequence corresponding to first amino acid residue of amino acid sequence corresponding to first to first amino acid residue of amino acid sequence corresponding to first to first amino acid residue of amino acid sequence corresponding to first to first to first amino acid residue of amino acid sequence corresponding to first to fir	, *=Stop , IKKGOGC
corresponding to first to first amino acid residue of amino acid residue of amino acid sequence corresponding to first L=Leucine, M=Methionine, N=Asparagine P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threconine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, Codon, /=possible nucleotide deletion _=possible nucleotide insertion) DFYRKEIEV\DSSPSVAGISWTQQGTEQF\ASMRDLY	*=Stop ,
to first amino acid P=Proline, Q=Glutamine, R=Arginine, amino acid residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unknown, amino acid sequence Codon, /=possible nucleotide deletion \ DFYRKEIEV\DSSPSVAGISWTQQGTEQF\ASMRDLY	*=Stop '
to first amino acid P=Proline, Q=Glutamine, R=Arginine, amino acid residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unknown, amino acid sequence Codon, /=possible nucleotide deletion \=possible nucleotide insertion) DFYRKEIEV\DSSPSVAGISWTQQGTEQF\ASMRDLY	*=Stop '
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, Codon, /=possible nucleotide deletion \ =possible nucleotide insertion) DFYRKEIEV\DSSPSVAGISWTQQGTEQF\ASMRDLY	, IKKGOGC
residue of amino acid w=Tryptophan, Y=Tyrosine, X=Unknown, Codon, /=possible nucleotide deletion	, IKKGOGC
amino acid sequence Codon, /=possible nucleotide deletion	, IKKGOGC
sequence \=possible nucleotide insertion) DFYRKEIEV\DSSPSVAGISWTQQGTEQF\ASMRDLY	IKKGOGC
DFYRKEIEV\DSSPSVAGISWTQQGTEQF\ASMRDLY	IKKGQGC
DFYRKBIEV\DSSPSVAGISWTQQGTEQF\ASMRDLY	IKKGQĞC VCN\ SVD
	ACM / GADA
ILVYSLVNQQSFQ\DIKPMRDQIIRVKVSEKVPVI\L	- Jay 13 VD
LESEREVSSSEGRALAEEWGCPFMETSAKSKIMVDEL	FAEIVRO
MNYAAQPDKDDPCCSACNIQ	-
6131 3 1811 SSPREKTSDSSHRPSRHGFLFLRLVGLSPFSYLCVPP	SRPVPGS
PRSLSAMRLLPLAPGRLRRGSPRHLFSCSPALLLLVL	CCCI CVE
GVAAGTRRPNVVLLLTDDQDEVLGGMTPLKKTKALIG	GGCDGAL
CAMURAL CORPORATION TO THE CORPORATION OF THE CORPO	EMGMTFS
SAYVPSALCCPSRASILTGKYPHNHHVVNNTLEGNCS	
QEPNTFPAILRSMCGYQTFF\AGKYLNEYGAPDAGGL	EHVPLGW
SYWYALEKNSKYYNYTLSINGKARKHGENYSVDYLTD	
DFLDYKSNFEPFFMMTATP\APHSPWTAAPQYQKAFQ	NVFAPRN
KNFNIHGTNKHWLIRQAKTPMTNSSIQFLDNAFRKRW	QTLLSVD I
DLVEKLVKRLEFTGELNNTYIFYTSDNGYHTGQFSLP	IDKROLY
EFDIKVPLLVRGPGIKPNQTSKMLVANIDLGPTILDI.	AGYDINIK
TQMDGMSLLPILRGASNLTWRSDVLVEYQGEGRNVTD	
PGVSQCFPDCVCEDAYNNTYACVRTMSALWNLQYCEF	LICESTS
EVYNLTADPDQITNIAKTIDPBLLGKMNYRLMMLQSC	SGPTCRT
PGVFDPGYRFDPRLMFSNRGSVRTRRFSKHLL	
6132 96 1241 AAGLLPPGLVPEDPRRTRNLLPFGIQGPPFALSRPLF:	
AWEAMEPEFLYDLLQLPKGVEPPAEEELSKGGKKKYL	PPTSRKD
PKFEELQKPA\VLMEWINATLLPEHIVVRSLEEDMFD0	GLILHHL
FQRLAALKLEAEDIALTATSQKHKLTVVLEAVNRS\C:	SWRSGRP
SGA/WESIFNKDLLSTLHLLVALAKRFQPDLSLPTNV	WEVITT
ESTKSGLKSEKLVEQLTEYSTDKDEPPKDVFDELFKL	DEMINI
VKEAIVNFVNQKLDRIGLSVQNLDTQFADGVILLLIG	
LHLKEFYLTPNSPAEMLHNVTLALELL/IGRGPAQLPO	C/LALK/
TIVNKDAKSTLRVLYGLFCKHTQKAHRDRTPHGAPN	
6133 2 4256 FVHGSMADTDLFMECEBEELEPWQKISDVIEDSVVED	
TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGA	NSDSTK
KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTM	TOPVLR
PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQI	IAMNOVG
IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQI	MENDE
STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTI	
TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVS	
VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSN	MICONEY
GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQI	KVTEAL
RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEK	
/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMI	
GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNF	
LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPY	
KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSS	LYSEVD
VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHOKF	/HYVN/
CNKCRVQFLFAKDKI EHKLQHHKTFRKPKQLEGLKPGI	KVTTPA
SRGQPRTVPVSSNDTPPSALQEAPLTSSMDPLPVFLY	DDMODE
IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCS	
CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACT	
SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTR	
NVKNMYPPPSFPTNKAATVKSAGATPARPEELLTPLAF	
STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSF	
LASGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAE	HFRNPO
RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTO	
VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLT	
VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAID	ETCLET
DIEUL SCHIBERMAL OTHER AND	PETSUFF
DTEVLSSDDRKENALQTVGTGBPWCDVVLAILADGTVL	
RGQMDQPANMPDSILLEAKESGYSDDEIMRLWSTRVWQ	
RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCS	SKIQPL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
INO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	to first amino acid		S=Serine, T=Threonine, V=Valine,
		residue of	
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sedneuce		\=possible nucleotide insertion)
			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
j l			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
'		, 	LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
			FYGFEEADLDLMEI
6134	2	4256	FVHGSMADTDLFMECEEEELEPWQKISDVIEDSVVEDYNSVDKT
\			TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
[KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
			PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
1			STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
			TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
1			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
1			GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
			RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
			/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
			GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
1			LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
İ			KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
			VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
			CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
l			SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
			IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
			CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
į.			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
1			NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
			STATPPPTPTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
]			LASGGGGSGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
i	Í		RRIRRWLRRFQASQGENLEGKYLSFEAEEKLAEWVLTQREQQLP
	j		VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
			DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
	·		RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
			RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
i			LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
			FYGFEEADLDLMEI
6135	2	4256	FVHGSMADTDLFMECEEEBLEPWQKISDVIEDSVVEDYNSVDKT
			TTVSVSQQPVSAPVPIAAHASVAGHLSTSTTVSSSGAQNSDSTK
			KTLVTLIANNNAGNPLVQQGGQPLILTQNPAPGLGTMVTQPVLR
	1		PVQVMQNANHVTSSPVASQPIFITTQGFPVRNVRPVQNAMNQVG
			IVLNVQQGQTVRPITLVPAPGTQFVKPTVGVPQVFSQMTPVRPG
i			STMPVRPTTNTFTTVIPATLTIRSTVPQSQSQQTKSTPSTSTTP
			TATQPTSLGQLAVQSPGQSNQTTNPKLAPSFPSPPAVSIASFVT
			VKRPGVTGENSNEVAKLVNTLNTIPSLGQSPGPVVVSNNSSAH\
1	i	[GSQRTSGPESSMKVTSSIPVFDLQDGGRKICPRCNAQFRVTEAL
1	1		RGHMCYCCPEMVEYQKKGKSLDSEPSVPSAAKPPSPEKTAPVAS
	1	1	/THPSSTPIPALSPPY/TKVPEPNENVGDAVQTKLIMLVDDFYY
	1		GRDGGKVAQLTNFPKVATSFRCPHCTKRLKNNIRFMNHMKHHVE
]		LDQQNGEVDGHTICQHCYRQFSTPFQLQCHLENVHSPYESTTKC
1	ľ		KICEWAFESEPLFLQHMKDTHKPGEMPYVCQVCQYRSSLYSEVD
!			VHFRMIHEDTRHLLCPYCLKVFKNGNAFQQHYMRHQKR\NVYH\
	1.	1	CNKCRVQFLFAKDKIEHKLQHHKTFRKPKQLEGLKPGTKVTIRA
1			SRGQPRTVPVSSNDTPPSALQEAAPLTSSMDPLPVFLYPPVQRS
			IQKRAVRKMSVMGRQTCLECSFEIPDFPNHFPTYVHCSLCRYST
1	1		CCSRAYANHMINNHVPRKSPKYLALFKNSVSGIKLACTSCTFVT
	L		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:		1	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
Î	corresponding	to first	
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ĺ	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			SVGDAMAKHLVFNPSHRSSSILPRGLTWIAHSRHGQTRDRVHDR
1	1		NVKNMYPPPSFPTNKAATVKSAGATPAEPEELLTPLAPALPSPA
			STATPPPTTTHPQALALPPLATEGAECLNVDDQDEGSPVTQEPE
	į.		LASGGGGGGGVGKKEQLSVKKLRVVLFALCCNTEQAAEHFRNPQ
1	i		RRIRRWLRRFQASQGENLEGKYLSFEABEKLAEWVLTQREQQLP
			VNEETLFQKATKIGRSLEGGFKISYEWAVRFMLRHHLTPHARRA
ļ			VAHTLPKDVAENAGLFIDFVQRQIHNQDLPLSMIVAIDEISLFL
			DTEVLSSDDRKENALQTVGTGEPWCDVVLAILADGTVLPTLVFY
ļ			RGQMDQPANMPDSILLEAKESGYSDDEIMELWSTRVWQKHTACQ
-			RSKGMLVMDCHRTHLSEEVLAMLSASSTLPAVVPAGCSSKIQPL
			DVCIKRTVKNFLHKKWKEQAREMADTACDSDVLLQLVLVWLGEV
			LGVIGDCPELVQRSFLVASVLPGPDGNINSPTRNADMQEELIAS
1			LEEQLKLSGEHSESSTPRPRSSPEETIEPESLHQLFEGESETES
i			FYGFEEADLDLMEI
		 	
6136	1704	539	PGVRMALEGMSKRKRKRSVQEGENPDDGVRGSPPEDYRLGQVAS
ł			SLFRGEHHSRGGTGRLASLFSSLEPQIQPVYVPVPK\ESALASA
İ		1	DLEEEIHQKQGQKRKNSQPGVKVADRKILDDTEDTVVSQRKKIQ
}			INQEEERLKNERTVFVGNLPVTCNKKKLKSFFKEYGQIESVRFR
			SLIPAEGTLSKKLAAIKRKIHPDQKNINAYVVFKEESAATQALK
1			RNGAQIADGFRIRVDLASETSSRDKRSVFVGNLPYKVEESAIEK
{			HFLDCGSIMAVRIVRDKMTGIGKGFGYVLFENTDSVHLALKLNN
			SELMGRKLRVMRSVNKEKFKQQNSNPRLKNVSKPKQGLNFTSKT
			AEGHPKSLFIGEKAVLLKTKKKGQKKSGRPKKQRKQK
6137	141	2656	RALRKRRCGPGRRGALGSGPGPGRRPGRVPEERPAPPRERKHPG
1			MWNMLIVAMCLA/LLGLPGKAQELQGHVS/IILAGEQLGDLAKK
			YLWQG\LFQLYLDEAGRGHSFSFHGAALTAPKQGQELMAKALES
			LSCPKDMAPSHCAEHKDQFLQLSQYRQLKTAEDYQALNKDIEAQ
•			LQHAGLREAGGIFYFSVPPFAYEDIARNINSSCRPGPGAWLRVV
		1	LEKPFGHDHFSAQQLATELGTFFQBEEMYRVDHYLGKQAVAQIL
		1	PFRDONRKALDGLWNRHHVERVEIIMKETVDAEGRTSFYEEYGV
		1	IRDVLQNHLTEVLTLVAMELPHNVSSAEAVLRHKLQVFQALRGL
			QRGSAVVGQYQSYSEQVRRELQKPDSFHSLTPTFAGVLVHIDNL
1			RWEGVPFILMSGKALDERVGYARILFKNQACCVQSEKHWAAAQS
			QCLPRQLVFHIGHGDLGSPAVLVSRNLFRPSLPSSWKEMEGPPG
ļ	i		LRLFGSPLSDYYAYSPVRERDAHSVLLSHIFHGRKNFFITTENL
			LASWNFWTPLLESLAHKAPRLYPGGAENGRLLDFEFSSGRLFFS
			QQQPEQLVPGPGPGPMPSDFQVLRAKYRESSLVSAWSEELISKL
1		1	ANDIEATAVRAVRRFGQFHLALSGGSSPVALFQQLATAHYGFPW
			ANDIEATAVRAVRAFGGFREADSGGSSFVADFQQEATANIGFFR AHTHLWLVDERCVPLSDPBSNFQGLQAHLLQHVRIPYYNIH\AM
		1	PVHLQQRLCAEEDQGAHIYAREISALGANSSFDLVLLGMGADGH
1			TASLFPOSPTGLDGEOLVVLTTSPSOPHRRMSLSLPLINRAKKV
1			
1			AVLVMGRMKREITTLVSRVGHEPKKWPISGVLPHSGQLVWYMDY
			DAFLG
6138	4587	934	EFSKLTDRWQNAVQGVRQRKGDVDGLVRQWQDFTTSVENLFRFL
1		1	TDTSHLLSAVKGQERFSLYQTRSLIHELKNKEIHFQRRRTTCAL
1			TLEAGEKLLLTTDLKTKESVGRRISQLQDSWKDMEPQLAEMIKQ
			FQSTVETWDQCEKKIKELKSRLQVLKAQSEDPLPELHEDLHNEK
1			ELIKELEQSLASWTQNLKELQTMKADLTRHVLVEDVMVLKEQIE
			HLHRQWEDLCLRVAIRKQEIBDRLNTWVVFNEKNKELCAWLVQM
			ENKVLQTADISIEEMIEKLQKDCMEEINLFSENKLQLKQMGDQL
			IKASNKSRAAEIDDKLNKINDRWQHLFDVIGSRVKKLKETFAFI
			QQLDKNMSNLRTWLARIESELSKPVVYDVCDDQEIQKRLAEQQD
		1	LORDIEQHSAGVESVFNICDVLLHDSDACANETECDSIQQTTRS
			LDRRWRNICAMSMERRMKIEETWRLWQKFLDDYSRFEDWLKSAB
1	1	1	
i .	1	· I	RTAACPNSSEVINTSAKEELKRFEAFOROIHERLTOLELINKOY
			RTAACPNSSEVLYTSAKEELKRFEAFQRQIHERLTQLELINKQY RRLARENRTDTASRLKQMVHEGNQRWDNLQRRVTAVLRRLRHFT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	- 3	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	location		
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence		\=possible nucleotide insertion)
		T	NOREEFEGTRESILVWLTEMDLQLTNVEHFSESDADDKMRQLNG
			FOOEITLNTNKIDQLIVFGEQLIQKSEP\LDAVLIEDELEELHR
Į			YCOEVFGRVSRFHRRLTSCTPGLEDEKEASENETDMEDPREIQT
	1	1	DSWRKRGESEEPSSPQSLCHLVAPGHERSGCETPVSVDS\IPLE
1			WDHTGRRGGPSSSH\EEDERAOYY\SALSGKSISDGHSWHVPDS
l	1	[PSCPEHHYKOMEGDRNVPPVPPASSTPYKPPYGKLLLPPGTDGG
1			KEGPRVLNGNPOOEDGGLAGITEOOSGAFDRWEMIQAQEL\HNK
i			
į			LKIKQNLQQLNSDISAITTWLKKTEAELEMLKMAKPPSDIQEIE
			LRVKRLQEILKAFDTYKALVVSVNVSSKEFLQTESPESTELQSR
		i	LRQLSLLWEAAQGAVDSWRGGLRQSLMQCQDFHQLSQNLLLWLA
ł			SAKNRRQKAHVTDPKADPRALLECRRELMQLEKELVERQPQVDM
			LQEISNSLLIKGHGEDCIEAEEKVHVI\EKKLKQLREQVSQDLM
'		1	ALQGTQNPASPLPSFDEVDSGDQPPATSVPAPRAKQFRAVRTTE
			GEEETESRVPGSTRPQRSFLSRVVRAALPLQLLLLLLLLLACLL
l			PSSEEDYSCTQANNF\ARSFYPMLRYTNGPPPT
6139	52	1131	LGDWVWSRTCGVLETPTSVLRRARARGPCPTDSKWALPRLREGE
			TERRPWEASSWKTL/LAGWIGGAASVIVGHPLDTVKTRLQAGVG
1			YGNTLSCIRVVYRRESMFGFFKGMSFPLASIAVYNSVVFGVFSN
Į.			TORFLSOHRCGEPRASPPRTLSDLLLASMVAGVVSVGLGGPVDL
l			IKIRLOMOTPPVSGROPRFEVQGSGSCG\EPAYQGPVHCITTIV
1			RNEGLAGLYRGASAMLLRDVPGYCLYFIPYVFLSEWITPEACTG
ļ			PSPCAVWLAGGMAGAISWGTATPMDVVKSRLQADGVYLNKYKGV
1			LDCISQSYQKEGLKVFFRGITVNAVRGFPMSAAMFLGYELSLQA
			IRGDHAVTSP
		126-	RPELELWRLRSRSWRPLGVPRRCHRRNWKEPVRAQPLSVTVWAP
6140	694	136	
1			RCQRP/QPPAPEPSSPNAAVPEAIPTPRAAASAALELPLGPAPV
	1		SVAPQAEAEARSTPGPAGSRLGPETFRQRFRQFRYQDAAGPREA
	l .	1	FRQLREL/SPRQWLRPDI\RTKEQ\IVEMLVQEQLLAILPEAAR
			ARRIRRRTDVRITG
6141	2	984	AQVGPRSRPCKMPLKLRGKKKAKSKETAGLVEGEPTGAGGGSLS
	1	}	ASRAPARRLVFHAQLAHGSATGRVEGFSSIQELYAQIAGAFEIS
	1		PSEILYCTLNTPKIDMERLLGGQLGLEDFIFAHVKGIEKEVNVY
			KSEDSLGLTITDNGVGYAFIKRIKDGGVIDSVKTICVGDHIESI
	1		NGENIVGWRHYDVAKKLKELKKEELFTMKLIEPKKAFEIELRSK
1	!		AGKSSGEKIGCGRATLRLRSKGPATVEEMPSETKAK\AIEKIDD
1			VLELYMGIRDIDLATTMFEAGKDKVNPDEFAVALDETLGDFAFP
	Ţ	}	DEFVFDVWGVIGDAKRRGL
6142	116	602	EAEGEQVCGAKCCGDAPHVENREEETARIGPGVMESKEERALNN
			LIVENVNOENDEKDEKEQVANKGEPLALPLNVSEYCVPRGNRRR
			FRVRQPILQYRWDIMHRLGEPQARMREENMERIGEEVRQLMEKL
			REKOLSHSLRAVSTDPPHHDHHDEFC\LMP
6143	2002	270	
6143	2802	270	FRMRIFLHCPWNQQMWKIWNLLETSLESCKAHLSIQKLLKER\Q \OLPVFKHRDSIVETLKRHRVVVVAGET\GSGKSTQVPHFLLED
			1
			LLLNEWEASKCNIVCTQPRRISAVSLANRVCDBLGCENGPGGRN
1			SLCGYQIRMESRACESTRLLYCTTGVLLRKLQEDGLLSNVS/HM
1			FIVDEV\HER\SVQSDFLLIILKEILQKRSDLHLILMSATVDSE
1			KFSTYFTHCPILRISGRSYPVEVFHLEDIIEETGFVLEKDSEYC
			QKFLEEEEEVTINVTSKAGGIKKYQEYIPVQTGAHADLNPFYQK
	,		YSSRTQHAILYMNPHKINLDLILELLAYLDKSPQFRNIEGAVLI
			FLPGLAHIQQLYDLLSNDRRFYSERYKVIALHSILSTQDQAAAF
1			TLPPPGVRKIVLATNIAETGITIPDVVFVIDTGRTKENKYHESS
			QMSSLVETFVSKASALQRQGRAGRVRDGFCFRMYTRERFEGFMD
			YSVPEILRVPLEELCLHIMKCNLGSPEDFLSKALDPPQLQVISN
1			AMNLLRKIGACELNEPKLTPLGQHLAALPVNVKIGKMLIFGAIF
			GCLDPVATLAAVMTEKSPFTTPIGRKDEADLAKSALAMADSDHL
			TIYNAYLGWKKAROEGGYRSEITYCRRNFLNRTSLLTLEDVKQE
1	1	ŀ	TITTED THE BOOTHEST LOUGH THE TOTAL AND AND

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
			Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid		
1		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
Į.			LIKLVKAAGFSSSTTSTSWEGNRASQTLSFQEIALLKAVLVAGL
1	l.		YDNVGKIIYTKSVDVTEKLACIVETAQGKAQVHPSSVNRDLQTH
	ŀ		GWLLYQEKIRYARVYLRETTLITPFPVLLFGGDIEVQHRERLLS
Į.	1		IDGWIYFQAPVKIAVIFKQLRVLIDSVLRKKLENPKMSLENDKI
	I		LQIITELIKTENN
	1000		<u> </u>
6144	1289	568	SGPGSMSGQRVDVKVVMLGKEYVGKTSLVERYVHDRFLVGPYQN
į	1	1	VSASGGARHGGRGSGGPVICTYGPDLFPLVA\TIGAAFVAKVMS
			VGDRTVTLGIWDTAGSERYEAMSRIYYRGAKAAIVCYDLTDSSS
1			FERAKFWVKELRSLEEGCQIYLCGTKSDLLEEDRRRRRVDFHDV
	•	İ	QDYADNIKAQLFETSSKTGQSVDELFQKVAEDYVSVAAFQVMTE
1		1	
63.45	1100	100	DKGVDLGQKPNPYFYSCCHH
6145	1109	196	GGMDLSELERDNTGRCRLSSPVPAVCRKEPCVLGVDEAGRGPVL
			GPMVYAICYCPLPRLADLEALKVADSKTLLESERERLFAKMEDT
			DFVGWALDVLSPNLISTSMLGRVKYNLNSLSHDTATGLIQYALD
		1	QGVNVTQVFVDTVGMPETYQARLQQSFPGIEVTVKAKADALYPV
	ļ		\VSAASICAKVARDQAVKKWQFVEKLQDLDTDYG\SGYPNDPOD
	1		/TKAWLKEHVEPVF\GFP\QFVRF\SWRTAQTI\LEKEAEDVIR
ſ			EDSASENQEGLRKITSYFLNEGSQARPRSSHRYFLERGLESTTS
		<u></u>	L
6146	428	781	LKKKGKEKAEAQQVEALPGPSLDQWHRSAGEEEDGPVLTDEQKS
		İ	R/YPGHEAHDQGG\WDARQSIIRKVVDPETGRTRLIKGDGEVLE
			BIVTKERHREINKQATRGDCLAFQMRAGLLP
6147	1	2304	GTRQLPPPSPGSGPGDSPEGPEGEAPERRRKAHGMLKLYYGLSE
1	_	1	
			GEAAGRPAGPDPLDPTDLNGAHFDPEVYLDKLRRECPLAQLMDS
			ETDMVRQIRALDSDMQTLVYENYNKFISATDTIRKMKNDFRKME
			DEMDRLATNMAVITDFSARISATLQDRHERITKLAGVHALLRKL
J	J.	,	QFLFELPSRLTKCVELGAYGQAVRYQGRAQAVLQQYQHLPSFRA
			IQDDCQVITARLAQQLRQRFREGGSGAPEQAECVELLLALGEPA
1			EELCEEFLAHARGRLEKELRNLEAELGPSPPAPDVLEFTDHG\S
			SGFVGGLCQVAAAYQELFAAQGPAGAEKLAAFARQLGSRYFALV
ł			ERRLAGEOGGGDNSLLVRALDRFHRRLRAPGALLAAAGLADAAT
l	1		
			EIVERVARERLGHHLQGLRAAFLGCLTDVRQALAAPRVAGKEGP
1			GLAELLANVASSILSHIKASLAAVHLFTAKEVSFSNKPYFRGEF
I		†	CSQGVREGLIVGFVHSMCQTAQSFCDSPGEKGGATPPALLLLLS
1			RLCLDYETATISYILTLTDEQFLVQDQFPVTPVSTLCAEARETA
l			RRLLTHYVKVQGLVISQMLRKSVETRDWLSTLEPRNVRAVMKRV
]			VEDTTAIDVQVLPRLAGVALTQAGGTVPSRGAGAAEDHWQSLPG
1	}		GGDMCIWASHGASSVARASVREPQGNKSPRMNTKRAGECLCPRS
1			CSFSAQDYDIFAPILPVEKQRLRVTQEVRAGLVLVLKIRPQTNS
İ			CILPLPHSTGSINSDHVPTK
6148	3056	353	
0148	3036	333	VPAVGGTFADGAMGEAEKFHYIYSCDLDINVQLKIGSLEGKREQ
1			KSYKAVLEDPMLKFSGLYQETCSDLYVTCQVFAEGKPLALPVRT
1			SYKAFSTRWNWNEWLKLPVKYPDLPRNAQVALTIWDVYGPGKAV
			PVGGTTVSLFGKYGMFRQGMHDLKVWPNCRSQMDQKPTKTPGRT
1	i		SSTLSEDQMSRLAKLTKAHRQGHMVKVDWLDRLTFREIEMINES
			VKRSSNFMYLMGGFRCVKCDDKEYGIVYYEKDGDESSPILTSFE
ŀ			LVKVPDPQMSLENLVESKHHNLPRSLRSGPSDHDLKPYPSPRDQ
i	1		
1			LKNIVSYPPSKPPTYEEQDLVWEFRYYLTNQDKALTKILTSVIW
l			DLPQGAKQALALLGKWKPMDVEDSLELLSSHYTNPTVRRYAVAR
1			LRQADDEDLLMYLLQLVQALKYENFDDIKNGLEPTKKDSQSSVS
ł	1		ENVSNSGINSAEIDSSQIIT/SAPFPSVSSPPP\ASKTKEVPDG
I			ENLEQDLCTFLISRASKNSTLANYLYWYVIVECEDQDTQQRDPK
			THEMYLNVMRRFSQALLKGDKSVRVMRSLLAAQOTFVDRLVHLM
1			
			KAVQRESGNRKKKNERLQALLGDNEKMNLSDVELIPLPLEPQVK
1			IRGIIPETATLFKSALMPAQLFFKTEDGGKYPVIFKHGDDLRQD
L	<u></u>		QLILQIISLMDKLLRKENLDLKLTPYKVLATSTKHGFMQFIQSV

CEO.	T 6	Thursday 1	
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide location	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
1	location	corresponding	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine,
İ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			PVAEVLDTEGSIQNFFRKYAPSENGPNGISAEVMDTYVKSCAGY
			CVITYILGVGDRHLDNLLLTKTGKLFHIDFGYILGRDPKPLPPP
		İ	MKLNKEMVEGMGGTQSEQYQEFRKQCYTAFLHLRRYSNLILNLF
1			SLMVDANIPDIALEPDKTVKKVQDKFRLDLSDEEAVHYMQSLID
6140			ESVHALFAAVVEQIHKFAQYWRK
6149	1	1413	RVDPRVRENGTANPIKNGKTSPASKDQRTGKKTSVQGQVQKGND
1		}	ESESDFESDPPSPKSSEEEEQDDEEVLQGEQGDFNDDDTEPENL
			GHRPLLMDSEDEEEEEKHSSDSDYEQAKAKYSDMSSVYRDRSGS
1			GPTQDLNTILLTSAQLSSDVAVETPKQEFDVFGAVPFFAVRAQQ PQQEKNEKNLPQHRFPAAGLEQEEFDVFTKAPFSKKVNVQECHA
ł			VGPEAHTIPGYPKSVDVFGSTPFQPFLTSTSKSESNEDLFGLVP
ŀ			FDEITGSQQQKVKQRSLQKLSSRQRRTKQDMSKSNGKRHHGTPT
İ			STKKTLKPTYRTPERARRHKKVGRRDSQSSNEFLTISDSKENIS
1			VALTDGKDRGNVLQPEESLLDPFGAKPFHSPD\LSWHPP\HQGL
			S\DIRADHNT\VLPGR\PRQNSLHGSFHSADVLKMDDFGAVP/F
			LTELVVQSITPHQSQQSQPV\ELDPFGAAPFPSKQ
6150	372	37	MSNIKKYIIDYDWKASIEIEIDHDVMTEEKLHQINNFWSDSEYR
		ĺ	LNKHGSVLNAVLIMLAQHALLIAISSDLNAYGVVCEFDWNDGNG
			QEGWPPMDGSEGIRITDIDTSGIF
6151	1555	521	DSNQQSVSGTAASTLLHSFKATIYYQGTGHVQQFYGVTSPYSQT
			TPPIVQSYAQPSLQYIQGQQIFTAHPQGVVVQPAAAVTTIVAPG
1 :			QPQPLQPSEMVVTNNLLDLPPPSPPKPKTIVLPPNWKTARDPEG
1			KIYYYHVITRQTQWDPPTWESPGDDASLEHEAEMDLGTPTYDEN
1			PMK\ASKKPKTAEADTSSELAKKSKEVFRKEMSQFIVQCLNPYR KPDCKVG\RITTTEDFKHLARKLTHGVMNKELKYCKNPE\DLEC
			NENVKHKTKEYIKKYMQKFGAVYKPKEDTEFRVTVGPGWEDGWS
			GKTDSRERKSCGPFCSTPVSTVLLMIHHPGEFNPADVN
6152	1366	648	NRTWSTPSTWMGVALPPLCSTGPWPVTRQITARTTCGAVPAKCP
			PWC/DVHEPRCQPPDCHGHGTCVDGHCQCTGHFWRGPGCDELDC
			GPSNCSQHGLCTETGCRCDAGWTGSNCSEECPLGWHGPGCQRPC
			KCEHHCPCDPKTGNCSVSRVKQCLQPPEATLRAGELSFFTRTAW
			LALTLALAFLLLISTAANLSLLLSRAERNRRLHGDYAYHPLQEM
			NGEPLAAEKEQPGGAHNPFKD
6153	2	3368	GRVGARSPGRAYALLLLICFNVGSGLHLQVLSTRNENKLLPKH
			PHLVRQKRAWITAPVALLEGEDLSKKNPIAKIHSDLAEERGLKI
			TYKYTGKGITEPPFGIFVFNKDTGELNVTSILDREETPFFLLTG
			YALDARGNNVEKPLELRIKVLDINDNEPVFTQDVFVGSVEELSA
			AHTLVMKINATDADEPNTLNSKISYRIVSLEPAYPPVFYLNKDT GEIYTTSVTLDREEHSSYTLTVEARDGNGEVTDKPVKQAQVQIR
			ILDVNDNIPVVENKVLEGMVEENQVNVEVTRIKVFDADEIGSDN
			WLANFTFASGNEGGYFHIETDAQTNEGIVTLIKEVDYEEMKNLD
			FSVIVANKAAFHKSIRSKYKPTPIPIKVKVKNVKEGIHFKSSVI
			SIYVSESMDRSSKGQIIGNFQAFDEDTGLPAHARYVKLEDRDNW
			ISVDSVTSEIKLAKLPDFESRYVQNGTYTVKIVAISEDYPRKTI
			TGTVLINVEDINDNCPTLIEPVQTICHDAEYVNVTAEDLDGHPN
			SGPFSFSVIDKPPGMAEKWKIARQESTSVLLQQSEKKLGRSEIQ
]			FLISDNQGFSCPEKQVLTLTVCEVLHGS\GCREAQHDSYVGLGP
			AAIALMILAFLLLLLVPLLLLMCHCGKGAKGFTPIPGTIEMLHP
			WNNEGAPPEDKVVPSFLPVDQGGSLVGRNGVGGMAKEATMKGSS
			SASIVKGQHEMSEMDGRWEEHRSLLSGRATQFTGATGAI\MTTE
			TTITARATGASRDVAGAQAAAVALNEEFLKNYFTDKAASYTEED
	1		ENHTAKDCLLVYSQEETESLNASIGCCSFIEGELDDRFLDDLGL
			KFKTLABVCLGQKIDINKEIEQRQKPATETSMNTASHSLCEQTM
			VNSENTYSSGSSFPVPKSLQEANAEKVTQEIVTERSVSSRQAQK
			VATPLPDPMASRNVIATETSYVTGSTMPPTTVILGPSQPQSLIV TERVYAPASTLVTODYAMEGTTAVTEDVIODEGGCND EGTOV
			TERVYAPASTLVDQPYANEGTVVVTERVIQPHGGGSNPLEGTQH

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			LQDVPYVMVRERESFLAPSSGVQPTLAMPNIAVGQNVTVTERVL
i			APASTLQSSYQIPTENSMTARNTTVSGAGVPGPLPDFGLEESGH
Ì			SNSTITTSSTRVTKHSTVQHSYS
6154	3660	2146	KKKTKMKNTLQKTVNFGAWPKPTISDKSHLLQMVSKLDLTDAKN
025.			SDTAHIKSIEITSILNGLQASESSAEDSEQEDERGAQDMDNNGK
			EESKIDHLTNNRNDLISKEEQNSSSLLEENKVHADLVISKPVSK
			SPERLRKDIEVLSEDTDYEEDEVTKKRKDVKKDTTDKSSKPQIK
i			RGKRRYCNTEECLKTGSPGKKEEKAKNKESLCMENSSNSSSDED
ł	1	Í	EEETKAKMTPTKKYNGLEEKRKSLRTTGFYSGFSEVAEKRIKLL
			1
			NNSDERLQNSRAKDRKDVWSSIQGQWPKKTLKELFSDSDTEAAA
			SPPHPAPEEGVAEESLQTVAEEESCSPSVELEKPPPVNVDSKPI
1			EEKTVEVNDRKAEFPSSGSNFSA*IPLPYLHLNRLHQSL*QKGS
		1	RQQSSVTVSEPLAPNQEEVRSIKSETDSTIEVDSVAGELQDLQS
			ERE*LASRF*CQCELEQ**SARTRTS*KSLYRSEKSERCSGRRK
			FIKKAEKKP*SNSGKQQKEGK
6155	869	121	HLLPELRGKSWITMKYVFYLGVLAGTFFFADSSVQKEDPAPYLV
	1		YLKSHFNPCVGVLIKPSWVLAPAHCYLPNLKVMLGNFKSRVRDG
ļ			TEQTINPIQIVRYWNYSHSAPQDDLMLIKLAKPAMLNPKVQALN
i		1	P\PTTNVRPGTVCLLSGLDWSQENSGRHPDLRQNLEAPVMSDRE
	Ì	Ì	CQKTEQGKSHRNSLCVKFVKVFSRIFGEVAVATVICKDKLQGIE
1			VGHFMGGDVGIYTNVYKYVSWIENTAKDK
6156	5725	3984	GTSTVTMATKKHFSIILNLLGMLLKKDNQDTRKLLMTWALEVAV
0230			VMKKSETYAPLFCLPSFHKFCKGLLADTLVEDVNICLQACSSLH
ł			ALSSSLPDDLLQRCVDVCRVQLVHRGTCIRQAFGKLLKSIPLGV
ŀ		· ·	FLSNNNHTEIQEISLALRSHMSKAPSNTFHPQDFSD/VISFILY
Í			GNSHRTGKDNWLERLFYSCQRLDKRDQSTIPRNLLKTDAVLWQW
	1		AIWEAAQFTVLSKLRTPLGRAQDTFQTIEGIIRSLAGHTLNPDQ
			DVSOWTTADNDEGHGNNQLRLVLLLQYLENLEKLMYNAYEGCAN
	1		ALTSPPKVIRTFLYTNRQTCQDWLTRIRLSIMRVGLLAGQPAVT
ļ			VRHGFDLLTEMKTTSLSQGNELEVSIMMVVEALCELHCPEAIQG
1	ŀ		IAVWSSSIVGKHLLWINSVAQQAEGRFEKASVEYQEHLCAMTGV
			DCCISSFDKSVLTLASAGCKSASLKHCLNGESRKSVLSKPTDSS
1			
			PEVINYLGNKACECYISTADWAAVQEWQNAIHDLKKSTSSTSLN
1			LKADFNYIKSLSSFESGKFVECTEQLELLPGENINLLAGGSKEK
			IDMKKLLRNM
6157	946	329	MANRGPSYGLSREVQEKIEQKYDADLENKLVDWIILQCAEDIEH
			PPPGRAHFQKWLMDGTVLCKLINSLYPPGQEPIPKISESKMAFK
			QMEQISQFLKAAETYGVRTTDIFQTVDLWEGKDMAAVQRTLMAL
			GSVAVTKDDGCYRGEPSWFHRKAQQNRRGFSEEQLRQGQNVIGL
1			QMGSNKGASQAGMTGYGMPRQIM*DAASCP
6158	441	1482	LGSLIVLSLHCKVIFSSQSLERAMKEKAVDLVPILAQNPGLAQN
			PILEGKDHNQNTGVDPIIDHVQDRKTD/SRSKSPHKKRSKSRER
İ		ì	RKSRSRSHSRDKRKDTREKIKEKERVKEKDREKEREREKEREKE
			KERGKNKDRDKBREKDREKDKEKDREREREKEHEKDRDKEKEKE
		1	ODKEKEREKDRSKEIDEKRKKDKKSRTPPRSYNASRRSRSSSRE
			RRRRRSRSSSRSPRTSKTIKRKSSRSPSPRSRNKKDKKREKERD
			HISERRERESTSMRKSSNDRDGKEKLEKNSTSLKEKEHNKEPD
1			SSVSKEVDDKDAPRTEENKIQHNGNCQLNEENLSTKTEAV
6350		84	AVIAPLHISLGDRARPYLKNTEKSSTTCSRRRNQSFPPVMSLTH
6159	53	54	
		1	RLHLCKYWGCAVSNVCRFWEGRPLPLMIVVPYTLPVSLPVGSCV
1		1	IITGTPILTFVKDPQLEVNFYTGMDEDSDIAFQFRLHFGHPAIM
1		1	NSCVFGIWRYEEKCYYLPFEDGKPFELCIYVRHKEYKVMVNGQR
1			IYNFAHRFPPASVKMLQVFRDISLTRVLISD*GRCVRITAVQEF
1			DVSVSCDCTTAYQPG
6160	1626	1790	AGAKPFP*F*KVADAQPTESEKEIYNQVNVVLKDAEGILEDLQS
			YRGAGHEIREAIQHPADEKLQEKAWGAVVPLVGKLKKFYEFSQR
			<u> </u>

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
]	sequence		\=possible nucleotide insertion)
	<u> </u>		LEAALRGLLGALTSTPYSPTQHLEREQALAKQFAEILHFTLRFD
			ELKMTNPAIONDFSYYRRTLSRMRINNVPAEGENEVNNELANRM
l			SLFYAEATPMLKTLSDATTKFVSENKNLPIENTTDCLSTMASVC
1	,	}	RVMLETPEYRSRFTNEETVSFCLRVMVGVIILYDHVHPVGAFAK
			TSKIDMKGCIKVLKDQPPNSVEGLLNALRYTTKHLNDETTSKOI
Į.			KSMLQ*QLLTLVNKG
6161	455	1569	PVSGSESSLRRAWASILRLMLGPRVAVSILCEDGISH*LLEKH*
0202	120		KSHVLEPLSSLALERQCLALSLDWSTGKTGRAGDQPLKIISSDS
			TGQLHLLMVNETRPRLQKVASWQAHQFEAWIAAFNYWHPEIVYS
			GGDDGLLRGWDTRVPGKFLFTSKRHTMGVCSIQSSPHREHILAT
		1	GSYDEHILLWDTRNMKQPLADTPVQGGVWRIKWHPFHHHLLLAA
1		l	CMHSGFKILNCQKAMEERQEATVLTSHTLPDSLVYGADWSWLLF
		1	RSLQRAPSWSFPSNLGTKTADLKGASELPTPCHECREDNDGEGH
			ARPQSGMKPLTEGMRKNGTWLQATAATTRDCGVNPEEADSAFSL
1	1	1	LATCSFYDHALHLWEWEGN
6162	1	586	RTIHATGRAGAS PMHRLIVWRLAEANKOHVRCOKCLEFGHWTYE
	_		CTGKRKYLHRPSRTAELKKALKEKENRLLLQQSIGETNVERKAK
		1	KKRSKSVTSSSSSSDSSASDSSSESEETSTSSSSEDSDTDESS
			SSSSSASSTTSSSSSDSDSDSSSSSKQ*HOHR*OL*R*TTKEE
		j	EKEIELLHSYWTDGLKTLM
6163	1081	785	RIRSTTEGCAVRLHPTONTGKARIMILLSVSLGRHWAFTYKFFL
0200	2002	,	TPVVFVFFFFFFHRKE*VMQKNPMKSREDEWMEKLNNLHVORAD
		ł	MNRLIMNYLVTEGFKEAAEKFRMESGIEPSVDLETLDERIKIRE
İ			MILKGQIQEAIALINSLHPELLDTNRYLYFHLQQQHLIELIRQR
			ETRAALEFAQTQLAEQGEESRECLTEMERTLALLAFDSPEESPF
			GDLLHTMQRQKVWSEVNQAVLDYENRESTPKLAKLLKLLLWAQN
ļ			ELDQKKVKYPKMTDLSKGVIEEPK
6164	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
			SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGONGFOOWYDALKA
i			VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
l		1	NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
			WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
1			YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
1	1	1	GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
1		1	RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
]	LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
}		1	KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE
!			PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
1		1	ALKRQYSRIKKKQQQQVHQVYIRADKGPVTSILPSQVNSSPVIN
]	1	1	HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
1			PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
İ		1	EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
1			VQAKLGALELNQRDAAAETELRVHPPCQRHCPEPPSAPEENKAT
	1	Ì	SKAPQGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
			HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
1		1	GGERFG
6165	90	406	PCQSPGRSRMRQDKLTGSLRRGGRCLKRQGGGVGTILSNVLKKR
]			SCISRTAPRLLCTLEPGVDTKLKFTLEPSLGQNGFQQWYDALKA
		!	VARLSTGIPKEWRRKVWLTLADHYLHSIAIDWDKTMRFTFNERS
İ		1	NPDDDSMGIQIVKDLHRTGCSSYCGQEAEQDRVVLKRVLLAYAR
1			WNKTVGYCQGFNILAALILEVMEGNEGDALKIMIYLIDKVLPES
	1	1	YFVNNLRALSVDMAVFRDLLRMKLPELSQHLDTLQRTANKESGG
		1	GYEPPLTNVFTMQWFLTLFATCLPNQTVLKIWDSVFFEGSEIIL
		1	RVSLAIWAKLGEQIECCETADEFYSTMGRLTQEMLENDLLQSHE
		1	LMQTVYSMAPFPFPQLAELREKYTYNITPFPATVKPTSVSGRHS
		1	KARDSDEENDPDDEDAVVNAVGCLGPFSGFLAPELQKYQKQIKE
	-l		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
~ .		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
1	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
:	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
į į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
t I	sequence	_	\=possible nucleotide insertion)
			PNEEQSLRSNNIAELSPGAINSCRSEYHAAFNSMMMERMTTDIN
			ALKROYSRIKKKOOOOVHOVYIRADKGPVTSILPSQVNSSPVIN
			HLLLGKKMKMTNRAAKNAVIHIPGHTGGKISPVPYEDLKTKLNS
1 1			PWRTHIRVHKKNMPRTKSHPGCGDTVGLIDEQNEASKTNGLGAA
			EAFPSGCTATAGREGSSPEGSTRRTIEGQSPEPVFGDADVDVSA
1			VOAKLGALELNORDAAAETELRVHPPCORHCPEPPSAPBENKAT
1			SKAPOGSNSKTPIFSPFPSVKPLRKSATARNLGLYGPTERTPTV
1			-
1			HFPQMSRSFSKPGGGNSGP*KMVFSSGTMLSRQLPGYPQEYQRN
			GGERFG
6166	2	1206	HKLWRTVAMAGAEWKSLEECLEKHLPLPDLQEVKRVLYGKELRK
			LDLPREAFEAASREDFBLQGYAFBAAEEQLRRPRIVHVGLVQNR
] !			IPLPANAPVAEQVSALHRRIKAIVEVAAMCGVNIICFQEAWTMP
			FAFCTREKLPWTEFAESAEDGPTTRFCQKLAKNHDMVVVSPILE
1			RDSEHGDVLWNTAVVISNSGAVLGKTRKNHIPRVGDFNESTYYM
1			EGNLGHPVFQTQFGRIAVNICYGRHHPLNWLMYSINGAEIIFNP
1		1	SATIGALSESLWPIEARNAAIANHCFTCAINRVGTEHFPNEFTS
1 1			GDGKKAHQDFGYFYGSSYVAAPDSSRTPGLSRSRDGLLVAKLDL
1 1			NLCQQVNDVWNFKMTGRYEMYARELAEAVKSNYSPTIVKE*PAS
1			VPALG
6167	1220	1844	YGIVTGPSLCAGDKOPKKQEKNPVLVSPEFVDEALCACEEYLSN
010,	1220	1011	LAHMDIDKDLEAPLYLTPEGWSLFLQRYYQVVHEGAELRHLDTQ
1 1			VORCEDILOOLOAVVPQIDMEGDRNIWIVKPGAKSRGRGIMCMD
			HLEEMLKLVNGNPVVMKDGKWVVQKYIERPLLIFGTKFDLRQWF
1 1		1	LVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDK*APLYLTPEGWS
1			
			LFLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDMEG
		Ì	DRNIWIVKPGAKSRGRGIMCMDHLBEMLKLVNGNPVVMKDGKWV
1			VQKYIERPLLIFGTKFDLRQWFLVTDWNPLTVWFYRDSYIRFST
1		ł	QPFSLKNLDK
6168	84	1392	VWPVPSVSAMPPKKQAQAGGSKKAEQKKKEKIIEDKTFGLKNKK
		ļ	GAKQQKFIKAVTHQVKFGQQNPRQVAQSEAEKKLKKDDKKKELQ
1 1		1	ELNELFKPVVAAQKISKGADPKSVVCAFFKQGQCTKGDKCKFSH
		1	DLTLERKCEKRSVYIDARDEELEKDTMDNWDEKKLEEVVNKKHG
			EAEKKKPKTQIVCKHFLEAIENNKYGWFWVCPGGGDICMYRHAL
			PPGFVLKKKKKKKKKEDEISL*DLIERERSALGPNVTKITLESF
		1	LAWKKRKRQEKIDKLEQDMERRKADFKAGKALVISGREVFEFRP
		1	ELVNDDDEEADDTRYTQGTGGDEVDDSVSVNDIDLSLYIFRDVD
		1	ETGITVASLERFSTYTSDKDENKLSEASGGRAENGERSDLEEDN
[EREGTENGAIDAVPVDENLFTGEDLDELEEELNTLDLEE
6169	112	662	APAAAMAERPEDLNLPNAVITRIIKEALPDGVNISKEARSAISR
6979	114	002	AASVFVLYATSCANNFAMKGKRKTLNASDVLSAMEEMEFQRFVT
1 1			PLKEALEAYRRBOKGKKEASEQKKKDKDKKTDSBEQDKSRDBDN
1			
1 1			DEDEBRLEEEEQNEEEEVDN*KGRETVAPWKVPLEMRRATCFCE
			AFPCWAE
6170	62	667	STKVMLPNTGRLAGCTVFITGASRGIGKAIALKAAKDGANIVIA
1			AKTAQPHPKLLGTIYTAAEEIEAVGGKALPCIVDVRDEQQISAA
1			VEKAIKKFGGIDILVNNASAISLTNTLDTPTKRLDLMMNVNTRG
			TYLASKACIPYLKKSKVAHIPNISPPLNLNPVWFKQHCGRW*VV
	•		G*GDGLCLICFELNLCMSDVITICT
6171	382	941	HFMQSDVELDCDIEPCGHTKFPPTLPLSTTVIVCSCHPVATAST
			MAEAFSKTTSEEDQSIQEPKEANSMTAQKQKK*GLRGSRRRHAN
			SGGDIFGDSFAAYFPRVLKQVHQALSLSQEAVSVMDSMVRDILD
[1		1	RIATEAGHLAHYSKCVTITSRDIRMAVCLLLPGKMGKLAESQGT
1 1		,	The same of the sa
l l			NATI DVTKCK
7		ļ	NATLRYTKSK GLODACCAUDESDEUUEAAL KNI. DDEADL PDEVI VPKAPERAOR
6172	651	54	GLCRAGGAHRFSRTHVEAALKMLRREARLRREYLYRKAREEAQR
6172	651	54	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	, ,	location	
NO:	nucleotide		Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
•	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	1	sequence	
	sequence	<u> </u>	\=possible nucleotide insertion)
		1	QRMNRGRHEVGALVRACKANGVTDLLVVHEHRGTPVGLIVSHLP
		1	FGPTAYFTLCNVVMRHDIPDLGTMSEAKPHLITHGFSSRLGKRV
	1		SDILRYLFPVPKDDSHRVITFANQDDYISFRHHVYKKTDHRNVE
	1		LTEVGPRFELKLYMIRLGTLEQEATADVEWRWHPYTNTARKRVF
	1		LSTE*AAPRPLGOLL
6173	 	200	
61/3	3	288	SVDHREVQVLSQSMPLTPHQAVLRGERPYMCVECGKCFGRSSHL
1			LQHQRIHTGEKPYVCSVCGKAFSQSSVLSKHRTIHTGEKPYECN
	1		ECGKAFRVSSDLAQHHKIHTGEKPHECLECRKAFTQLSHLIQHQ
	}		RIHTGERPYVCPLCGKAFNHSTVLRSHQRVHTGEKPHRCNECGK
	1		TFSVKRTLLQHQRIHTGEKPYTCSECGKAFSDRSVLIQHHNVHT
1	1		GEKPYECSECGKTFSHRSTLMNHERIHTEEKPYACYECGKAFVQ
1		1	HSHLIQHQKVHRKL*PTCVLSVGSALAGVPTSFSISVSTLERSP
		<u>L</u>	MCAVYVGRPSARAQSLVNTGQFTQVRSPMSVMSVEKPLE
6174	1060	959	PRPPGKRWMVAGLGNPGLPGTRHSVGMAVLGQLARRLGVAESWT
1			RDRHCAADLALAPLGDAQLVLLRPRRLMNANGRSVARAAELFGL
1			TAEEVYLVHDELDKPLGRLALKLGGSARGHNGVRSCISCLNSNA
)		MPRLRVGIGRPAHPEAVQAHVLGCFSPAEQELLPLLLDRATDLI
	ļ		LDHIRERSQGPSLGP*H*WFSKKA
6175	2204	334	RYFRADPRSRSGQPRAEGLGAFAEGPLRAMAAPVKGNRKQSTEG
	1	1	DALDPPASPKPAGKQNGIQNPISLEDSPEAGGEREEEQEREEEQ
			AFLVSLYKFMKERHTPIERVPHLGFKQINLWKIYKAVEKLGAYE
			LVTGRRLWKNVYNELGGSPGSTSGATCTRRHY*RLVLPYVRHLK
			GEDDKPLPTSKPRKQYKMAKENRGDDGATERPKKAKEERRMDOM
1	1	ł	
		1	MPGKTKADAADPAPLPSQEPPRNSTEQQGLASGSSVSFVGASGC
		İ	PEAYKRLLSSFYCKGTHGIMSPLAKKKLLAQVSKVEALQCQEEG
ļ	İ	1	CRHGAEPQASPAVHLPESPQSPKGLTENSRHRLTPQEGLQAPGG
1	1	1	SLREEAQAGPCPAAPIFKGCFYTHPTEVLKPVSQHPRDFFSRLK
			DGVLLGPPGKEGLSVKEPQLVWGGDANRPSAFHKGGSRKGILYP
i	1	1	KPKACWVSPMAKVPAESPTLPPTFPSSPGLGSKRSLEEEGAAHS
	i	1	GKRLRAVSPFLKEADAKKCGAKPAGSGLVSCLLGPALGPVPPEA
	1		· ·
			YRGTMLHCPLNFTGTPGPLKGQAALPFSPLVIPAFPAHFLATAG
	1		PSPMAAGLMHFPPTSFDSALRHRLCPASSAWHAPPVTTYAAPHF
	j		FHLNTKL
6176	1040	402	PLSALRAMAEVHVIGQIIGASGFSESSLFCKWGIHTGAAWKLLS
ł			GVREGQTQVDTPQIGDMAYWSHPIDLHFATKGLOGWPRLHFOVW
1	1		SQDSFGRCQLAGYGFCHVPSSPGTHQLACPTWRPLGSWRBQLAR
	1		
	1		AFVGGGPQLLHGDTIYSGADRYRLHTAAGGTVHLEIGLLLRNFD
J			RYGVEC*GTLPPTSPPSTPRTPSDGGGWHSGQEHRL
6177	1400	992	VPIESLVGKVHNFPLIAFYCCEKGKRQPHKSLHDRCFGEALDPN
1		1	CSHCYLDQIKRSDFLGFSGYSPHFVAISTNSEHKMQPSSMQQAL
1	1	1	PSQ*PYWTDPRPALVPCCSHRPDVHRSRPGPGLPGTSGCSDRPP
1	1	ĺ	VCPI
6178	1027	254	
51,8	1021	434	STORGGIKGVARAASLVGRRRAGTGMALLLCLVCLTAALAHGCL
1			HCHSNFSKKFSFYRHHVNFKSWWVGDIPVSGALLTDWSDDTMKE
1	1	1	LHLAIPAKITREKLDQVATAVYQMMDQLYQGKMYFPGYFPNELR
1			NIFREQVHLIQNAIIESRIDCQHRCGIFQYETISCNNCTDSHVA
1	1		CFGYNCESSAQWKSAVQGLLNYINNWHKQDTSMRPRSSAFSWPG
1	1	1	THRAAPAFLVLPALRCLEPPHLANLSLEDAA*CLKOH
6179	806	276	
"1"	1 300	4/0	RGETREMAGNLLSGAGRRLWDWVPLACRSFSLGVPRLIGIRLTL
	1	1	PPPKVVDRWNEKRAMFGVYDNIGILGNFEKHPKELIRGPIWLRG
1	1		WKGNELQRCIRKRKMVGSRMFADDLHNLNKRIRYLYKHFNRHGK
1	1		FR*KRKLRTSEKAHLSPWRRETVLFPVRKRLCIFSVIKWGFFGI
6180	156	1833	DHHILKAASTTHVCARGNIFAIPNTRCLEC*ATATPSSLECON*
			SHLSLCPLPATTSGLTPNSMIPEKERQNIAERLLRVMCADLGAL
1		1	
1	1	1	SVVSGKEFLKLAQTLVDSGARYGAFSVTEILGNFNTLALKHLPR
L			MYNQVKVKVTCALGSNACLGIGVTCHSQSVGPDSCYILTAYQAE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide		(A-Alamine, C-Cysteine, D-Aspartic Acid, E-
NO:	1	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	bequeenee	
	sequence		\=possible nucleotide insertion)
		l	GNHIKSYVLGVKGADIRDSGDLVHHWVQNVLSEFVMSEIRTVYV
1 1			TDCRVSTSAFSKAGMCLRCSACALNSVVQSVLSKRTLQARSMHE
1			VIELLNVCEDLAGSTGLAKETFGSLEETSPPPCWNSVTDSLLLV
1			HERYEQICEFYSRAKKMNLIQSLNKHLLSNLAAILTPVKQAVIE
			LSNESQPTLQLVLPTYVRLEKLFTAKANDAGTVSKLCHLFLEAL
		i	KENFKVHPAHKVAMILDPQQKLRPVPPYQHEEIIGKVCELINEV
1		-	
			KESWAEEADFEPAAKKPRSAAVENPAAQEDDRLGKNEVYDYLQE
1		1	PLFQATPDLFQYWSCVTQKHTKLAKLAFWLLAVPAVGARSGCVN
	L	1	MCEQALLIKRRRLLSPEDMNKLMFLKSNML
6181	169	1032	TRTLLSPVLLPGPRWKPWRRRPMGPLALPAWLQPRYRKNAYLFI
į į			YYLIQFCGHSWIFTNMTVRFFSFGKDSMVDTFYAIGLVMRLCQS
			VSLLELLHIYVGIBSNHLLPRFLQLTERIIILFVVITSQEEVQE
j			KYVVCVLFVFWNLLDMVRYTYSMLSVIGISYAVLTWLSQTLWMP
]	}		· -
			IYPLCVLAEAFAIYQSLPYFESFGTYSTKLPFDLSIYFPYVLKI
i		1	YLMMLFIGMYFTYSHLYSERRDILGIFPIKKKKM*STAFQCDTR
			KDRLWIQCSK*NTGSILVEKFLVF
6182	1769	1224	AS*IDYQLNTLLKEFQLTEENTKLRYLTCSLIEDMAAAYFPDCI
			VRPFGSSVNTFGKLGCDLDMFLDLDETRNLSAHKISGNFLMEFQ
	•	ľ	VKNVPSERIATQKILSVLGECLDHFGPGCVGVQKILNARCPLVR
1			FSHQASGFQCDLTTNNRIALTSSELLYIYGALDSRVRALVFSVR
		į ,	CWARAHSLTSSIPGAWITNFSLTMMVIFFLQRRSPPILPTLDSL
			KTLADAEDKCVIEGNNCTFVRDLSRIKPSQNTETLELLLKEFFE
]]	İ	l	YFGNFAFDKNSINIRQGREQNKPDSSPLYIQNPFETSLNISKNV
1			SQSQLQKFVDLARESAWILQQEDTDRPSISSNRPWGLVSLLLPS
1 1		1	APNRKSFTKKKSNKFAIETVKNLLESLKGNRTENFTKTSGKRTI
			STQT
6183	1118	452	HLDRYIKSPGSGSSTPAPPSHLLLYLLHPOSTRTMGCCGCSRGC
]			GSGCGGCGSSCGGCGSGCGGCGSGCGGCSSCGGCGS
1 1			RCYVPVCCCKPVCSWVPACSCTSCGSCGGSKGGCGSCGGSKGGC
; ;			GSCGCSQSSCCKPCCCSSGCGSSCCQSSCCKPCCCQSSCCVPVC
1 1		1	CQSSCCKPCCCQSNCCVPVCCQCKI*GSGPRPSGFSCLVKAFLM
	· · · · · · · · · · · · · · · · · · ·		VP
6184	1	2191	IVTVREEDGAPAVAPPGVVVSRANKRSGAGPGGSGGGGARGAEE
			EPPPPLQAVLVADSFDRRFFPISKDQPRVLLPLANVALIDYTLE
			FLTATGVQETFVFCCWKAAQIKEHLLKSKWCRPTSLNVVRIITS
1 1			ELYRSLGDVLRDVDAKALVRSDFLLVYGDVISNINITRALEEHR
			LRRKL*KNVSVMTMIFKESSPSHPTRCHEDNVVVAVDSTTNRVL
			HFQKTQGLRRFAFPLSLFQGSSDGVEVRYDLLDCHISICSPQVA
			QLFTDNFDYQTRDDFVRGLLVNEEILGNQIHMHVTAKEYGARVS
1			
			NLHMYSAVCADVIRRWVYPLTPEANFTDSTTQSCTHSRHNIYRG
			PEVSLGHGSILEENVLLGSGTVIGSNCFITNSVIGPGCHIEPGD
1			NVVLDQTYLWQGVRVAAGAQIHQSLLCDNAEVKERVTLKPRSVL
1			TSQVVVGPNITLPEGSVISLHPPDAEEDEDDGEFSDDSGADQEK
1 1			DKVKMKGYNPAEVGAAGKGYLWKAAGMNMEEEBELQQNLWGLKI
			NMEEESESESEQSMDSEEPDSRGGSPOMDDIKVFONEVLGTLOR
[GKEENISCONLVLEINSLKYAYNISLKEVMQVLSHVVLEFPLQQ
1			, · · · · · · · · · · · · · · · · · · ·
1			MDSPLDSSRYCALLLPLLKAWSPVFRNYIKRAADHLEALAAIED
		j	FFLEHEALGISMAKVLMAFYQLEILAEETILSWFSQRDTTDKGQ
<u></u>			QLRKNQQLQRFIQWLKEAEEESSEDD
6185	791	44	PCTSCVLWATLHLPASTRKAPQAECGMISITEWQKIGVGITGFG
			IFFILFGTLLYFDSVLLAFGNLLFLTGLSLIIGLRKTFWFFFQR
			HKLKGTSFLLGGVVIVLLRWPLLGMFLETYGFFSLFKGFFPVAF
]			GFLGNVCNIPFLGALFRRLQGTSSMV*KTEMSSLNLDHWLKGAK
, ,			
1 1			
			REEWEPPPQSPALTHSPTYPGPPQVQKERNGAEQLTSNPQVDSR
6186	569	238	

CPO -	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
	sequence		KERKVKNKVKNKADTEEVPNNSPTNQEKMPTSAILPDFSGSVIS
			NIRNOMETLHSQPHQEENLCFENSFSLINLLPINAVEPTSSQQI
			PNRETSEANKERRKMTSKSSESNIYSPLTSFITADSELHDIIKD
ł			LEDCLMVGLHTCGDLAPNTLRIFTSNSEIKGVCSVGCCYHLLSE
		İ	EFENOHKERTQEKWGFPMCHYLKEERWCCGRNARMSACLALERV
ļ			AAGOGLPTESLFYRAVLQDIIKDCYGITKCDRHVGKIYSKCSSF
ĺ			LDYVRRSLKKLGLDESKLPBKIIMNYYEKYKPRMNELEAFNMLK
		}	VVLAPCIETLILLDRLCYLKEQEDIAWSALVKLFDPVKSPRCYA
			VIALKKOO*FPLKQIIRCISL*DSAGCAEEVSVGDGGPALRDAP
1			PSGSRVGSRYD
	1701	771	DAWGPETRLARILNPDSFIEPRPGRLPBLEATRPHMEPKASCPA
6187	1,01	,,,,	AAPLMERKFHVLVGVTGSVAALKLPLLVSKLLDIPGLEVAVVTT
1			ERAKHFYSPODIPVTLYSDADEWEMWKSRSDPVLHIDLRRWADL
	ŀ		LLVAPLDANTLGKVASGICDNLLTCVMRAWDRSKPLLFCPAMNT
			AMWEHPITAQQVDQLKAFGYVEIPCVAKKLVCGDEGLGAMAEVG
			TIVDKVKEVLFOHSGFQQS*PGISVMGVPLYSEWVQAKSVKMDV
J			GKIGGYPHLLNGGPALSLPRGQACSRLNWTEGPGLSFFQPGEAA
			A
6100	238	1534	KGFVNAGPLMAELOVSPOWKAPEMSQICLSCGHPSA*GPRWASW
6188	236	1534	NIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCMQEMG
			NGKANRLYEAYLPETFRRPQIDPAVEGFIRDKYEKKKYMDRSLD
1			INAFRKEKDDKWKRGSEPVPEKKLEPVVFEKVKMPQKKEDPQLP
			RKSSPKSTAPVMDLLGLDAPVACSIANSKTSNTLEKDLDLLASV
1			PSPSSGSRKVVGSMPTAGSAGSVPENLNLFPEPGSKSEEIGKK
			QLSKDSILSLYGSQTPQMPTQAMFMAPAQMAYPTAYPSFPGVTP
}			PNSIMGSMMPPPVGMVAQPGASGMVAPMAMPAGYMGGMQASMMG
			VPNGMMTTQQAGYMAGMAAMPQTVYGVQPAQQLQWNLTQMTQQM
ì		1	AGMNFYGANGMMNYGQSMSGGNBQAANQTLSPQMWK
6189	1297	793	LGEPLGDLCELIPGDVQQLQMGEVHPGTGAQGSAAQSVAGEVQL
0105	1	1.22	TOLSHARORPSCOGSQLIALDLQHMDISRQPRWQHVQPVARQVQ
1			RAQQAQLAEGVAVHLWAGDAVVAEVELLQEVGGGKVFAANACDL
1			VVQDHEGAHAARQATGHALQRVIVQVRRVQPLEAL*RVPSGLPR
1			RVRAFMILHNQITGIGREDFATTYFLEELNLSYNRITSPQVHRD
1		1	AFRKLRLLRSLDLSGNRLHMLPPGLPRNVHVLKVKRNELAALAR
1			GALAGMAOLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQ
			LTEIPEGLPESLEYLYLQNNKISAVPANAFDSTPNLKGIFLRFN
			KLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKDRGRLGKEKE
[EEEEDEVEREETR
6190	66	1309	ILVGNVSFLLSFAEYVCNCSVVGSLNVNRCNQTTGQCECRPGYQ
			GLHCETCKEGFYLNYTSGLCQPCDCSPHGALSIPCNSSGKCQCK
		1	VGVIGSICDRCQDGYYGFSKNGCLPCQCNNRSASCDALTGACLN
			COENSKGNHCEECKEGFYQSPDATKECLRCPCSAVTSTGSCSIK
			SSELEPECDQCKDGYIGPNCNKCENGYYNFDSICRKCQCHGHVY
		1	PVKTPKICKPESGECINCLHNTTGFWCENCL*GYVHDLEGNCIK
			KVILPTPEGSTILVSNASLTTSVPTPVINSTFTPTTLQTIFSVS
			TSENSTSALADVSWTQFNIIILTVIIIVVVLLMGFVGAVYMYRE
	1		YONRKLNAPFWTIELKEDNISFSSYHDSIPNADVSGLLEDDGNE
			VAPNGQLTLTTPIHNYKA
6191	1212	1511	VNLCHGGLLHLSTHHLGIKPSMH*LFFLMLSFPHLTPQQPKCPS
1			MIDWIKKIWYIYTMEYYATIKRNEIMFFAGTWMEMEAIILSKLM
			ODYMFSLISGS
6192	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
31,72			KGGLVSDAYGEDDFSRLGGDEDGYEBEEDENSRQSEDDDSETEK
1			PEADDPKDNTEAEKRDPQBLVASFSERVRNMSPDEIKIPPEPPG
1			RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
1			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
1		_l	1 -

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
			DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
			IVKKAKQ
6193	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
	1		KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
	ĺ		PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
j			RCSNHLQDKIQKLYBRKIKEGMDMNYIIQRKKEFRNPSIYEKLI
	ļ		QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
ĺ			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
	İ		DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
	L		IVKKAKQ
6194	3	950	TRGCGNKMAGKKNVLSSLAVYAEDSEPESDGEAGIEAVGSAAEE
		}	KGGLVSDAYGEDDFSRLGGDEDGYEEEEDENSRQSEDDDSETEK
			PEADDPKDNTEAEKRDPQELVASFSERVRNMSPDEIKIPPEPPG
			RCSNHLQDKIQKLYERKIKEGMDMNYIIQRKKEFRNPSIYEKLI
			QFCAIDELGTNYPKDMFDPHGWSEDSYYEALAKAQKIEMDKLEK
}			AKKERTKIEFVTGTKKGTTTNATSTTTTTASTAVADAQKRKSKW
			DSAIPVTTIAQPTILTTTATLPAVVTVTTSASGSKTTVISAVGT
		225	IVKKAKQ
6195	736	235	VANGLQSNMPKFYCDYCDTYLTHDSPSVRKTHCSGRKHKENVKD
	İ	İ	YYQKWMEEQAQSLIDKTTAAFQQGKIPPTPFSAPPPAGAMIPPP
			PSLPGPPRPGMMPAPHMGGPPMMPMMGPPPPGMMPVGPAPGMRP
6100	1510	623	PMGGHMPMMPGPPMMRPPARPMMVPTRPGMTRPDR
6196	1512	623	KTGKRRSAAYVRNILDNAEQVISNLEARNLGPRLTPLLQEEDSH
}			QRLLMGLMVSELKDHFLRHLQGVEKKKIEQMVLDYISKLLDLIC HIVETNWRKHNLHSWVLHFNSRGSAAEFAVFHIMTRILEATNSL
			FLPLPPGFHTLHTILGVQCLPLHNLLHCIDSGVLLLTETAVIRL
ļ	İ		MKDLDNTEKNEKLKFSIIVRLPPLIGQKICRLWDHPMSSNIISR
			NHVTRLLONYKKOPRNSMINKSSFSVEFLPLNYFIEILTDIESS
			NOALYPFEGHDNVDAEFVEEAALKHTAMLLGL
6197	3	819	ADPEGTEEAVMSRYTRPPNTSLFIRNVADATRPEDLRREFGRYG
0237	1	1	PIVDVYIPLDFYTRRPRGFAYVQFEDVRDAEDALYNLNRKWVCG
1			RQIEIQFAQGDRKTPGOMKSKERHPCSPSDHRRSRSPSORRTRS
			RSSSWGRNRRRSDSLKESRHRRFSYSQSKSRSKSLPRRSTSARQ
			SRTPRRNFGSRGRSRSKSLQKRSKSIGKSQSSSPQKQTSSGTKS
			RSHGRHSDSIARSPCKSPKGYTNFETKVQTAKHSHFRSHSRSRS
	1		YRHKNSW
6198	111	1912	SEAALSPSFISPACFLLRKLPALEDGTLPHPDTLGMNYEGARSE
			RENHAADDSEGGALDMCCSERLPGLPQPIVMEALDEAEGLQDSQ
			REMPPPPPPSPPSDPAQKPPPRGAGSHSLTVRSSLCLFAASQFL
			LACGVLWFSGYGHIWSQNATNLVSSLLTLLKQLEPTAWLDSGTW
			GVPSLLLVFLSGGLVLVTTLVWHLLRTPPEPPTPLPPEDRRQSV
			SRQPSFTYSEWMBEKIEDDFLDLDPVPBTPVFDCVMDIKPEADP
			TSLTVKSMGLQERRGSNVSLTLDMCTPGCNEEGFGYLMSPREES
			AREYLLSASRVLQAEELHEKALDPFLLQAEFFEIPMNFVDPKEY
			DIPGLVRKNRYKTILPNPHSRVCLTSPDPDDPLSSYINANYIRG
1			YGGEEKVYIATQGPIVSTVADFWRMVWQBHTPIIVMITNIEEMN
			EKCTEYWPEEQVAYDGVEITVQKVIHTEDYRLRLISLKSGTEER
	1		GLKHYWFTSWPDQKTPDRAPPLLHLVREVBEAAQQEGPHCAPII
			VHCSAGIGRTGCFIATSICCQQLRQEGVVDILKTTCQLRQDRGG
			MIQHCEQYQFVHHVMSLYEKQLSHQSPE
6199	144	1211	MARENGESSSSWKKQAEDIKKIFEFKETLGTGAFSEVVLAEEKA
			TGKLFAVKCIPKKALKGKESSIENEIAVLRKIKHENIVALEDIY
			BSPNHLYLVMQLVSGGELFDRIVEKGFYTEKDASTLIRQVLDAV
			YYLHRMGIVHRDLKPENLLYYSQDEESKIMISDFGLSKMEGKGD
1		<u> </u>	VMSTACGTPGYVAPEVLAQKPYSKAVDCWSIGVIAYILLCGYPP
I			The state of the s

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	residue of	residue of amino acid	S=Serine, T=Threonine, V=Valine,
ĺ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
		·	FYDENDSKLFEQILKAEYEFDSPYWDDISDSAKDFIRNLMEKDP
			NKRYTCEQAARHPWIAGDTALNKNIHESVSAQIRKNFAKSKWRQ
		ļ	AFNATAVVRHMRKLHLGSSLDSSNASVSSSLSLASOKDCASGTF
1			HAL*
6200	702	96	LPEVPHSLRPRVKPHLCCAQPAVRVMARLPKLAVFDLDYTLWPF
			WVDTHVDPPFHKSSDGTVRDRRGQDVRLYPEVPEVLKRLQSLGV
1			PGAAASRTSEIEGANQLLELFDLFRYFVHREIYPGSKITHFERL
1			QQKTGIPFSQMIFFDDERRNIVDVSKLGVTCIHIQNGMNLQTLS
			QGLETFAKAQTGPLRSSLEESPFEA
6201	2809	2383	GQTPRVRWKMRRSLRAGKRRQTAGRKSKSPPKVPIVIQDDSLPA
			GPPPQIRILKRPTSNGVVSSPNSTSRPTLPVKSLAQREAEYAEA
1			RKRILGSASPEEEQEKPILDRPTRISQPEDSRQPNNVIRQPLGP
6202	2	426	DGSQGFKQRR INADRAAVASSLLSRPTRKMAPQKDRKPKRSTWRFNLDLTHPVE
"""	_	120	DGIFDSGNFEQFLREKVKVNGKTGNLGNVVHIERFKNKITVVSE
1	İ		KQFSKRYLKYLTKKYLKKNNLRDWLRVVASDKETYELRYFQISQ
1			DEDESESED
6203	419	2550	RCPRPPATAGAAASRPDRSPPSGISGSEAAAGAGAAAPASOHPA
			TGTGAVQTEAMKQILGVIDKKLRNLEKKKGKLDDYQERMNKGER
			LNQDQLDAVSKYQEVTNNLEFAKELQRSFMALSQDIQKTIKKTA
Į.			RREQLMREEAEQKRLKTVLELQYVLDKLGDDEVRTDLKQGLNGV
			PILSEEELSLLDEFYKLVDPERDMSLRLNEQYEHASIHLWDLLE
ļ			GKEKPVCGTTYKVLKEIVERVFQSNYFDSTHNHQNGLCEEEEAA
]			SAPAVEDQVPEAEPEPAEEYTEQSEVESTRYVNRQFMAETQFTS
			GEKEQVDEWTVETVEVVNSLQQQPQAASPSVPEPHSLTPVAQAD
Į			PLVRRQRVQDLMAQMQGPYNFIQDSMLDFENQTLDPAIVSAQPM NPTQNMDMPQLVCPPVHSESRLAQPNQVPVQPEATQVPLVSSTS
			EGYTASQPLYQPSHATEQRPQKEPIDQIQATISLNTDQTTASSS
ĺ			LPAASQPQVFQAGTSKPLHSSGINVNAAPFQSMQTVFNMNAPVP
j	1		PVNEPETLKQQNQYQASYNQSFSSQPHQVEQTELQQEQLQTVVG
ļ			TYHGSPDQSHQVTGNHQQPPQQNTGFPRSNQPYYNSRGVSRGGS
			RGARGLMNGYRGPANGFRGGYDGYRPSFSNTPNSGYTQSQFSAP
			RDYSGYQRDGYQQNFKRGSGQSGPRGAPRGRGGPPRPNRGMPQM
			NTQQVN
6204	2933	787	CTHNLISLLGGRALIHFNRFLNLKIQEGEAHNIFCPAYDCFQLV
			PGDIIKSVVSKEMDKRYLQFDIKAFVENNPAIKWCPTPGCDRAV
			RLTKQGSNTSGSDTLSFPLLRAPAVDCGKGHLFCWECLGBAHEP CDCQTWKNWLQKITEMKPEELVGVSEAYEDAANCLWLLTNSKPC
]	}		ANCKSPIQKNEGCNHMQCAKCKYDFCWICLEEWKKHSFVHWEVI
			YRCTRYEVIQHVEEQSKEMTVEAEKKHKRFQELDRFMHYYTRFK
			NHEHSYQLEQRLLKTAKEKMEQLSRALKETEGGCPDTTFIEDAV
			HVLLKTRRILKCSYPYGFFLEPKSTKKEIFELMQTDLEMVTEDL
			AQKVNRPYLRTPRHKIIKAACLVQQKRQEFLASVARGVAPADSP
			EAPRRSFAGGTWDWEYLGFASPEEYAEFQYRRRHRQRRRGDVHS
			LLSNPPDPDEPSESTLDIPEGGSSSRRPGTSVVSSASMSVLHSS
			SLRDYTPASRSENQDSLQALSSLDEDDPNILLAIQLSLQESGLA
			LDEETROFLSNEASLGAIGTSLPSRLDSVPRNTDSPRAALSSSE
			LLELGDSLMRLGAENDPFSTDTLSSHPLSEARSDFCPSSSDPDS
			AGQDPNINDNLLGNIMAWFHDMNPQSIALIPPATTEISADSQLP
			CIKDGSEGVKDVELVLPEDSMFEDASVSEGRGTQIEENPLEBNI PGGGKQHPQAW
6205	i	1200	RAHRGKMALEVGDMEDGQLSDSDSDMTVAPSDRPLQLPKVLGGD
	_	1200	SAMRAFQNTATACAPVSHYRAVESVDSSEESFSDSDDDSCLWKR
			KRQKCFNPPPKPBPFQFGQSSQKPPVAGGKKINNIWGAVLQEQN
			QDAVATELGILGMEGTIDRSROSETYNYLLAKKLRKESQEHTKD
			LDKELDEYMHGGKKMGSKEEBNGQGHLKRKRPVKDRLGNRPEMN
			

	•		
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ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
İ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ł	\=possible nucleotide insertion)
			YKGRYEITAEDSQEKVADEISFRLQEPKKDLIARVVRIIGNKKA
1		<u> </u>	IELLMETAEVEONGGLFIMNGSRRRTPGGVFLNLLKNTPSISEE
			QIKDIFYIENQKEYENKKAARKRRTQVLGKKMKQAIKSLNFQED
i .	1	,	DDTSRETFASDTNEALASLDESQEGHAEAKLEAEEAIEVDHSHD
		· ·	-
			LDIF
6206	10	1442	IISERRERSCLHLVCIRCSCDVVEMGSVLGLCSMASWIPCLCGS
1		1	APCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGMEEQ
1			LNKIPGFCENEKGVVPCNILVGYKAVYRLCFGLAMFYLLLSLLM
i		1	IKVKSSSDPRAAVHNGFWFFKFAAAIAIIIGAFFIPEGTFTTVW
			FYVGMAGAFCFILIQLVLLIDFAHSWNESWVEKMEEGNSRCWYA
1			ALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMLLC
			VGASVMSILPKIQESQPRSGLLQSSVITVYTMYLTWSAMTNEPE
1	1		TNCNPSLLSIIGYNTTSTVPKEGQSVQWWHAQGIIGLILFLLCV
		1	FYSSIRTSNNSOVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
			RAVDNERDGVTYSYSFFHFMLFLASLYIMMTLTNWYRYEPSREM
			KSQWTAVWVKISSSWIGIVLYVWTLVAPLVLTNRDFD
6207	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
]	Ì		GGGGGSDGSGGGWTKQVTCRYFMHGVCKEGDNCRYSHDLSDSPY
1		1	SVVCKYFQRGYCIYGDRCRYEHSKPLKQEEATATBLTTKSSLAA
	[SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP
{		1	GOPYCGRTAPSCTEAPLOGSVTKEESEKEQTAVETKKQLCPYAA
j	i		VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
'	1	1	HEKDMELSFAVORSKDMVCGICMEVVYEKANPSERRFGILSNCN
ļ	1		1
1	1		HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE
	1		KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
1	1	1	GRREEPQRQKVGTSSRYRAQRRNHFWELIEERENSNPFDNDEEE
	1	1	VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
6208	2924	1471	TVMAEAATPGTTATTSGAGAAAATAAAASPTPIPTVTAPSLGAG
ł	1		GGGGGSDGSGGGWTKQVTCRYFMHGVCKBGDNCRYSHDLSDSPY
	Į.	l	SVVCKYFQRGYCIYGDRCRYEHSKPLKQBEATATELTTKSSLAA
Į.			SSSLSSIVGPLVEMNTGEAESRNSNFATVGAGSEDWVNAIEFVP
		ì	GOPYCGRTAPSCTEAPLOGSVTKEESEKKOTAVETKKOLCPYAA
1	i	1	VGECRYGENCVYLHGDSCDMCGLQVLHPMDAAQRSQHIKSCIEA
1			HEKDMELSFAVQRSKDMVCGICMEVVYEKANPSERRPGILSNCN
1	1		
1	i		HTYCLKCIRKWRSAKQFESKIIKSCPECRITSNFVIPSEYWVEE
1			KEEKQKLILKYKEAMSNKACRYFDEGRGSCPFGGNCFYKHAYPD
1			GRREEPQRQKVGTSSRYRAQRRNHFWELIBERENSNPFDNDEEE
L			VVTFELGEMLLMLLAAGGDDELTDSEDEWDLFHDELEDFYDLDL
6209	1758	829	ERLCFPCMQSKIYSYMSPNKCSGMRFPLQEENSVTHHEVKCQGK
1	1	,	PLAGIYRKREEKRNAGNAVRSAMKSEEQKIKDARKGPLVPFPNQ
Į			KSEAAEPPKTPPSSCDSTNAAIAKQALKKPIKGKQAPRKKAQGK
			TOONRKLTDFYPVRRSSRKSKAELQSEERKRIDELIESGKEEGM
1			KIDLIDGKGRGVIATKQFSRGDFVVEYHGDLIEITDAKKREALY
			AQDPSTGCYMYYFQYLSKTYCVDATRETNRLGRLINHSKCGNCQ
1			TKLHDIDGVPHLILIASRDIAAGEELLYDYGDRSKASIBAHPWL
		1	
	1		KH
6210	3761	387	IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT
			SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV
	1 2	1	SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
			CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGR1E
			IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
1			SGPIWFDDLICNGNESALWNCKHOGWGKHNCDHAEDAGVICSKG
j]	ADLSLRLVDGVTECSGRLEVRFOGEWGTICDDGWDSYDAAVACK
			QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE
i	,		WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL
			The state of the s
L	<u> </u>		LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ļ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	· -	\=possible nucleotide insertion)
ļ			FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV
	,		GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV
			SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
1	•		SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
Į.	İ	ļ	IEDAHVLCOOLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ
I			HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
1			RPTIPEESAVACIESGOLRLVNGGGRCAGRVEIYHEGSWGTICD
			DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
	1		GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
			ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
]		ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
1			WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV
			VCQQLGCGPALKAFKEAEFGQGTGPIWLNEVKCKGNESSLWDCP
			ARRWGHSECGHKEDAAVNCTDISVOKTPOKATTGRSSROSSFIA
1			VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR
			EMNSCLNADDLDLMNSSGGHSEPH
6211	3761	387	IFGMSKLRMVLLEDSGSADFRRHFVNLSPFTITVVLLLSACFVT
i i			SSLGGTDKELRLVDGENKCSGRVEVKVQEEWGTVCNNGWSMEAV
ţ			SVICNQLGCPTAIKAPGWANSSAGSGRIWMDHVSCRGNESALWD
}			CKHDGWGKHSNCTHQQDAGVTCSDGSNLEMRLTRGGNMCSGRIE
ļ			IKFQGRWGTVCDDNFNIDHASVICRQLECGSAVSFSGSSNFGEG
1			SGPIWFDDLICNGNESALWNCKHQGWGKHNCDHAEDAGVICSKG
			ADLSLRLVDGVTECSGRLEVRFQGEWGTICDDGWDSYDAAVACK
İ			QLGCPTAVTAIGRVNASKGFGHIWLDSVSCQGHEPAVWQCKHHE
			WGKHYCNHNEDAGVTCSDGSDLELRLRGGGSRCAGTVEVEIQRL
			LGKVCDRGWGLKEADVVCRQLGCGSALKTSYQVYSKIQATNTWL
1			FLSSCNGNETSLWDCKNWQWGGLTCDHYEEAKITCSAHREPRLV
1			GGDIPCSGRVEVKHGDTWGSICDSDFSLEAASVLCRELQCGTVV
			SILGGAHFGEGNGQIWAEEFQCEGHESHLSLCPVAPRPEGTCSH
İ			SRDVGVVCSRYTEIRLVNGKTPCEGRVELKTLGAWGSLCNSHWD
ł			IEDAHVLCQQLKCGVALSTPGGARFGKGNGQIWRHMFHCTGTEQ
1	İ		HMGDCPVTALGASLCPSEQVASVICSGNQSQTLSSCNSSSLGPT
1			RPTIPEESAVACIESGQLRLVNGGGRCAGRVEIYHEGSWGTICD
		į	DSWDLSDAHVVCRQLGCGEAINATGSAHFGEGTGPIWLDEMKCN
1			GKESRIWQCHSHGWGQQNCRHKEDAGVICSEFMSLRLTSEASRE
1			ACAGRLEVFYNGAWGTVGKSSMSETTVGVVCRQLGCADKGKINP
1	•		ASLDKAMSIPMWVDNVQCPKGPDTLWQCPSSPWEKRLASPSEET
1	}		WITCDNKIRLQEGPTSCSGRVEIWHGGSWGTVCDDSWDLDDAQV VCQQLGCGPALKAFKEABFGQGTGPIWLNEVKCKGNESSLWDCP
1	1		ARRWGHSECGHKEDAAVNCTDISVQKTPQKATTGRSSRQSSFIA
1	1		VGILGVVLLAIFVALFFLTKKRRQRQRLAVSSRGENLVHQIQYR
1			EMNSCLNADDLDLMNSSGGHSEPH
6212	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCQTNPGPPSSLRRAFRR
0212	1	1:34	RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL
			GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPAERHMISSWE
		1	OKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI
			SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS
	•	1	VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALYWHFLT
		1	DTFTAYYRLLITHLGLPOWOYAFTSYGISPQAKORVSMYKPITY
			NTNLLTEETDSFVNKLDPSKVFKSKNKIVIPKKKGPVQPAGGQK
			GPSGPSGPSTSTSKSSSGSGNPTRK
6213	1	1134	LKWELRPGGAVWGTGRGAGTGAPRSCCCOTNPGPPSSLRRAFRR
0213	1	1134	RELPFPACHEIGLGAEAGSGPPPAPAARESRSRAMEEEASSPGL
			GCSKPHLEKLTLGITRILESSPGVTEVTIIEKPPABRHMISSWE
İ			QKNNCVMPEDVKNFYLMTNGFHMTWSVKLDEHIIPLGSMAINSI
			SKLTQLTQSSMYSLPNAPTLADLEDDTHEASDDQPEKPHFDSRS
L		J	PARTABLIAGOLITORI MAN TRUDBRODI MINICOPONE BULLEDONO

Predicted Predicted end nucleotide location No: nucleotide location Corresponding to first amino acid residue of amino acid sequence Sequenc	, E= ne, Stop WHFLT KPITY AGGQK FVGWV FSAYN RRQVH
NO: nucleotide location corresponding to first amino acid amino acid residue of amino acid sequence Se	Stop WHFLT KPITY AGGQK FVGWV FSAYN RRQVH
location corresponding to first amino acid amino acid residue of amino acid sequence Particle Particle Particle Particle	Stop WHFLT KPITY AGGQK FVGWV FSAYN RRQVH
Leucine, M=Methionine, N=Asparagine, amino acid amino acid residue of amino acid sequence Seserine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Codon, /=possible nucleotide deletion, \possible nu	WHFLT KPITY AGGQK FVGWV FSAYN RRQVH
to first amino acid residue of amino acid residue of amino acid sequence P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, S=Serine, T=Threonine, X=Unknown, *= Codon, /=possible nucleotide deletion, Ap	WHFLT KPITY AGGQK FVGWV FSAYN RRQVH
amino acid residue of amino acid sequence sequen	WHFLT KPITY AGGQK FVGWV FSAYN RRQVH
residue of amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide insertion) VifeLDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALM DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQVSWM NTMLITEETDSFVMKLDPSKVFKSKNKIVIPKKKGPVQU GPSGPSGPSTSSTSKSSSGSGNPTKK FURLEDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALM DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQVSWM NTMLITEETDSFVMKLDPSKVFKSKNKIVIPKKKGPVQU GPSGPSGPSTSSTSKSSSGSGNPTKK GPSGPSGPSTSSTSKSSSGSGNPTKK HELAPSAIRRAARIGLGPARWQSRAAAFYFVRGFRTGWS VLGTSAKRTRLFFILSKMAASSRAQVLALYRAMLRESKK YRTYAVKRIRDAFRENKNVKDPVEIQTLVNKAKRDLGVI IGQLYSTDKLIIENRDMPRT FVAGGPRGSGSAAETMPEIRVTTPJGAGQDVGRSCILVS: MLDCGMHMGFNDDRRFPDFSVITONGRUTDFLDCVIISK CGALPYFSEMWGYDGPIYMTHPTQAICPILLEDYKKIAN AMPGIKVGSESVVYTGDYNMTPDRHLGAAWIDKCPNLI YATTIRDSKRCRERDFLKKVLETVERGGKVLLPVFALGI LLETTWERNNLKVPIYFSTGLTEKANHYYKLFIPWTMK FVQRNMFERFKHIKAFDRAFADNPGFMVVFATFGMLHAGG RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGK KKEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKKGL LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEH RVHLHDTRKRQETALRVYSHLKSVLKDHCVQHLPGSV LQAAAPSEDCTKVLLVSWTYQDEELIGSFLTSLLKKGL LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEH RVHLHDTRKRQEFTALRVYSHLKSVLKDHCVQHLPGSV LQAAAPSEDCTKVLLVSWTYQDEELIGSFLTSLLKKGL GARGEEGSARMWKTLTFFVALPGVAVSMLNVVLKSHHGG FLAYPHLRIRTKFPFWGGNNTLFHNPHVDPLPTGYED GARGEEGSARMWKTLTFFVALPGVAVSMLNVVLKSHHGG FLAYPHLRIRTKFPFWGGNNTLFHNPHVDPLPTGYED LRKLFIGGLSFETTDDSLREHEEKWGTLTDCVVMRDPQ GFFVTYSCVERVDAAMCARPHKVDGRVVFPKRAVSRED HLTVKKIFVGGIKEDTESYNLRDYFEKYGKIETIEVME KRGPAFVFFDDHDTVDKITVQKYHTINGHNCSVKKALS AGSQRGGGGGSGNFGGGGGNFGGGGGNFGGGGNFGGGGNFGGGGNFGGGGNFGGGGNFGGGGNFGGGGNFGGGGNFGGGGNFGGGGNFGGGGNFGGGGNFGGGGNFGGGGNFGGGGGNFGGGGGNFG	WHFLT KPITY AGGQK FVGWV FSAYN RRQVH
amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion) VIFELDSCNGSKVCLVYKSGKPALAEDTEEWFLDRALY DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSMY NTMLLTEETDSFVMKLDPSKVFKSRKRLVIPKKGPVQI GPSGPSGPSTSSTSKSSSGSGNPTKK HELAPSÄIRRAARLGLGPARWGSRAAAFYFVRGFRTGWS VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKI YRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGVI IGGLYSTDKLIIENROMPRT FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVS: MLDCGMHMGFNDDRRFPDFSYITDNGRLTDFLDCVIISI CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIA' ANFFTSGMIKDCMKKVVAVHLHGTVQVDDELEIKAYYAK AMPGIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLI LLETFWERNNLKVPIYFSTGLITEKANHYYKLFIPWTN FVQRNMFEFKHIKAFDRAFADNPGPMVVFATPGMLHAGG RKWAGNEKNNVIMPGYCVQGTVEHKILSGQRKLEMEGRK MQVEYMSFSAHDANKG IMQLVGQABPESVLLVHGEAKK KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKRI LPBAKKFRLHGTLIMKDSNFRLUSSEQALKEDLGKK KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKRI LPBAKKFRLHGTLIMKDSNFRLUSSEQALKEGLEGSFRFGLG GARGEGGSARMAVTLTFFVALDFVANSHUNYLKSHGG FLAYPHLBIRTKFPPFWGDGNHTLFHNPHVNPLPTGYEDL GARGEGGSARMAVTLTFFVALDFVANSHUNYLKSHGG FLAYPHLRIRTKFPFPWGGGNHTLFHNPHVNPLPTGYEDL LRILFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ' FGFVTYSCVERVDAMACARPHKVDGRVYBFRRVSEEDL KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGRGGGGGNFGRGGGNFGRGGGNFGRGGNFGGRGGNFGGGGNFGGRGGNFGGRGGNFGGGNFGGGNFGGGNFGGGNFGGGNFGGGNFGGGNFGGGNFGGGNFGGGGNFGGGGNFGG	WHFLT KPITY AGGQK FVGWV FSAYN RRQVH
Sequence Sequence	KPITY AGGQK FVGWV FSAYN RRQVH
Sequence Sequence	KPITY AGGQK FVGWV FSAYN RRQVH
VIFELDSCNGSGKVCLVYKSGKPALAEDTEIWFLDRALV DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSM NTMLLTEETDSFVMKLDPSKVFKSKNKIVIPKKKGPVQI GPSGPSGPSTSSTSKSSSGSGNPTRK 6214 2 460 HELAPSAIRRAARLGLGPARWGSRAAAFYFVRGFRTGW VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKE YRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGV: IGQLYSTDKLIIENRDMPRT 6215 2 1849 FVAGGPRGSGSAETMPEIRVFLGAGQDVGRSCILVS: CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDTRKIAN ANFFTSQMIKDCMKKVVAVHLHCTVQVDDELBIKAYYAA AMPQIKVGSESVVTTGDYNMTPDRHLGAAWIDKCRPNLI YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGI ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTN FVQRNMFEFKHIKAFDRAFADDRGPMVVFATPGMLHAG RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRK KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKRI CPBAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEH RVHLHDTRKEQETALRVYSHLKSVIKDHCVQHLPDGSV LQAAAPSEDPGTKVLLVSWTYQDEBLGSFTTSLLKKGL GAHGEEGSARMWKTLTFVALPGVAVSMLNVYLKSHGI FIAYPHLRIRTKFFFWGDONHTLFHNPHVNPLPTGYED GAHGEEGSARMWKTLTFVALPGVAVSMLNVYLKSHGI FIAYPHLRIRTKFFFWGDONHTLFHNPHVNPLPTGYED LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDDQ FGFVTYSCUEBUDAMCARPHKVDGRVVFFRRAVSRED HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME KRGRAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGRGGGGGNFGRGGGGGNFGRGGRGNFGRGGGGGGGRFGRGRGGGGGGGG	KPITY AGGQK FVGWV FSAYN RRQVH
DTFTAYYRLLITHLGLPQWQYAFTSYGISPQAKQRVSM NTMLLTEETDSFVMKLDPSKVFKSKMKLVIPKKKGPVQI GPSGPSGPSTSSTSKSSSGGMPTTK HELAPSAIRRARLGLGPARWGSRAAAFYFVRGFRTGWS VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKE YRTYAVRRIRDAFRENKMVKDFVEIQTLVNKAKRDLGVI IGQLYSTDKLIIENRDMPRT FVAGGPRGSGSAAETMPETRVTPLGAGQDVGRSCILVSI MLDCGMHMGFNDDRRFPDFSYITQNGRLTDFLDCVILISA CGALPYPSEMWGYDGPIYMTHPTQAICPILLEDYRKILSA ANFFISQMIKDCMKKVVAVHLHCTVQVDDELBIKAYYAK AMMOIKVGSESVVYTGDYMMTPDRHLGAAWIDKCRPNLI YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGEI ILLETFWERMMLKVPIYFATDHSCPMVVFATPGMLHAGG RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRG MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKK KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKRI LPBAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEH RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV LQAAAPSEDPGTKVLLVSMTYQDEELGSFLTSLLKKGLL FBAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEH RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV LQAAAPSEDPGTKVLLVSMTYQDEELGSFLTSLLKKGLI GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGI FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYED GHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGI FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYED HLTVKKIPVGGIKEDTEEYNLRDYFEKYGKIETIEVME KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGRGGGGGNFMGRGGGGGNFGGRGGNFGGRGGGGGGNFGGRGGNFGGRGGGGGNFGGRGGNFGGRGGGGGNFGGRGGNFGGRGGGGGNFGGRGGGGGNFGGRGGNFGGRGGGGGNFGGRGGNFGGRGGGGGNFGGRGGNFGGRGGGGGNFGGRGGNFGGRGGGGGNFGGRGGNFGGRGGGGGGNFGGRGGNFGGRGGGGGNFGGRGGNFGGRGGGGGNFGGRGGNFGGRGGNFGGRGGNFGGRGGNFGGRGGNFGGRGGNFGGRGGNFGGRGGNFGGRGGNFGGRGGGGGNFGGRGGNFGGRGGNFGGRGGNFGGRGGNFGGRGGGGGNFGGRGGGGGNFGGRGGNFGGGGGNFGGGGGNFGGRGGGGGNFGGGGGNFGGGGGNFGGGGGNFGGGGGNFGGGGGNFGGGGGNFGGGGGNFGGGGGG	KPITY AGGQK FVGWV FSAYN RRQVH
NTNLLTEETDSFVNKLDPSKVFKSRNKIVIPKKGPVQI GPSGPSGPSGPSTSTSKSSSGSGNPTRK 6214 2 460 HELAPSAIRRAARLGLGPARWGSRAAAFYFVRGFRTGWS VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKE YRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGVI IGQLYSTDKLIIENRDMPRT 6215 2 1849 FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVS: MLDCGMHMGFNDDRRFPDFSYITQNGRLTDFLDCVIISE CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAN ANFFISKMIKDCMKKVVAVHLHQTVQVDDELEIKAYYAC AMPGIKOGSESVVYTGDYNMYPDRHLGAAMIDKCRPNLI YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGI ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTN FVQRNMFEFKHIKAFDRAFADNPGPMVVFATPGMLHAGC RKWAGNERNMVIMPGYCVQGTVGHKILSGQRKLEMEGRK KIEQELRVNCYMPANGETVTLPTSPSIPVGISLIGLIKRI LPEAKKPRLLHGTLIMKDSNFFLVSSEQALKBLGLAEH RVHLHDTRKBQETALRVYSHLKSVLKDHCVQHLPDGSV- LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGL FLAYAPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYED GAHGEGSARMWKTLTFFVALPGVAVSMLNYYLKSHGI FLAYPHLRIRTKFPFWGDGNHTLFHNPHVNPLPTGYED LRKLFIGGLSFETTDGLSFFTTDCVVMRDPQ- FGFVTYSCVEEVDAAMCARPHKVDGRVVEFKRAVSRED- HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME- KRGPAFVTTDDHDTVDKLVVQKYHTINGHNCEVKALS- AGSQRGGGGSGNFGGGGGNFGGRGG	AGGQK FVGWV FSAYN RRQVH
GPSGPSGPSTSSTSKSSSGSGNPTRK 6214 2 460 HELAPSAIRRARIGJGPARWGSRAAAFYFVRGFRTGWS VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKE YRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGV: IGQLYSTDKLIIENRDMPRT 6215 2 1849 FVAGGPRGSGSAAETWEIRVTPLGAGODVGRSCILVS: MLDCGMINGFNDDRRFPDFSYITQNGRLTDFLDCVIISE CGALPYPSEMVGYDGPIYMTHPTQAICPILLEDTKIAN ANFTSQMIKDCMKKVVAVHLHQTVQVDDELEIKAYYAK AMFQIKVGSESVVYTGDYNMTPDRHLGAAMIDKCRPNLI YARTIRDSKRCRERDFLKKVHETVERGKVLIPVFALGE ILLETFWERMIKVPIVFSTGLIFEKANHYYKLFIPWTRM FVORNMFEFKHIKAFDRAFADNPGPMVVFATPGMLHAGK RKWAGNEKNMVIMPGYCVOGTVGHKILSGORKLEMEGRK MQVEYMSFSAHADAKGIMQLVQQAEPESVLLVHGEAKKE KIEQELRVNCYMPANGETVTLDTSPSIPVGISLGLLKRI LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHK RVHLHDTRKQETALRVYSHLKSVLKDHCVQHLPPGSV- LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLLKKGLI GAHGEGSARMKTLITFVALPGVAVSMLNVYLKSHGI FIAYPHLRIRTKFPPWGDGNHTLFHNPHVNPLPTGYEDI GAHGEGSARMKTLITFVALPGVAVSMLNVYLKSHGI FIAYPHLRIRTKFPPWGDGNHTLFHNPHVPLPTGYEDI LRKLFIGGLSFFTTDDSLREHFEKWGTLTDCVVMRDPCY FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSRED HLTVKKIPVGGIKEDTEYNLRDYFEKYGKIETIEVME KRGPAFVTFDDHDTVDKLVVQKYHTINGHNCEVKKALSI AGSQRGGGGSGNFMGRGGNFGGRG GGSRGSYGGGDGGYNGFGGGGGNFGGRG	FVGWV FSAYN RRQVH
6214 2 460 HELAPSAIRRAARLGLGPARWGSRAAAFYFVRGFRTGWS VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKE YRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGVI IGQLYSTDKLIIENRDMPRT 6215 2 1849 FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVSI MLDCGMHMGFNDDRFPDFSYITQNGRLTDFLDCVIISE CGALPYFSEMVGYDGPIYMTHPTQAICPLLLEDYRKIAN ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELEIKAYYAK AMFQIKVGSESVVYTGDYMMTPDRHLGAAWIDKCRPNLI YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGE ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTNN FVQRNMFERKHIKAFDRAFADNPGPMVVFATPGMLHAGG RKWAGNEKNMVIMPGYCVOGTVGHKILSGQRKLEMEGRG MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKH KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKRI LPEAKKPRLHGTLIMKOSNFRLVSSEQALKBLGLAEHG RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLLKKGL GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGI FIAYPHLRIRTKFPFWGDMHTLFHNPHVNPLPTGYEDI LRKLFIGGLSFETTDDSLREHFEKMGTLTDCVVMRDPQ FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSRED HLTVKKIFVGGIKEDTEEYMLRDYFEKYGKIETIEVME KRGFAFVTFDDHDTVDKIVVQKYTINGHNCEVKKALS: AGSQRGGGGGSGNFMGRGGGFGGGGGNFGRGGNFGGGGGGGGGGGGGGGGG	FSAYN RRQVH
VLGTSAKRTRLFFFLSKMAASSRAQVLALYRAMLRESKE YRTYAVRRIRDAFRENKINVKOPVEIQTLVNKAKRDLGVI IGQLYSTDKLIIENDMPRT FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVS: MLDCGMHMGFNDDRRPPDFSYITQNGRLTDFLDCVIISE CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAN ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELEIKAYYAK AMFQIKVGSESVVYTGDYMTPDRHLGAAWIDKCRPNLI YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGE ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTM FVQRMMFEFKHIKAPPRAFADNPGPMVVFATPGMLHAG RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRG MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKE KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKRE LPEAKKPRLLHGTLIMKDSNFFLVSSEQALKBLGLAEH RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLLKKGL GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGE GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGE FIAYPHLRIRTKPFPMGDGNHTLFHNPHVNPLPTGYED LKKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSRED HLTVKKIFVGGIKEDTEFYNLRDYFEKYGKIETIEVME KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGRGG	FSAYN RRQVH
YRTYAVRRIRDAFRENKNVKDPVEIQTLVNKAKRDLGVI IGQLYSTDKLIIENRDMPRT FVAGGPRGSGAAETMPEIRVTPLGAGQDVGRSCILVS MLDCGMHMGFNDDGRFPDFSYITQNGRLTDFLDCVIISH CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAV ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELBIKAYYAG AMFQIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLI YATTIRDSKRCRERDFLKKVHETVERGGKVLIFVFALGI ILLETFWERMNLKVPIYFSTGLTBKANHYYKLFIPWTNG FVQRNMFEFKHIKAFDRAFADDMGPMVVFATPGMLHAGG RKWAGNEKNNVIMPGYCVQGTVGHKILSGQRKLEMEGRG MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKH KIEQELRVNCYMPANGETVTLFTSPSIPVGISLGLLKRN LPEAKKPRLHHGTLIMKDSNFRLVSSEQALKELGLAEHG RVHLHDTRKBQBTALRVYSHLKSVLKDHCVQHLPDGSV LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLI GAHGEEGSARWWKTLTFVALPGVAVSMLNVYLKSHGI FIAYPHLRIRTKFFPWGDGNHTLFHNPHVNPLPTGYEDI FIAYPHLRIRTKFFPWGDGNHTLFHNPHVNPLPTGYEDI LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ FGFVTYSCVEBVDAAMCARPHKVDGRVVEPKRAVSRED HLTVKKIFVGGIKEDTEYNLRDYFEKYGKIETIEVME KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGGGGGSGNFMGRGGGGGGGFGRGGRGGGGGGGGGGGGGGGGGGGGG	RRQVH
IGQLYSTDKLIIENRDMPRT FVAGGPRGSGSAAETMPETRVTPLGAGQDVGRSCILVS. MLDCGMHMGFNDDRFPDFSYITQNGRLTDFLDCVIISE CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAN ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELEIKAYYAG AMFQIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLI YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGI ILLETFWERMNLKVPIYFSTEJTEKANHYYKLFIPWTNG FVQRNMFEFKHIKAPDRAFADNPGPMVVFATPGMLHAGG RKWAGNEKNMVIMPGYCVGGTVGHKILSGQRKLEMEGRG MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKI KIEQELRVNCYMPANGETTTLPTSPSIPVGISLGLLKRI LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKBLGLAEHG RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLI GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGI FIAYPHLRIRTKFPWGDGNHTLFHNPHVNPLPTGYEDI GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGI FIAYPHLRIRTKFPWGDGNHTLFHNPHVNPLPTGYEDI LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ' FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSRED: HLTVKKIFVGGIKEDTEEYMLRDYFEKYGKIETIEVME KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGRGGGGGNFGRGGGFGGRGGGGGGGFGRGGGFGGRGGGGGGGG	
6215 2 1849 FVAGGPRGSGSAAETMPEIRVTPLGAGQDVGRSCILVS: MLDCGMHMGFNDDRRPDFSYITQNGRLTDFLDCVIISI CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRLIAV ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELBIKAYYAG AMFQIKVGSESVVYTGDYNMTPDRHLGAAMIDKCRPNLI YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGI ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTMG FVQRNMFEFKHIKAFDRAFADNBGPMVVFATPGMLHAGG RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRG MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKN KIEQELRVNCYMPANGETVTLPTSPSIPVGTSLGLLKRI RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV' LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLL RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV' LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLL GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGI GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGI FIAYPHLBIRTKPFFPMGGNHTLFHNPHVNPLPTGYED LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ' FGFVTYSCVEBVDAAMCARPHKVDGRVVEPKRAVSRED HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGGGGGGNFMGRGGNFGGGGGGNFGRGGNFGGGGGGGGGG	A CIVATO
MLDCGMHMGFNDDRRFPDFSYITQNGRLTDFLDCVIISI CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAV ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELBIKAYYAC AMFQIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLI YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGI ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTNC FVQRNMFEFKHIKAFDRAFADNPGPMVVFATPGMLHAGG RKWAGNEKNMVIMPGYCVQGTVGHKILLSGQRKLEMEGGK MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKN KIEQELRVNCYMPANGETVTLPTSPSIPVGTSLGLLKRI LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHC RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV* LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLL GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGI GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGI FIAYPHLRIRTKPFFPMGGNHTLFHNPHVNPLPTGYED LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ* FGFVTYSCVEBVDAAMCARPHKVDGRVVEPKRAVSRED HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME KRGPAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGRGGGSGNFMGRGGGTNGFGGGGTNFGRGGNFGGGGGGFGGGGNFGGGGGGGFGGGGNFGGGGGGGFGGGGNFGGGGGG	ACTIVITY
MLDCGMHMGFNDDRRFPDFSYITQNGRLTDFLDCVIISI CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAV ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELBIKAYYAC AMFQIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLI YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGI ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTNC FVQRNMFEFKHIKAFDRAFADNPGPMVVFATPGMLHAGG RKWAGNEKNMVIMPGYCVQGTVGHKILLSGQRKLEMEGGK MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKN KIEQELRVNCYMPANGETVTLPTSPSIPVGTSLGLLKRI LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHC RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV* LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLL GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGI GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGI FIAYPHLRIRTKPFFPMGGNHTLFHNPHVNPLPTGYED LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ* FGFVTYSCVEBVDAAMCARPHKVDGRVVEPKRAVSRED HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME KRGPAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGRGGGSGNFMGRGGGTNGFGGGGTNFGRGGNFGGGGGGFGGGGNFGGGGGGGFGGGGNFGGGGGGGFGGGGNFGGGGGG	nunu v
CGALPYFSEMVGYDGPIYMTHPTQAICPILLEDYRKIAN ANFFTSQMIKDCMKKVVAVHLHGTVQVDDBLBIKAYYAG AMFQIKVGSESVVYTGDYMTPDRHLGAAWIDKCRPNLI YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGI ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTNG FVQRNMPEFKHIKAFDRAFADNPGPMVVFATPGMLHAGG RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRI MQVEYMSFSAHADAKGIMQLVGQABPESVLLVHGEAKKI KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKRI LPEAKKPRLIHGTLIMKDSNFRLVSSEQALKELGLAEHG RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLI GAHGEGSARMKVLTFFVALPGVAVSMLNVYLKSHGJI GAHGEGSARMKVLTFFVALPGVAVSMLNVYLKSHGJI FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDI LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ FGFVTYSCVEBVDAAMCARPHKVDGRVVEPKRAVSRED HLTVKKIFVGGIKEDTESYNLRDYFEKYGKIETIEVME KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGGGGGGGGGGGGGGGG	FHLDH
ANFFTSQMIKDCMKKVVAVHLHQTVQVDDELBIKAYYAC AMFQIKVGSESVVYTGDYNMTPDRHLGAAWIDKCRPNLI YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGI ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTNG FVQRNMFEFKHIKAFDRAFADNPGPMVVFATFGMLHAGG RKWAGNEKNMVIMPGYCVQGTVGHKILSGORKLEMEGGK MQVEYMSFSAHADAKGIMQLVGQABPESVLLVHGEAKKI KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKRI LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEH RVHLHDTRKEQETALRVYSHLKSVLKKDHCVQHLPDGSVV LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLI GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGI GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGI FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDI LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ' FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSRED: HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEL KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGCNFGGGGGGGGGGGGGGGGGGGGG	
AMFQIKVGSESVYTGDYNMTPDRHLGAAWIDKCRPNLI YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGE ILLETFWERMILKVPIYFSTGLTEKANHYYKLFIPWTNG FVQRNMPEFKHIKAFDRAFADNPGPMVVFATPGMLHAGG RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRR MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKI KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKRI LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHG RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV: LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLLKKGLI GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGI FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDI 6217 9 1178 TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHD LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ' FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSRED: HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME: KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGRGGGSGNFMGRGGNFGGGGGFGRGCMFGRGGMFGGGGGFGGGGGFGGGGGFGGGGGFGGGGGFGGGGGFGGGG	
YATTIRDSKRCRERDFLKKVHETVERGGKVLIPVFALGI ILLETFWERMILKVPIYFSTGLTEKANHYYKLFIPWTM FVQRIMMEFKHIKAFDRAFADNPGPMVVFATPGMLHAGG RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRG MQVEYMSFSAHADAKGIMQLVGQABPESVLLVHGEAKKI KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKRI LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHG RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV LQAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLI GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGG FIAYPHLRIRTKPFFWGDGNHTLFHNPHVNPLPTGYED AGHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGG FIAYPHLRIRTKPFFWGDGNHTLFHNPHVNPLPTGYED LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ FGFVTYSCVEBVDAAMCARPHKVDGRVVEPKRAVSRED HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGCMFGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	TTPPOT
ILLETFWERMNLKVPIYFSTGLTEKANHYYKLFIPWTM FVQRNMFEFKHIKAFDRAFADNEGPMVVFATPGMLHAGG RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRG MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKN KIEQELRVNCYMPANGETVTLPTSPSIPVGTSLGLLKRI LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHG RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV LQAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLI GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGI FIAYPHLBIRTKPFPMGDGNHTLFHNPHVNPLPTGYEDI LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ FGFVTYSCVEBVDAAMCARPHKVDGRVVEPKRAVSRED HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEL KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGGGGGGGGGGGGGGGG	
FVQRNMFEFKHIKAFDRAFADNPGPMVVFATFGMLHAGG RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRG MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKI KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKRI LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHG RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV- LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLL GAHGEEGSARMWKTLTFFVALPGVAVSMLNYYLKSHGJI GAHGEEGSARMWKTLTFFVALPGVAVSMLNYLKSHGJI FIAYPHLRIRTKPFPMGGNHTLFHNPHVNPLPTGYEDI LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ- FGFVTYSCVEBVDAAMCARPHKVDCRVVEPKRAVSRED- HLTVKKIFVGGIKEDTESYNLRDYFEKYGKIETIEVMEL KRGPAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGGGGGGGGGGGGGGGG	
RKWAGNEKNMVIMPGYCVQGTVGHKILSGQRKLEMEGRC MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKI KIEQELRVNCYMPANGETVTLPTSPSIPVGTSLGLLKRI LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGAEHC RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV' LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLI 6216 11 393 QTTRPEPRNSALRQSRSKMAVVGVSSVSRLIGRSRPQLG GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGI FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDI LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ' FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDS HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEE KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGRGG	
MQVEYMSFSAHADAKGIMQLVGQAEPESVLLVHGEAKKI KIEQELRVNCYMPANGETVTLPTSPSIPVGTSLGLLKRI LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGAEHK RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSV' LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTTSLLKKGLI 6216 11 393 QTTRPEPRNSALRQSRSKMAVVGYSSVSRLIGRSRPQLI GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGI FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDI LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ' FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSRED KRGPAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGRGGGSGNFMGRGGNFGGGGNFGRGCNFGRGG	
KIEQELRVNCYMPANGETVTLPTSPSIPVGISLGLLKRI LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEH RVHLHDTRKEQETALRVYSHLKSVLKKDHCVQHLPDGSV LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLI 6216 11 393 QTTRPEPRNSALRQSRSKMAVVGVSSVSRLLGRSRPQLG GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGI FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDI 178 TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHD LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSRED HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGRGGGSGNFMGRGGNFGRGGNFGRGGNFGRGG GGSRGSYGGGDGGYNGFGGDGNYGGGPGYSSRGGYGG	VLEVK
LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHG RVHLHDTRKQETALRVYSHLKSVLKCHCVQHLPDGSV: LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLLKKGL: LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLKKGL: LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLKKGL: LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLKKGL: GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGG FIAYPHLRIRTKPFFPMGDGNHTLFHNPHVNPLPTGYED FIAYPHLRIRTKPFFPMGDGNHTLFHNPHVNPLPTGYED LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ' FGFVTYSCVEBVDAAMCARPHKVDCRVVEPKRAVSRED: HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME: KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGCNFGGGGGGGGGGGGGGGGGGGGG	EFLKQ
LPEAKKPRLLHGTLIMKDSNFRLVSSEQALKELGLAEHG RVHLHDTRKQETALRVYSHLKSVLKCHCVQHLPDGSV: LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLLKKGL: LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLKKGL: LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLKKGL: LQAAAPSEDPGTKVLLVSWTYQDEELGSFLTSLKKGL: GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHGG FIAYPHLRIRTKPFFPMGDGNHTLFHNPHVNPLPTGYED FIAYPHLRIRTKPFFPMGDGNHTLFHNPHVNPLPTGYED LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ' FGFVTYSCVEBVDAAMCARPHKVDCRVVEPKRAVSRED: HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME: KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGCNFGGGGGGGGGGGGGGGGGGGGG	MAQGL
RVHLHDTRKEQETALRVYSHLKSVLKDHCVQHLPDGSVL LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLL 6216 11 393 QTTRPEPRNSALRQSRSKMAVVGVSSVSRLLGRSRPQLG GAHGEEGSARMWKTLTFFVALDGVAVSMLNVYLKSHHGI FIAYPHLRIRTKPFPMGDGNHTLFHNPHVNPLPTGYEDI 178 TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHD LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ FGFVTYSCVEBVDAAMCARPHKVDCRVVEPKRAVSREDI HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVMEL KRGPAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGGGGGGGGGGGGGGGG	LRFTC
LQAAAPSEDPGTKVLLVSWTYQDEBLGSFLTSLLKKGLI 6216 11 393 QTTRPEPRNSALRQSRSKMAVVGYSSVSRLLGRSRPQLI GAHGEEGSARMKTLTFFVALPGVAVSMLNVYLKSHHGI FIAYPHLRITKFPFWGDGNHTLFHNPHVNPLPTGYEDI 6217 9 1178 TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHDI LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ' PGFVTYSCVEBVDAAMCARPHKVDGRVVEPKRAVSREDI HLTVKKIFVGGIKEDTESYNLRDYFEKYGKIETIEVME KRGPAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGGGGGGGGGGGGGGGG	VESVL
6216 11 393 QTTRPEPRNSALRQSRSKMAVVGVSSVSRLLGRSRPQLG GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGI FIAYPHLRIRTKPFPMGDGNHTLFHNPHVNPLPTGYEDI 6217 9 1178 TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHD LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ PGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDI HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME KRGPAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALSI AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGGG GGSRGSYGGGDGGYNGFGGDGNYGGGPGYSSRGGYGG	OAPS
GAHGEEGSARMWKTLTFFVALPGVAVSMLNVYLKSHHGI FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYEDI 6217 9 1178 TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHD LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ' PGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSREDG HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME KRGPAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGRG GGSRGSYGGGDGGYNGFGGDGGNYGGGPGYSSRGGYGG	PDMSS
FIAYPHLRIRTKPFPWGDGNHTLFHNPHVNPLPTGYED 6217 9 1178 TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHD LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ FGFVTYSCVEEVDAAMCARPHKVDGRVVEPKRAVSRED HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME KRGPAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGGGGSGNFMGRGGNFGGGGGNFGRGCNFGGRG GGSRGSYGGGDGGYNGFGGDGGNYGGGPGYSSRGGYGG	
6217 9 1178 TRVGRGESGLKMEVKPPPGRPQPDSGRRRRRGEEGHD LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ' FGFVTYSCVEEVDAAMCARPHKVDCRVVEPKRAVSRED: HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME: KRGFAFVTFDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGCNFGRGG GGSRGSYGGGDGGYNGFGGDGNYGGGPGYSSRGGYGG	
LRKLFIGGLSFETTDDSLREHFEKWGTLTDCVVMRDPQ' FGFVTYSCVEBVDAAMCARPHKVDCRVVEPKRAVSRED: HLTVKKIFVGGI KEDTEEYNLRDYFEKYGKIETIEVME: KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGRGGGGGGGGGGGGGGG	,
FGFVTYSCVEBVDAAMCARPHKVDGRVVEPKRAVSRED: HLTVKKIFVGGIKEDTEEYNLRDYFEKYGKIETIEVME: KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGRGGGGGGGGGGGGGG	
HLTVKKI FVGG I KEDTEE YNLRDYFE KYGKI ET I EVME KRGFAF VTFDDHDTVDKI VVQKYHTINGHNCE VKKALS AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGGGGGGGGGGGGGGGG	
KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGRGGGSGNFMGRGGNFGGGGGNFGGRGGGGGGGGGGGGGGGGGGGG	VKPGA
KRGFAFVTFDDHDTVDKIVVQKYHTINGHNCEVKKALS: AGSQRGRGGGSGNFMGRGGNFGGGGGNFGGRGGGGGGGGGGGGGGGGGGGG	RQSGK
AGSQRGRGGGSGNFMGRGGNFGGGGGNFGRGGNFGGRGGGGGGGGGGGGGG	QEMQS
GGSRGSYGGGDGGYNGFGGDGGNYGGGPGYSSRGGYGG	
NQGGGYGGGGGYDGYNEGGNYGGGGNYNDFGNY	
NGGGGGGGGTGTNBGGNTGGGNTANDGNTNBGNTANDGNTNBGNTNBGNTNBGNTNBGNTNBGNTNBGNTNBGNT	~****
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6218 1305 906 SCERRGFIMADDLKRFLYKKLPSVEGLHAIVVSDRDGV	VATUAN
NDNAPEHALRPGFLSTFALATDQGSKLGLSKNKSIICY	MITION
VQFNRLPLVVSFIASSSANTGLIVSLEKELAPLFEELR	144EA2
6219 2 890 AGPGEGAGAGTRCAGAEAEMASAGGEDCESPAPEADRP	IORPFL
IGVSGGTASGKSTVCEKIMELLGQNEVEQRQRKVVILS)DRFYK
VLTAEQKAKALKGQYNFDHPDAFDNDLMHRTLKNIVEG	CIVEAD
TYDFVTHSRLPETTVVYPADVVLFEGILVFYSQEIRDM	HLRLF
VDTDSDVRLSRRVLRDVRRGRDLEOILTQYTTFVKPAF	
TKKYADVIIPRGVDNMVAINLIVQHIQDILNGDICKWH	
RSYKRTFSEPGDHPGMLTSGKRSHLESSSRPH	
TO A STATE OF THE PARTY OF THE	זא. ז אַ יִידְּיוֹיִר
6220 227 764 EQNISLEMSCTIEKALADAKALVERURDHDDAAESLIE	(DEL VV
KRVEAMKQYQEEIQELNEVARHRPRSTLVMGIQQENRQ	
ENKELRTSLEEHQSALELIMSKYREQMFRLLMASKKDD	V17744
LKEQHSKIDMVHRNKSEGFFLDASRHILEAPQHGLERR	PGIIMK
NVH	PGIIMK
6221 98 916 RWIWDLNPVSDGLELRPKYNGILHCLTTIWKLDGLRGL	PGIIMK HLEANQ
NIWGAGLSWGLYFVFYNAIKSYKTEGRAERLEATEYLV	PGIIMK HLEANQ YQGVTP
AMTLCITNPLWVTKTRLMLQYDAVVNSPHRQYKGMFDT	PGIIMK HLEANQ YQGVTP SAAEAG
YEGVRGLYKGFVPGLFGTSHGALQFMAYELLKLKYNQH	PGIIMK HLEANQ YQGVTP SAAEAG
AQLSTVEYISVAALSKIFAVAATYPYQVVRARLQDQHM	PGIIMK HLEANQ YQGVTP SAAEAG LVKIYK
DVITKTWRKEGVGGFYKGIAPNLIRVTPACCITFVVYE	PGIIMK HLEANQ YQGVTP SAAEAG LVKIYK INRLPE
	PGIIMK HLEANQ YQGVTP SAAEAG LVKIYK INRLPE FYSGVI
LDLREKRK	PGIIMK HLEANQ YQGVTP SAAEAG LVKIYK INRLPE FYSGVI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:			H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ľ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
. 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6222	2	2116	MARELRALLLWGRRLRPLLRAPALAAVPGGKPILCPRRTTAQLG
	_		PRRNPAWSLOAGRLFSTOTAEDKEEPLHSIISSTESVQGSTSKH
ĺ			EFOAETKKLLDIVARSLYSEKEVFIRELISNASDALEKLRHKLV
1		ľ	SDGOALPEMEIHLQTNAEKGTITIQDTGIGMTQEELVSNLGTIA
. !		1	RSGSKAFLDALQNQAEASSKIIGQFGVGFYSAFMVADRVEVYSR
			SAAPGSLGYOWLSDGSGVFEIAEASGVRTGTKIIIHLKSDCKEF
1		ļ	1 ~
			SSEARVRDVVTKYSNFVSFPLYLNGRRMNTLQAIWMMDPKDVRE
!			WQHEEFYRYVAQAHDKPRYTLHYKTDAPLNIRSIFYVPDMKPSM
		1	FDVSRELGSSVALYSRKVLIQTKATDILPKWLRFIRGVVDSEDI
			PLNLSRELLQESALIRKLRDVLQQRLIKFFIDQSKKDAEKYAKF
		1	FEDYGLFMREGIVTATEQEVKEDIAKLLRYESSALPSGQLTSLS
			EYASRMRAGTRNIYYLCAPNRHLAEHSPYYEAMKKKDTEVLFCF
}	•	1	EOFDELTLLHLREFDKKKLISVETDIVVDHYKEEKFEDRSPAAE
			CLSEKETEELMAWMRNVLGSRVTNVKVTLRLDTHPAMVTVLEMG
		İ	AARHFLRMOOLAKTOEERAOLLOPTLEINPRHALIKKLNQLRAS
		1	EPGLAQLLVDQIYENAMIAAGLVDDPRAMVGRLNELLVKALERH
6223	3	715	DAWARTMAGMVDFQDEEQVKSFLENMEVECNYHCYHEKDPDGCY
			RLVDYLEGIRKNFDEAAKVLKFNCEENQHSDSCYKLGAYYVTGK
			GGLTQDLKAAARCFLMACEKPGKKSIAACHNVGLLAHDGQVNED
· 1		1	GQPDLGKARDYYTRACDGGYTSSCFNLSAMFLQGAPGFPKDMDL
1 1		1	ACKYSMKACDLGHIWACANASRMYKLGDGVDKVEAKAEVLKNRA
			QQVHKEQQKGVQPLTFG
6224	1	133	LRTISSMAWGPLLLTLLAHCTGSWAQSVLTQPPSVSGARIPHBK
6225	3259	938	LLSCHRLAICKLPFSVESRKTVMGPQGARRQAFLAFGDVTVDFT
			OKEWRLLSPAORALYREVTLENYSHLVSLGILHSKPELIRRLEQ
[Į.	GEVPWGEERRRRPGPCAGIYAEHVLRPKNLGLAHQRQQQLQFSD
1			QSFQSDTAEGQEKEKSTKPMAFSSPPLRHAVSSRRRNSVVEIES
į l			SQGQRENPTEIDKVLKGIENSRWGAFKCABRGQDFSRKMMVIIH
i			KKAHSRQKLFTCRECHQGFRDESALLLHQNTHTGEKSYVCSVCG
			RGFSLKANLLRHORTHSGEKPFLCKVCGRGYTSKSYLTVHERTH
i 1]	-
]	ļ	1	TGEKPYECQECGRRFNDKSSYNKHLKAHSGEKPFVCKECGRGYT
1		1	NKSYFVVHKRIHSGEKPYRCQECGRGFSNKSHLITHQRTHSGEK
		į.	PFACRQCKQSFSVKGSLLRHQRTHSGEKPFVCKDCERSFSQKST
		1	LVYHQRTHSGEKPFVCRECGQGFIQKSTLVKHQITHSEEKPFVC
	1	ł	KDCGRGFIQKSTFTLHQRTHSEEKPYGCRECGRRFRDKSSYNKH
ļ			
1			LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE
ł			LRAHLGEKRFFCRDCGRGFTLKPNLTIHQRTHSGEKPFMCKQCE KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH
		į į	
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN
6226	70	266	KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS
6226	29	266	KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHORTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLBEKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA
6226	29	266 890	KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHORTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHORTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLECRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLECRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHQRTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFQQPGALGSTPFLQQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHORTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQBCKRGYTSKSDLTVHERIHTGERPYBCQBCGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLQQHGFNFPPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDCGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHORTHSGEKPFVCNVCGQGFSWKRSLTRHMRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLQQHGFNFFPSGIDFS AWGNNSSQGQSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPQPAQLSVQQQAAQPTRWV
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHORTHSGEKPFVCNVCGQGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLQQHGFNFFPSGIDFS AWGNNSSQGGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVYVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHORTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVYVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHORTHSGEKPFVCNVCQGGFSWKRSLTRHHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLBEKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLLECRPKGGGNKVQNGSVHQKDGLNDDDFEFYLSPQARP NNAYTAMSDSYLPSYYSFSIGFSYSLGEAMSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVPKVVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPFIKHNMDIGTWDNKGFVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPQPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK RLDAAYRSMNGKGPVYLLFSVNGSGHFCGVAEMKSAVDYNTCAG
			KSFSLKANLLRHQWTHSGERPFNCKDCGRGFILKSTLLFHQKTH SGEKPFICSECGQGFIWKSNLVKHQLAHSGKQPFVCKECGRGFN WKGNLLTHORTHSGEKPFVCNVCGQGFSWKRSLTRHWRIHSKE KPFVCQECKRGYTSKSDLTVHERIHTGERPYECQECGRKFSNKS YYSKHLKRHLREKRFCTGSVGEASS TKVSELLGGSQRLFFLPLWRRLCRCGLGPRVSPMAGPRVEVDGS IMEGGGQSLRVSTGLSWLLSLPWRAQRIRAGRSYA MSASSLEQRPKGQGNKVQNGSVHQKDGLNDDDFEPYLSPQARP NNAYTAMSDSYLPSYYSPSIGFSYSLGEAAWSTGGDTAMPYLTS YGQLSNGEPHFLPDAMFGQPGALGSTPFLGQHGFNFFPSGIDFS AWGNNSSQGGSTQSSGYSSNYAYAPSSLGGAMIDGQSAFANETL NKAPGMNTIDQGMAALKLGSTEVASNVYVGSAVGSGSITSNI VASNSLPPATIAPPKPASWADIASKPAKQQPKLKTKNGIAGSSL PPPPIKHNMDIGTWDNKGPVAKAPSQALVQNIGQPTQGSPQPVG QQANNSPPVAQASVGQQTQPLPPPPPPPAQLSVQQQAAQPTRWV APRNRGSGFGHNGVDGNGVGQSQAGSGSTPSEPHPVLEKLRSIN NYNPKDFDWNLKHGRVFIIKSYSEDDIHRSIKYNIWCSTEHGNK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
}	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\-possible nucleotide insertion)
6228	47	1978	GRRCRRGAVMELAQEARBLGCWAVEEMGVPVAARAPESTLRRL
]			CLGQGADIWAYILQHVHSQRTVKKIRGNLLWYGHQDSPQVRRKL
			ELEAAVTRIRAEIQELDQSLELMERDTEAQDTAMEQARQHTQDT
1			QRRALLLRAQAGAMRRQQHTLRDPMQRLQNQLRRLQDMERKAKV
			DVTFGSLTSAALGLEPVVLRDVRTACTLRAQFLQNLLLPQAKRG
			SLPTPHDDHFGTSYQQWLSSVETLLTNHPPGHVLAALEHLAAER
		1	EAEIRSLCSGDGLGDTEISRPQAPDQSDSSQTLPSMVHLIQEGW
			RTVGVLVSQRSTLLKERQVLTQRLQGLVEEVERRVLGSSERQVL
			ILGLRRCCLWTELKALHDQSQELQDAAGHRQLLLRELQAKQQRI
1			LHWRQLVEETQEQVRLLIKGNSASKTRLCRSPGEVLALVQRKVV
			PTFEAVAPQSRELLRCLEEEVRHLPHILLGTLLRHRPGELKPLP
			TVLPSIHQLHPASPRGSSFIALSHKLGLPPGKASELLLPAAASL
1			RQDLLLLQDQRSLWCWDLLHMKTSLPPGLPTQELLQIQASQEKQ
			QKENLGQALKRLEKLLKQALERIPELQGIVGDWWEQPGQAALSE
	:		ELCQGLSLPQWRLRWVQAQGALQKLCS
6229	1571	560	GPSLLGTRGTPNPARTLQIFFLIIGRRLTGRMAAVDDLQFEEFG
			NAATSLTANPDATTVNIEDPGETPKHQPGSPRGSGREEDDELLG
			NDDSDKTELLAGQKKSSPFWTFEYYQTFFDVDTYQVFDRIKGSL
1			LPIPGKNFVRLYIRSNPDLYGPFWICATLVFAIAISGNLSNFLI
			HLGEKTYHYVPEFRKVSIAATIIYAYAWLVPLALWGFLMWRNSK
			VMNIVSYSFLEIVCVYGYSLFIYIPTAILWIIPHKAVRWILVMI
			ALGISGSLLAMTFWPAVREDNRRVALATIVTIVLLHMLLSVGCL
	_		AYFFDAPEMDHLPTTTATPNQTVAAAKSS
6230	1723	600	SKMSGRSGKKKMSKLSRSARAGVIFPVGRLMRYLKKGTFKYRIS
			VGAPVYMAAVIEYLAAEILELAGNAARDNKKARIAPRHILLAVA
1			NDEELNQLLKGVTIASGGVLPRIHPELLAKKRGTKGKSETILSP
			PPEKRGRKATSGKKGGKKSKAAKPRTSKKSKPKDSDKEGTSNST
			SEDGPGDGFTILSSKSLVLGQKLSLTQSDISHIGSMRVEGIVHP
			TTAEIDLKEDIGKALEKAGGKEFLETVKELRKSQGPLEVAEAAV
İ			SQSSGLAAKFVIHCHIPQWGSDKCEEQLEETIKNCLSAAEDKKL
			KSVAFPPFPSGRNCFPKQTAAQVTLKAISAHFDDSSASSLKNVY
			FLLFDSESIGIYVQEMAKLDAK
6231	149	870	LIFSSSTMDRSLRNVLVVSFGFLLLFTAYGGLQSLQSSLYSEEG
i			LGVTALSTLYGGMLLSSMFLPPLLIERLGCKGTIILSMCGYVAF SVGNFFASWYTLIPTSILLGLGAAPLWSAQCTYLTITGNTHAEK
l .			AGKRGKDMVNQYFGIFFLIFQSSGVWGNLISSLVFGQTPSQETL
			PEEOLTSCGASDCLMATTTTNSTORPSOOLVYTLLGIYTGSGVL
1	1		AVLMIAAFLQPIRDVQRESE
6232	3679	1476	FVAGTTMAGFWVGTAPLVAAGRRGRWPPQQLMLSAALRTLKHVL
0232	3375	1 11/0	YYSROCLMVSRNLGSVGYDPNEKTFDKILVANRGEIACRVIRTC
			KKMGIKTVAIHSDVDASSVHVKMADEAVCVGPAPTSKSYLNMDA
1			IMEAIKKTRAQAVHPGYGFLSENKEFARCLAAEDVVFIGPDTHA
1			IOAMGDKIESKLLAKKAEVNTIPGFDGVVKDAEEAVRIAREIGY
			PVMIKASAGGGGKGMRIAWDDEETRDGFRLSSQEAASSFGDDRL
			LIEKFIDNPRHIEIQVLGDKHGNALWLNERECSIQRRNQKVVEE
1			APSIFLDAETRRAMGEQAVALARAVKYSSAGTVEFLVDSKKNFY
İ			FLEMNTRLQVEHPVTECITGLDLVQEMIRVAKGYPLRHKQADIR
		Į	INGWAVECRVYAEDPYKSFGLPSIGRLSQYQEPLHLPGVRVDSG
		i	IQPGSDISIYYDPMISKLITYGSDRTEALKRMADALDNYVIRGV
ľ			THNIALLREVIINSRFVKGDISTKFLSDVYPDGFKGHMLTKSEK
			NOLLAIASSLFVAFOLRAOHFOENSRMPVIKPDIANWELSVKLH
	1		DKVHTVVASNNGSVFSVEVDGSKLNVTSTWNLASPLLSVSVDGT
1			QRTVQCLSREAGGNMSIQFLGTVYKVNILTRLAAELNKFMLEKV
1	1		TEDTSSVLRSPMPGVVVAVSVKPGDAVAEGQEICVIEAMKMQNS
1 .	1		MTAGKTGTVKSVHCQAGDTVGEGDLLVELE
6233	1	2654	HSTRENLNAGNPNFPSEGHLVRSTGPGGSFAKHMVAQCVSPKGP
<u> </u>			A CONTRACTOR OF THE PROPERTY O

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
l			Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	1
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	 		LACSRTYFFGATHVPYLGGDSKLPKKTEQIRLLSQIYAAVIEAV
ł		1	LAGIACYAKTSSLTKAKEVAEQTLGSGLDSFELIPFKAALRSKM
ļ	i	{	TFHIHAVNNQGRIVPLDSEDSLSFVKTACMAVYDIPDLLGGNGC
1			LGSVVFSESFLTSQILVKEKDGTVTTETSSVVLTAAVPRFCSWL
-	1		VEDNEVKLSEKTHOAVRGDESFLGTYLTGGEGAYLYSSNLOSWP
į	}	l .	
	1	1	EEGNVHFFSSGLLFSHCRHGSIIISKDHMNSISFYDGDSTSTVA
	1	ľ	ALLIDFKSSLLPHLPVHFHGSSNFLMIALFPKSKIYQAFYSEVF
	1		SLWKQQDNSGISLKVIQEDGLSVEQKRLHSSAQKLFSALSQPAG
		!	EKRSSLKLLSAKLPELDWFLQHFAISSISQEPVMRTHLPVLLQQ
			AEINTTHRIESDKVIISIVTGLPGCHASELCAFLVTLHKECGRW
			MVYRQIMDSSECFHAAHFQRYLSSALEAQQNRSARQSAYIRKKT
	1		RLLVVLQGYTDVIDVVQALQTHPDSNVKASFTIGAITACVEPMS
·		-	CYMEHRFLFPKCLDQCSQGLVSNVVFTSHTTEQRHPLLVQLQSL
			IRAANPAAAFILAENGIVTRNEDIELILSENSFSSPEMLRSRYL
}	1		MYPGWYEGKLNAGSVYPLMVQICVWFGRPLEKTRFVAKCKAIQS
			SIKPSPFSGNIYHILGKVKFSDSERTMEVCYNTLANSLSIMPVL
			EGPTPPPDSKSVSQDSSGQQECYLVFIGCSLKEDSIKDWLRQSA
}			KOKPORKALKTRGMLTQOEIRSIHVKRHLEPLPAGYFYNGTOFV
			NFFGDKTDFHPLMDQFMNDYVEEANREIEKYNQELEQQEYHDLF
	1		ETKb
6234	1731	404	PRVREDMDHKSPGNKGSLVYAGIKSIVKSSLGMVESSRHNWSGL
			DKQSDIQNLNEERILALQLCGWIKKGTDVDVGPFLNSLVQEGEW
	1	1	ERAAAVALFNLDIRRAIQILNEGASSEKGDLNLNVVAMALSGYT
(DEKNSLWREMCSTLRLQLNNPYLCVMFAFLTSETGSYDGVLYEN
ĺ		1	KVAVRDRVAFACKFLSDTQLNRYIEKLTNEMKEAGNLEGILLTG
	1		LTKDGVDLMESYVDRTGDVQTASYCMLQGSPLDVLKDERVQYWI
ļ			ENYRNLLDAWRFWHKRAEFDIHRSKLDPSSKPLAQVFVSCNFCG
Ì			KSISYSCSAVPHQGRGFSQYGVSGSPTKSKVTSCPGCRKPLPRC
		1	ALCLINMGTPVSSCPGGTKSDEKVDLSKDKKLAQFNNWFTWCHN
Į			CRHGGHAGHMLSWFRDHAECPVSACTCKCMQLDTTGNLVPAETV
i			OP
6235	 1	571	EKRDHRLPSWPRAALKVPGRGGRVGTTPELAAGGIMATRNPPPO
0235	+	3/1	DYESDDDSYEVLDLTEYARRHQWWNRVFGHSSGPMVEKYSVATQ
	1		-
			IVMGGVTGWCAGFLFQKVGKLAATAVGGGFLLLQIASHSGYVQI
1			DWKRVEKDVNKAKRQIKKRANKAAPEINNLIEEATEFIKQNIVI
			SSGFVGGFLLGLAS
6236	1	703	WDQNKGAAAGSGLTLPSLPSARFSAGPPTQRSRPTMSNMEKHLF
			NLKFAAKELSRSAKKCDKEEKAEKAKIKKAIQKGNMEVARIHAE
1			NAIRQKNQAVNFLRMSARVDAVAARVQTAVTMGKVTKSMAGVVK
			SMDATLKTMNLEKISALMDKFBHQFETLDVQTQQMEDTMSSTTT
			LTTPQNQVDMLLQEMADEAGLDLNMELPQGQTGSVGTSVASAEQ
	<u>†</u>		DELSQRLARLRDQV
6237	312	720	PTAMAEEGIAAGGVMDVNTALOBVLKTALIHDGLARGIREAAKA
1 5257	3,2	1	LDKROAHLCVLASNCDEPMYVKLVEALCABHOINLIKVDDNKKL
[GEWVGLCKIDREGKPRKVVGCSCVVVKDYGKESOAKDVIEEYFK
			-
		1555	CKK ERVPTOESVKWEINVIIKNPEIVFVADMTKNDAPALVITTOCEI
6238	2	4666	
			CYKGNLENSTMTAAIKDLQVRACPFLPVKRKGKITTVLQPCDLF
			YQTTQKGTDPQVIDMSVKSLTLKVSPVIINTMITITSALYTTKE
}			TIPEETASSTAHLWEKKDTKTLKMWFLEESNETEKIAPTTELVP
1			KGEMIKMNIDSIFIVLEAGIGHRTVPMLLAKSRFSGEGKNWSSL
			INLHCQLELEVHYYNEMFGVWEPLLEPLEIDQTEDFRPWNLGIK
			MKKKAKMAIVESDPEEENYKVPEYKTVISFHSKDQLNITLSKCG
			LVMLNNLVKAFTEAATGSSADFVKDLAPFMILNSLGLTISVSPS
	1	1	•
1			DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK
			DSFSVLNIPMAKSYVLKNGESLSMDYIRTKDNDHFNAMTSLSSK LFFILLTPVNHSTADKIPLTKVGRRLYTVRHRESGVERSIVCOI

ID	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Cortesponding Cofirst amino acid residue of amino acid residue of amino acid ami	ID	beginning	nucleotide	
Cortesponding Cofirst amino acid residue of amino acid residue of amino acid ami	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
corresponding to first amino acid residue of residue of amino acid residue of amino acid sequence service of amino acid sequence service of amino acid sequence seque		location	corresponding	
to first amino acid am		corresponding	to first	
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ABVTENTEVELPHKOLEAFKEBYKTASLUDQSQVSLYEYPHISP IKLHLSVSLSSGREEAKDSKQNGGLIPVHSLINLLIKSIGATLIN VQDVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLIL GLDVLGNPFGLIREFSEGVEAPPYBPYQGAIQGPEEFVEGMALG LKALVGGAVGGLAGAASKITGAMAKGVAAMTMDEDYQQKRREAM NKQPAGFREGITRGOKGLVSGFVSGITGIVTHPIKGAQKGAAG FFKGVGKGLVGAVARPTGGIIDMASSTPQGIRRATETSEVESLR PPRFFNEDGVIRPYRLRGGTGNQMLQKLQFYREMIMTHSSSSDD DDDDDDDDEDDEDLNH 6239 2108 634 KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTLGPVVLAVFSSPAVYVL SLLEMSKFYSGLIVGRVUGGUFFGLWTLQKEVRHFGAMVATM FCWVTAMQPHLMFYCTRTLPNVLALDRVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCHFIGLLLLLALGRKXVSVVRALRHAVPAGG ILCIGLTVAVDSYFWQGITWPEGKVLWYNTVLNKSSNMSTSFLL WYFYSALPRGLGCSLLFIPLGLUDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLWNYKKSMYKAGSLLVI GHLVVNAAYSATALVVSHFNYPGGVAMQRLQLVPPQTOVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSTRSSGTTTSTXKSLANQ TRNGSLSYDSLITPSDSDFESVQAGPBEPDPLGYTSPPLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLGREEEPGLGDSGTQSTPSGGHAPTTSSSSDDSKRSP GLGKTPLGRPRSVPRFGKFDGVGRGVGSPEPGCPTAPYLGRSMSYS GQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNQCPKSLGS ASPGPGGPFLSSPTRGGVKKVSGVGGTTTEISV RNAEEKKELSLQREKILARVSIDNRTRALVQALRRTTDPKLCIT RVEELTHLLEFPEGKGVAVKERIIPYLLRLRQIKDETIQAAVR EILALIGVVDPVKGRGIRILSIDGGGTGGVADLGTLRKLVGLTQ KPUHQLFDYICGVSTGAILAFMLGLFHMPLDECEBLYRKLGSDV FSQNVIVGTVKNSNSHAFYDSQTMENILKRDMGSALMIETARNP	1		ļ	SFRIQIYRIQIQNQIHGAVFPFVFYPVKPPKSVTMDSAPKPFTD
IKLHLSVSLSSGREAKDSKONGGLIPVHSLNLLLKSIGATLTD VQDVVFKLAFFELNYGFHTTSDLQSEVTRHYSKQAIKOMYVLIL GLDVLGNPGLIREFSEGVEAPPYEPYGGAIQGEPEPYEGMALG LKALVGGAVGGLAGASKITGAMAKGVAAMTMDEDYQQKRREAM NKQPAGFREGITRGGGLVSGFVYSGITGITVTKPIKGAQKGGAGA FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGIDMASSTFGGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNOMLQKIQFYREMIMTHSSSSDD DDDDDDDDDBDEDDLNH 6239 2108 634 KPGMAGKGSSGRRPLLIGLLVAVATVHLVICPYTKVEESFNLQA THDLLYHMQDLEQYDHLEFPGVVPRTFLGEVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGGVIFGLWTLQKEVRRHFGAMWATM FCWVTAMQPHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAITVFRVELCLIFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGUVDRRTHAFTVLALGFWALVSLL PHKELRFIIJAFPMLNITAARGCSYLLMYKKSSLLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVASAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSVDSLLTPSDSPDFESVQAGPEPPPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEERKL LRQSPPLPGREEEPGLGDSGIGSTPGSGHAPRTSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGPPLSSFTRGGVKKVSGGTTYEISV GKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGPPLSSFTRGGVKKVSGGTTYEISV FVMELTFHLLEFPEGKGVAVKERIIPYLLRRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIGOGGTRGVVALQTLRRLVSLTQ KPUHQLFPYLCGVSTGAILAFMIGLEFHMPLDECEBLYRKLGSDV FSQNVIVGTVKNSWSHAFYDSQTWENILKDRMGSALMIETARNF	, ,			VSIVMRSAGHSQISRIKYFKVLIQEMDLRLDLGFIYALTDLMTE
VQDVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLIL GLDVLIGNPFGLITREFSEGVEAFFYEPYGAIQGEEFVEGMALG LKALVGGAVGGLAGAASKITGAMAKGWAMTMDEDYQQKRREMA NKQPAGFREGITRGGKGLVSGFVSGITGIVTKPIKGAQKGGAAG FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR PPRFFNEDGVIRPYRLBGDTGNMALQKIQFYREWIMTHSSSSDD DDDDDDDDDDDDDDDDDDDDDDDDDDDDLNH 6239 2108 634 KPGMAGKGSSGRFPLLLGLLVAVATVHLVICPYTKVEESFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVLAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQPHLMFYCTRTJPNVLALPVVLLALAAMLRHEWARFI WLSAPAIIVHTVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPBGKVLWYNTVLNRSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLUDRRTHAFTVLALGFMALVSLL PHKELRFIIYAFFMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALTVSHNYPGGVAMQRLHQLVPPGTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKSPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFLQQLQSIRSEGTTTSTYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGFEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRVDNLSRHIVASLQEREKL LRQSPPLPGREEPGLGDSGIQSTPGSGHAPRTSSSSDDSRRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGGQPPLSSPTRGGVKKVSGVGGTTYSLSV 6241 3 1341 RNAEEKKRLSLQREKI LARVSIDNFTRALVQALRETTOPKLCIT RVEBLTFHLLEFPEGKGVAVKERIIPYLLRRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDOGGTGGVAALQTLRRLVSLTQ KPUHQLFDYICGVSTGAILAFMIGLEFHMPLDECEBLYRKLGSDV FSQNVIVGTVKNSWSHARFVDSQTWENILKDRMGSALMIETARNF				AEVTENTEVELFHKDIEAFKEEYKTASLVDQSQVSLYEYFHISP
GLDVLGNPFGLIREFSEGVEAFPYEPYQGAIQGPEEFVEGMALG LKALVGGAVGGLACAASKI TGAMAKGVAAMTMDEDYQQKRREAM NKQPAGFREGITRGSKGLVSGFVSGITGIVTKPI KGAQKGGAAG PFKGVGKGLVGAVARPTGGIIDMASSTPQGIKRATETSEVESLR PPRFFPEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD			ļ	IKLHLSVSLSSGREEAKDSKQNGGLIPVHSLNLLLKSIGATLTD
LKALVGGAVGGLAGAASKITGAMAKGVAAMTMDEDYQQKRREAM NKQPAGFRBGITRAGKGLVSGFVSGITGIVTKPIKGAQKGGAAG FFKGVGKGUVGAVARPTGGIIDMASSTPQGIKRATETSEVESLR PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDBBSDLNH 6239 2108 634 KFGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVLAVFSSPAVYVL SLLEMSKFYSQLIVRGVIGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQPHLMFYCTRTLPMVLALPVVLLALAAMLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTHPEGKVLWYMTVLINKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFFMIANITAARGSYLLNNYKKSWLYKAGSLLVI GHLVVMAAVSATALVSHFNVPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRVDKREDVQRGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFSSVQAGPBEDPPJGTTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGTQSTBGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNQQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV 6241 3 1341 RNAEEKKRLSLQREKITARVSIDNSTRALVQALRRTTDPKLCIT RVEBLTFHLLEFPEGKGVAVKERIIPYLLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLIKKUPLITQ KPVHQLFDYICGVSTGALAFMLGLFHMPLDECEBELFRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP				VQDVVFKLAFFELNYQFHTTSDLQSEVIRHYSKQAIKQMYVLIL
NKQPAGFREGITRGKKGLVSGFVSGITGIVTKPIKGAQKGGAAG FFKKVCKGLVGAVARPTGGIIMASSTFQGIKRATETSEVESLR PPRFPEDGUTRYRPDEGUTRYRDGTGNQMLQKIQFYREWIMTHSSSDD DDDDDDDDDDDDDDDDLNH 6239 2108 634 KPGMAGKGSSGRPLLLGLLVAVATVHLVICPYTKVEESFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVLAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGYIFGLWTLQKEVRRHFGAMVATM FCWVTAMQPHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFIGLLLLLALGRKKVSVVRALRHAVPAG ILCLGLTVAVDSYPWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFTPLGLUDRRTHAPTVLALGFMALYSLL PHKELRFIIVAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVONSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPSPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEERKL LRQSPPLPGREEEPGLGDSGIGSTPGSGHAPRTSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSSTEEVALQPLLTPRDEVQLKTTYSKSNQPKSLGS ASPGPQDPLSSPTRGVKVSGVGGTTYEISV 6241 3 1341 RNAEEKKRLSLQRSKILARVSIDNRTRALVQALRRTTDPKLCIT RVEBLTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLPTYLGGVSTGAILAFMLGIFMMPLDECEBLYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP				GLDVLGNPFGLIREFSEGVEAFFYEPYQGAIQGPEEFVEGMALG
FFKGVGKGLVGAVARPTGGIIDMASSTPGGIKRATETSEVESLR PPRFFPEDGGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDESDLNH 6239 2108 634 KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVLAVPSSPAVYVL SLLEMSKFYSQLIVRGVLGGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQPHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCHFLGLLLLLALGRRKKYSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLINKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLUDRRTHAPTVLALGFMALYSLL PHKELRFIIVAFPMLNITARAGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSFFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPPRS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTOFELGGLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPFSVQAGPEPPPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQREEKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGFTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDBVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGVKKVSGVGGTTYEISV 6241 3 1341 RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEBLTFHLLEFPBGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYDVDVKGRGIRILISLDGGGTRGVVALQTLRKLVELTQ KPVHQLFTYLGVSTGAILAFMLGLFFMPLDECEBLYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRRGSALMIETARNP				LKALVGGAVGGLAGAASKITGAMAKGVAAMTMDEDYQQKRREAM
PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD	1			NKQPAGFREGITRGGKGLVSGFVSGITGIVTKPIKGAQKGGAAG
DDDDDDDESDLNH 6239 2108 634 KPGMAGKGSSGRPPLLIGLUAVATVHLVICPYTKVEESFNLQA THDLLYHWQDLQYDHLEFPGVVPRTFIGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVIGLGVIFGLWTLQKEVRHIFGAMYATM FCWVTAMQPHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLIFLIGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFMRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGIGGSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVMAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELQQLQSIRSEGTTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPPLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFFGKPDGLRGGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPQPPLSSPTRGGVKKVSGVGGTTTYEISV 6241 3 1341 RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEBLTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKKRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEBLYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP				FFKGVGKGLVGAVARPTGGIIDMASSTFQGIKRATETSEVESLR
6239 2108 634 KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVLAVFSSPAVYVL SLLEMSKFYSQLIVRGYUGLGVJFGLWTTQKEVRRHFGAMVATM FCWVTAMQPHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGRRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAPPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLHH DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETTEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV 6241 3 1341 RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEBLTFHLLEFPEGKCVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEBLYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP				PPRFFNEDGVIRPYRLRDGTGNQMLQKIQFYREWIMTHSSSSDD
THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVIALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLALGNRKVSVVRALRHAVPAG ILCGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGGSLLFIFLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNNAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGFTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV 6241 3 1341 RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVV EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICCVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP	j .			DDDDDDDDESDLNH
SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCFLGLLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGGSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGFTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDBVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV 6241 3 1341 RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGTRGVVALQTLRKLVELTQ KPVHQLFDYICCVSTGAILAFMLGLFHMPLDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP	6239	2108	634	KPGMAGKGSSGRRPLLLGLLVAVATVHLVICPYTKVEESFNLQA
FCWVTAMQPHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPECKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALZVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKVGSVGGTTTEISV 6241 3 1341 RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEBLYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP				THDLLYHWQDLEQYDHLEFPGVVPRTFLGPVVIAVFSSPAVYVL
WLSAFAIIVFRVELCLFLGLLLLALGNRKVSVVRALRHAVPAG ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSILFIPLGLVDRRTHAPTVLALGFWALLYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLGSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGLQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKVSGVGGTTTEISV 6241 3 1341 RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMELDECEBLYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP				SLLEMSKFYSQLIVRGVLGLGVIFGLWTLQKEVRRHFGAMVATM
ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFI I YAFPMLNI TAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAQTGVSRFLQVNSAWRYDKREDVQDGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQS IRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKVSGVGGTTTEISV 6241 3 1341 RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMELDECBELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP	[FCWVTAMQFHLMFYCTRTLPNVLALPVVLLALAAWLRHEWARFI
WYFYSALPRGLGCSLLFIPLGLVDRRTHAPTVLALGFMALYSLL PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALTVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPPNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPBEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV 6241 3 1341 RNAEEKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMELDECBELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP				WLSAFAIIVFRVELCLFLGLLLLLALGNRKVSVVRALRHAVPAG
PHKELRFIIYAFPMLNITAARGCSYLLNNYKKSWLYKAGSLLVI GHLVVNAAYSATALVSHFNYPGGVAMQRLHQLVPPQTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV 6241 3 1341 RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMELDECEELYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP				ILCLGLTVAVDSYFWRQLTWPEGKVLWYNTVLNKSSNWGTSPLL
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GHLVVNAAYSATALYVSHFNYPGGVAMQRLHQLVPPQTTDVLLHI DVAAAQTGVSRFLQVNSAWRYDKREDVQPGTGMLAYTHILMEAA PGLLALYRDTHRVLASVVGTTGVSLNLTQLPPFNVHLQTKLVLL ERLPRPS 6240 2202 1176 HERGDSLKEPTSIAESSRHPSYRSEPSLEPESFRSPTFGKSFHF DPLSSGSRSSSLKSAQGTGFELGQLQSIRSEGTTSTSYKSLANQ TRNGSLSYDSLLTPSDSPDFESVQAGPPEPDPPLGYTSPFLSARL AQQREAERHPRLVPTGPTHREPSPVRYDNLSRHIVASLQEREKL LRQSPPLPGREEEPGLGDSGIQSTPGSGHAPRTSSSSDDSKRSP LGKTPLGRPAVPRFGKPDGLRGRGVGSPEPGPTAPYLGRSMSYS SQKAQPGVSETEEVALQPLLTPKDEVQLKTTYSKSNGQPKSLGS ASPGPGQPPLSSPTRGGVKKVSGVGGTTYEISV RNAEEKKRLSLQREKIIARVSIDNRTRALVQALRRTTDPKLCIT RVEELTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEBLYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP				
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RVEBLTFHLLEFPEGKGVAVKERIIPYLLRLRQIKDETLQAAVR EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEBLYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP	6241	2 -	1341	
EILALIGYVDPVKGRGIRILSIDGGGTRGVVALQTLRKLVELTQ KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEBLYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP	7271	1		
KPVHQLFDYICGVSTGAILAFMLGLFHMPLDECEBLYRKLGSDV FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP				
FSQNVIVGTVKMSWSHAFYDSQTWENILKDRMGSALMIETARNP				
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WQAIRASSAAPGYFAEYALGNDLHQDGGLLLNNPSALAMHECKC	1	1		
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TEEVHIMLDGLLPPDTYFRFNPVMCENIPLDESRNEKLDQLQLE		1		
GLKYİERNEQKMKKVAKILSQEKTTLQKINDWİKLKTDMYEGLP	L	<u> </u>	L	GUNITERNEGNMEKVAKILSGEKTTLGKINDWIKUKTDMYEGLP

CEO	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	1	sequence	\=possible nucleotide insertion)
	sequence		· · · · · · · · · · · · · · · · · · ·
		L	FFSKL
6242	198	1310	QHFLPGAETWSPGAAVCTARRFPGRSLAAFPRPAAPRRAVEMGE
			SSEDIDQMFSTLLGEMDLLTQSLGVDTLPPPDPNPPRAEFNYSV
		1	GFKDLNESLNALEDQDLDALMADLVADISEAEQRTIQAQKESLQ
		1	NOHHSASLQASIFSGAASLGYGTNVAATGISQYEDDLPPPPADP
	1		VLDLPLPPPPPPEPLSQEEEEAQAKADKIKLALEKLKBAKVKKLV
		1	VKVHMNDNSTKSLMVDERQLARDVLDNLFEKTHCDCNVDWCLYE
	1		IYPELQIERFFEDHENVVEVLSDWTRDTENKILFLEKEEKYAVF
		1	
Ì	ł	1	KNPQNFYLDNRGKKESKETNEKMNAKNKESLLEVRLILQSGRKE
ļ			KDVCSIFKSFASENNGKI
6243	1509	614	RSASRFSGCWSRDSTCCCCPSTCWSRSSASCPRARWPPSSAPAT
			TSRASSRRLACGPQTRAGAETRSTAMIRANSAARDTRRATCRSA
	1	1	AGTPSPTTMTCLTDVPTGCAAVEPTARLPAAAWASTITTGCCPA
	1	1	MGQAGAGPAGRKGSEAGGGPGRAHHAHPSPLPREPRVRTGPPAH
1	1		SPTPGSIDPSPELSWGSAGVTQESPLLDPVDFLLFRTRAVDPLR
			RVFFFFYQHLTFFSIQPQPPPCHAFHPRDPPAGTKRQLILVPLK
ļ	ł	Į.	GPPILAPILSLTPILSRWSCYFPRSRIAQGWHLS
			GPFILMFILISHTFILISMSCIFFRSKIAGOMILIS
6244	2119	1745	FEHAYASQFGTFLGNNESERCKLKLQQKTMSLWSWVNQPSELSK
1			FTNPLFEANNLVIWPSVAPQSLPLWEGIFLRWNRSSKYLDEAYE
	1	ļ	EMVNIIEYNKELQAKVNILRRQLAELETEDGMQESP
6245	81	1148	LSLRNAKYSFPQELISLFSMTDLNDNICKRYIKMITNIVILSLI
			ICISLAFWIISMTASTYYGNLRPISPWRWLFSVVVPVLIVSNGL
<u> </u>		i	KKKSLDHSGALGGLVVGFILTIANFSFFTSLLMFFLSSSKLTKW
ļ	1	1	KGEVKKRLDSEYKEGGQRNWVQVFCNGAVPTBLALLYMIENGPG
		Į.	EIPVDFSKQYSASWMCLSLLAALACSAGDTWASEVGPVLSKSSP
		1	
ì	1	1	RLITTWEKVPVGTNGGVTVVGLVSSLLGGTFVGIAYFLTQLIFV
		ł	NDLDISAPQWPIIAFGGLAGLLGSIVDSYLGATMQYTGLDESTG
ì	1	1	MVVNSPTNKARHIAGKPILDNNAVNLFSSVLIALLLPTAAWGFW
	ł	1	PRG
6246	1177	359	SLWPWILMDDSLMQISLQLLCVYTANFPNGCSSLCWSSCGQHPV
	_	•	OATHRGAVSNSLMLCILKLASQMPLENTTVQQMVFMLLSNLALS
1	1	i	HDCKGVIQKSNFLQNFLSLALPKGGNKHLSNLTILWLKLLLNIS
ł		1	SGEDGOOMILRLDGCLDLLTEMSKYKHKSSPLLPLLIFHNVCFS
i			PANKPKILANEKVITVLAACLESENQNAQRIGAAALWALIYNYQ
			KAKTALKSPSVKRRVDEAYSLAKKTFPNSEANPLNAYYLKCLEN
1		1	
	l		LVQLLNSS
6247	3	1678	NSRVWGPWTEPSAGSLRPMARKQNRNSKELGLVPLTDDTSHAGP
	1		PGPGRALLECDHLRSGVPGGRRRKDWSCSLLVASLAGAFGSSFL
		1	YGYNLSVVNAPTPYIKAFYNESWERRHGRPIDPDTLTLLWSVTV
			SIFAIGGLVGTLIVKMIGKVLGRKHTLLANNGFAISAALLMACS
			LOAGAFEMLIVGRFIMGIDGGVALSVLPMYLSEISPKEIRGSLG
			QVTAIFICIGVFTGQLLGLPELLGKESTWPYLFGVIVVPAVVQL
			LSLPFLPDSPRYLLLEKHNEARAVKAFQTFLGKAHVSQEVEEVL
1			
1			AESRVQRSIRLVSVLELLRAPYVRWQVVTVIVTMACYQLCGLNA
1			IWFYTNSIFGKAGIPPAKIPYVTLSTGGIETLAAVFSGLVIEHL
1			GRRPLLIGGFGLMGLFFGTLTITLTLQDHAPWVPYLSIVGILAI
			IASFCSGPGGIPFILTGEFFQQSQRPAAFIIAGTVNWLSNPAVG
1			LLFPFIQKSLDTYCFLVFATICITGAIYLYFVLPETKNRTYAEI
1			SQAFSKRNKAYPPEEKIDSAVTDGKINGRP
6240	+	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVQNPGAALDLCI
6248	56	1//3	AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
			WAS TARGED AND TARGET BACK OF BALL BECKENODE THE TARGET BACK OF THE TA
1	}		ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
			SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII
}	1		LNLVMVGLVSRLWVLYKGVLKRLILLYEPLFGLLQEVARIQPMP
Į			YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF
			LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF
L			<u> </u>

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
\	sequence		\=possible nucleotide insertion)
	bequeines		KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
			VIGTPHAKSFYORFREAESFTOLSEEIOMAVVWCRSKKLKAOAI
!			FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
ĺ			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
	}		ATDTSAKWRLSHCTVHRTDLYPNSKOLLNSGVSMPVIOTKEKMI
			HENLRGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6249	56	1773	VPPPRMMAAVPPGLEPWNRVRIPKAGNRSAVTVONPGAALDLCI
0243] 30	1,,,,	AAVIKECHLVILSLKSQTLDAETDVLCAVLYSNHNRMGRHKPHL
ł			ALKQVEQCLKRLKNMNLEGSIQDLFELFSSNENQPLTTKVCVVP
			SQPVVELVLMKVLGACKLLLRLLDCCCKTFLLTVKHLGLQEFII
			LNLVMVGLVSRLWVLYKGVLKRLILLYBPLFGLLQEVARIQPMP
			YFKDFTFPSDITEFLGQPYFEAFKKKMPIAFAAKGINKLLNKLF
1			LINEQSPRASEETLLGISKKAKQMKINVQNNVDLGQPVKNKRVF
		Į.	KEESSEFDVRAFCNQLKHKATQETSFDFKCSQSRLKTTKYSSQK
1			VIGTPHAKSFVORFREAESFTOLSEEIOMAVVWCRSKKLKAQAI
		1	FLGNKLLKSNRLKHLEAQGTSLPKKLECIKTSICNHLLRGSGIK
			TSKHHLRQRRSQNKFLRRQRKPQRKLQSTLLREIQQFSQGTRKS
		1	ATDTSAKWRLSHCTVHRTDLYPNSKQLLNSGVSMPVIQTKEKMI
			HENLEGIHENETDSWTVMQINKNSTSGTIKETDDIDDIFALMGV
6250	232	1306	LAALHIMALPFRKDLEKYKDLDEDELLGNLSETELKOLETVLDD
0230	232	1300	LDPENALLPAGFROKNOTSKSTTGPFDREHLLSYLEKEALEHKD
		i	REDYVPYTGEKKGKIFIPKQKPVQTFTEEKVSLDPELEEALTSA
			SDTELCDLAAILGMHNLITNTKFCNIMGSSNGVDQEHFSNVVKG
1		1	EKILPVFDEPPNPTNVEESLKRTKENDAHLVEVNLNNIKNIPIP
			TLKDFAKALETNTHVKCFSLAATRSNDPVATAFAEMLKVNKTLK
			SLNVESNFITGVGILALIDALRDNETLAELKIDNQRQQLGTAVE
			LEMAKMLEENTNILKFGYQFTQQGPRTRAANAITKNNDLVRKRR
			VEGDHO
6251	62	972	TPGSGPMSAWAAASLSRAAARCLLARGPGVRAAPPRDPRPSHPE
1		1	PRGCGAAPGRTLHFTAAVPAGHNKWSKVRHIKGPKDVERSRIFS
		k	KLCLNIRLAVKEGGPNPEHNSNLANILEVCRSKHMPKSTIETAL
ļ			KMBKSKDTYLLYEGRGPGGSSLLIEALSNSSHKCQADIRHILNK
			NGGVMAVGARHSFDKKGVIVVEVEDREKKAVNLERALEMAIEAG
			AEDVKETEDEEERNVFKFICDASSLHQVRKKLDSLGLCSVSCAL
			EFIPNSKVQLAEPDLEQAAHLIQALSNHEDVIHVYDNIE
6252	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLQTKRKKPRRYWEE
		}	ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
		1	PKKPREWKNPESQRGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
		1	KLPHSKAKTRSRLEVABAEEEETSIKAARSELLLAEEPGFLEGE
			DGEDTAKICQADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
			RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL
		1	AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
			TGFLTYLDVSVGKIVAALNARAGRLDVMSQNPYNAVIHLGHSNG
		1	TVSLWSPAMKEPLAKILCHRGGVRAVAVDSTGTYMATSGLDHQL
		1	KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA
	1		GQGKASPPSLEQPYLTHRLSGPVHGLQFCPFEDVLGVGHTGGIT
			SMLVPGAGEPNFDGLESNPYRSRKQRQEWEVKALLEKVPABLIC
		1	LDPRALAEVDVISLEQGKKEQIERLGYDPQAKAPFQPKPKQKGR
			SSTASLVKRKRKVMDEEHRDKVRQSLQQQHHKEAKAKPTGARPS
			ALDREVR
6253	27	1897	EEFCTWIAVRVGEMETAPKPGKDVPPKKDKLOTKRKKPRRYWEE
1			ETVPTTAGASPGPPRNKKNRELRPQRPKNAYILKKSRISKKPQV
		1	PKKPREWKNPESORGLSGAQDPFPGPAPVPVEVVQKFCRIDKSR
			KLPHSKAKTRSRLEVAEABEEETSIKAARSELLLAEEPGFLEGE
			DGEDTAKICOADIVEAVDIASAAKHFDLNLRQFGPYRLNYSRTG
			RHLAFGGRRGHVAALDWVTKKLMCEINVMEAVRDIRFLHSEALL
	.l		

NO: uncleotide location corresponding control corresponding control cont	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No: nucleotide cortesponding to first amino acid corresponding to first amino acid residue of amino acid residue of amino acid sequence S-Proline, Q-Glutamine, R-Arginine, P-Proline, Q-Glutamine, R-Arginine, S-Serine, T-Threonine, V-Valine, W-Typtophan, Y-Tyroseine, X-Unknown, *-Stop Codon, /-possible nucleotide deletion, \	l l			(A-Alanina C-Cysteina D-Aspartis Asid E-
corresponding to first amino acid uence sequence se	1		1	
corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence S-Peroline, Q-Goltumamine, X-Muknown, *-Stop Codon, V-possible nucleotide deletion, V-possible nucleotide insertion) AVAQNEWLHIYDNOGIEHCIRECREVITELEFJPHFILLATASE TOFILITLUDYSUGKIVAALMARAGRIDUMSQNPYNAVIHLEGHAA GCGKASPPSLEGVITHRLEGSVPHAAVDISTGTVANTSGLDHQL KIFDLUTYSUGKIVAALMARAGRIDUMSQNPYNAVIHLEGHAA GCGKASPPSLEGVITHRLEGSVPHOLGPCFPEDVLGVGHTGGIT SMLVPGAGSPNFDOLESSPYRGRGRUVAAVDSTGTVANTSGLDHQL KIFDLUTYGRGFPHEDVLSSPYRGRGRUVAAVDSTGTVANTSGLDHQL KIFDLUTYGRGFPHEDVLSSPYRGRGRUVAAVDSTGTVANTSGLDHQL KIFDLUTYGRGFPHEDVLSSPYRGRGRUVAAVDSTGTVANTSGLDHQL KIFDLUTYGRGFPHEDVLSSPYRGRGRUVAAVDSGTVANTSGLDHQL KIFDLUTYGRGFPHEDVLSSPYRGRGRUVAAVDSGTVANTSGLDHQL KIFDLUTYGRGFPHEDVLSSPYRGRGRUVAAVDSGTVANTSGLDHQL KIFDLUTYGRGFPHEDVLSSPYRGRGRUVAAVDSGTVANTSGLDHQL KIFDLUTYGRGFPHEDVLSSPYRGRGRUVAAVDSGTVANTSGLDHQL KIFDLUTYGRGFPHEDVLSSPYRGRGRUVAAVDSGTVANTSGLDHQL KIFDLUTYGRGFPHEDVLSSPYRGRGRUVAAVDSGTVANTSGRAFPHEDVLSSPYRGRGRUVAAVDSGTVANTSGRAFPHEDVLSSPYRGRGRUVAAVDSGTVANTSGRAFPHEDVLSGRAFPHEDVLSGRGFPHEVAARGARTSGRAFFHEVAARGARTSGRAFFHEVAARGARTSGRAFFHEVAARGARTSGRAFFHEVAARGARTSGRAFFHEVAARGARTSGRAFFHEVAARGARTSGRAFFHEVAARGARTSGRAFFHEVAARGARTSGRAFFHEVAARGARTSGRAFFHEVAARGARTSGRAFFHEVAARGARTSGRAFFHEVAARGARTSGRAFFHEVAARGARTSGRAFFHEVAARGARTSGRAFFH	NO.			
to first amino acid residue of samino acid amino acid sequence solvent the transport of amino acid sequence solvent sequence	1	l .		
amino acid residue of amino acid sequence S-Serine, T-Threonine, V-Valine, walknown, *-Stop Codon, /-possible nucleotide deletion, V-possible nucleotide insertion, V	1			
residue of amino acid sequence (Codon, /-possible nucleotide deletion, \-possible nucleotide deletion, \-possible nucleotide dissertion) AVAGNRALHIYDROGE ELECTRECEVTRIEFIPHFILLATASE TOFLTYIDLYSVEKIVALIMARAGRILDYSORPYNAVIHLGHENGE TYSLWSSAMKEPLAKILCHRGGVRAVADSTGTYMATSGLÜHGL KIFDLRGTVGDISTRTLPHGGAMLHASSGGLUAMGGVANAMGVANIMA GGGKASPFSLEGPYLTHRLSGPVHGLGFCFFEDVLGVHTGGIT SKLVPGAGSPPNFDGLISSNYFSKRÇAGRBEVKALLEKVPAELIC LDPRALAEVDVISLEGGKKEGIERLGYTDPOAKAPFORF KPKGKGR SSTASLVKRKRKVMDEHENDRVRGSLGQOHKKEAKAKPTGARPS ALDRRVR 6254 155 1139 HALGERGGSGGELSAAAGCFALRLRAPSGGRPLAFGARAFAGL GGAPRFPPRGSAAGRTHLKEYRICMPLTVDEVKIGQLYMISKE SSEGSRGGGVEVVQWEFFEDPHHGHGGPTEKKVINSLEGEM RAVVPKIFTVTFKAWNYTYSTITTSTCSPLEFKSHIHETKYEEN KOSNDTIFDNEAKDVEREVCFIDIACDEIPERTYKESEDPKHFK SSEKTGRGGLEGEWBSHGHG HESVSILLHETKYEEN KOSNDTIFDNEAKDVEREVCFIDIACDEIPERTYKESEDPKHFK SSKTGRGGLEGEWBSHGHG HESVSILLHETKYEEN KOSNDTIFDNEAKDVEREVCFIDIACDEIPERTYKESEDSWHFK VCNOHSSPYDIBESHAGTTE VCNOHSSPYDIBESHAGTTE LGFGLEGEMSSALSCLASSLKFYHKGLASSTORFT LGFGLEFKSTATATTHAF LGFGEFVLARLAUGHGLANGGARDHAGHG LGFGLEKTLAULAGASTLAULAGA	J	1		
amino acid sequence Codon, /-possible nuclectide deletion,	1	1) · · · · · · · · · · · · · · · · · · ·
A-posible nuclectide insertion	1	l .	1	
A VAONRHLHI YDNOGI ELHCITRCOB VTELEF, EPPEPILLATASE TOFILTIJUN YOKKI VAAALMAR ARGELUWAG NOPWAN VIHLGHSING TVSLMS PAMKEPLAKI LCHRGGVRAVAVOSTOTYMATSGLOHQL KI FOLROTYQPLSTRIPHGAGHLAFS GRGLLVAGHGUVAUN AA QQXASS PS BLEQPYLTHRILSGOWGLVAGHGUVAUN HAA QQXASS PS BLEQPYLTHRILSGOWGLVAGHGUVAUN HAA QQXASS PS BLEQPYLTHRILSGOWGLAVAGHGUVAUN HAA QQXASS PS BLEQPYLTHRILSGOWGLAVAGHGUVAUN HAA QQXASS PS BLEQPYLTHRILSGOWGLAVAGHGUVAUN HAA QQXASS PS BLEQPYLTHRILSGOWGLAVAGHGUVAUN HAA QQXASS PS BLEQPYLTHRILSGOWGLAVAGHGUVAUN HAA QQXASS PS BLEQPYLTSANGKAGHEVALLEKVYPALDIC LDPRALAEVUY SLEGGKEUGLERLSTPDAGPYPEP KOKKING SSTASLVKKKRKVMDEEHBDKVRQSLQQQHHKEAKAKPTGARPS ALDREVR ALDREVR BALGREGG GOLSAAAGCCFALLERARGSGEPALARGAAAFRGL GGAPRFP PRGSAAGCTFALLKRYRICQLIVMISKH SHEQSDRGGGVEVVQNEP FEDPHHIGNGQPTEKRVYINSKLPSHA RAVVFKLFYVTEKAMYYPYTITSTYCS FLOKKSGLYHINSKLPSHA RAVVFKLFYVTEKAMYYPYTITSTYCS FLOKKSGLYHINSKLPSHA RAVVFKLFYVTEKAMYYPYTITSTYCS FLOKKSGLYRUGDLYRUGDV HKVVROLLIGHGQAFAWDEWTMYMDUVERVENHEDTINK VCNQHSSPUDIESHAQTST VYRTARQASRMONIDHAKELYQSLLTOVASKHJOLFREYDEV HKVVROLLIGHGQAFAWDEWTMYMDUVERVENHEDTINK VCNQHSSPUDIESHAQTST VYRTARQASRMONIDHAKELYQSLLTOVASKHJOLFREYDENNOH LSPQCEFVELRIDLLQAFSQLICTCNSLKTSPPALATTIANTIL GGBLQRGGRISNOMKOSMBERSLASRYGDLYQASFDABATIR NVELQOSCALISHATEALILDESSASSQUSTGTHABDSYER RMMSVYNNYLEBVESINGKYTPVSYMHTACLONAILLKVPL SFOKFYFFKLQSTSIKLAISPSPRPAPABTIANTISMALA NUEQOSCALISHATEALILDESSASSQUSTGTHABDSYER RMMSVYNNYLEBVESINGKYTPVSYMHTACLONAILLKVPL SFOKFYFFKLQSTSIKLAISPSPRPAPABTIANTISMALA VENEQAAABSILINKLIRSKINDNITNOVEVLORDONSPLYSVKSFEL RIKKPQLLQOVYAMPKRPSKLUGNAILTIANTISMALA VEDEQAAABSILINKLIRSKINDNITNOVEVLORDONSPLYSVKSFEL RIKKPQLLQOVYAMPKRPSKLUGNAILTIANTISMALA VEDEQAAABSILINKLIRSKINDNITNOVEVLORDONSPLYSVKYREP ERKPQLLQOVYAMPKRPSKLUGNAILTIANTISMALA VEDEQAAABSILINKLIRSKINDNITNOVEVLUGNINGVYULCSB DEKPQALCULVANGKKERGROKISSGUVTGNUJOVYULCSB DEKPQALCULVANGKKERGROKISSGUVTGNUJOVYULCSB DEKPQALCULVANGKKERGROKISSGUVTGNUJOVYULCSB DEKPQALCULVANGKKERGROKISSGUVTGNUJOVYULCSB DEKPQALCULVANGKHERGROKISSGUVTGNUJOVYULCSB DEKPQALCULVANGKHERGROKISGUVTAVORAKIGANDAVOSKISM NIL	1	amino acid	sequence	
TOFLITILD/SVOKI/VALINARIAGRID/MSQNPYNAYHLGHSING TVSLWSPAMEPLARILLORGGVRAVAVDSTGTYWATSGLDHOL KIFDLRGTYQPLSTRTLPHGAGHLAFSQRGLLVAGNGDVVNTWA QGKASPPSLEGGPTJTHRLSGPVHGLGFCFFEDVYGGHTGGTT SMLVPGAGBPNFDGLESNPYRSKRQGBWEVKALLEKVPAELIC LDPRALAEVDVISLEGGKKBQIERLGYDPQAKAFPOFKPKOKGR SSTASIVKRKRKVMDEEHRKVRQSLQOGHHKAKAKAPTGARPS ALDRFVR 6254 155 1139 HALGREGGSOELSAAGCCFALELEAPDSGRPALAFGAAAPAGL GGAPFPPRGSAAGRTMLLKEVRICMPLTVDEYKIGQLYMISKH SHEGSBRGEVEVVQNEPFEDHHONGPTEKVYLINSLUPSMA RAVVPKIFYVTEKAMNYPTTTETTCFEPFKFSHIETKYEDN KOSNDTIFDNEAKDVEREVCFIDIACDEIPERYKESEDPKHFK SSKTGRGGLEGWRDSRIGPTMCSYKLIVVTSFEWGLGTRVEGDFV HKVVRDILLIGHRGAFAWUDEWTDMTMDDVREYEKMHEQTNIK VCNGHSSPVDDIESHAGTTST 1444 PTRPQOELLVSLATVIFVASQKALSVESKAVIKQOLESVSNGWT VYRZARQASRMGNHDMAKELYQSLLTQVASKHFYKMISLKEPS HAEQCLIFIGLGENNYSASLASILAESLKFYHGLINSLESSES HAEQCLIFIGLGENNYSASLASILAESLKFYHGLINSLESSES HAEQCLIFIGLGENNYSASLASILAESLKFYHGLIABLATAASTPLINF LSFQCEFVKLRIDLLQAFSQLICTCNSLKTSPPPAITTIAMTIL GRODLQRGGISNOMKOSWEFFRSLASRYGDLYGASFDADSATLR NVELOQOSCLLISHAIEALILDPESASFQCYSGTSTATABASEYE RRMSVVNINVLEVENSLINGKYTPVSYMHTACLCNAITALLKVPL SFQRYFFOKLQSTSIKLALSPSPRNPAEPIAVONNQQLALKVEG VVQHGKPGLFRKLIGSVCLNVSSTLQSKSQDYKITDMTHTEM OFFTTIFVKSLEDPYSQQIRLQQOOAQOPLQQQOQRAYTHF CGGGAGAPANNFSFSELVSSSTSTSYSPAFGTMATDSWALA VIEGGAAABSLSNLHLKERKIKPDTNGAVVKYNDANSKYTDESK EDRAAGSLINKLIRSNLVONTHOVEVLQDRSPLYSVSFSEE RRAAGSVLINKLIRSNLVONTHOVEVLQDRSPLYSVSFSEE BERRAAGSVLINKLIRSNLVONTHOVEVLQDRSPLYSVSFSEE SATFEDSWKFAQKVVPDDYNVIKKREBETITHKPNQMLLF STORTAAPVLAMLSVGRAAVERHEDGTDLDEIEKIAN NILNRIQBHFNKKIERLDTDDLDEIEKIAN NILNRIQBHRNKKERLDTDDLDEIEKIAN NILNRIQBHRNKKERLDTDDLDEIEKAN NILNRIQBHRNKKERLDTDDLDEIEKAN NILNRIQBHRNKKERLDTDDLDEIEKAN NILNKELALLDGSNVVPKLLGPVLVKQELGEARATVGKRLDYI TAEIKKYESQLRDLERQSEQORETLAQLQQEFQRAQAKKAGAPG KA APTPAMAELIGKKLQGEVEKYQOLQKDLSKNSGRQKLEAQLTE NNIVKEELALLDGSNVVPKLLGPVLVKQELGEARATVGKRLDYI TAEIKKYESQLRDLERQSEQORETLAQLQQEFQRAQAAKAGAPG KA APTPAMAELIGKKLQGEVEKYQOLQKDLSKSNSGRQKLEAQLTE NNIVKEELALLDGSNVVPKLLGPVLVKQELGEARATVGKRLDYI TAEIKKYESQLRDLERGSGRGKETLAQLQQEFQRAQAAKAGAPG KA		sequence		\=possible nucleotide insertion)
TYSLMSPAMKEPLAKILCHRGGYRAVAVDSTOTYWATSGLDHOL KI FDLRGTYOPILSTRTLPHGAGHLAFSQRGLLVAGMGDVVNIWA GQGKASPPSLEGPYLTRILGSEVHOLGFCPFEDVLGVGHTGGIT SMLVPGAGENPTGLESNPYRSRKQRGEMEVKALLEVYABLIC LDPRALAEVDVISLEGOKRGJERIGYDQAKAPFOPKPKRKKG SSTASLVKRKRKVMDEERDKVRQSLQQQHHKEAKAKPTGARPS ALDRRVR 6254 155 1139 HALGREGSQELSAAACGCFALRLRAPGSGRPALAFGAAAFAGL GGAPRFPPRGSAAGRTHLLKENYLCMLTVDEYKLGLYMISKH SHEQSDREGOVEVVQNDEPEDPHHIMOGPPTEKRVYLNSKLPSWA RAVVPKIFYYTEKANNYYPYTTENTCSPLPKFSYHLETKYEEN KOSNDTIFDNEAKDVERSVCPJDIACDGPTEKRVYLNSKLPSWA RAVVPKIFYYTEKANNYYPYTTENTCSPLPKFSYHLETKYEEN KOSNDTIFDNEAKDVERSVCPJDIACDGPTEKRVYLNSKLPSWA RAVVPKIFYYTEKANNYYPYTTENTCSPLPKFSYHLETKYEEN KOSNDTIFDNEAKDVERSVCPJDIACDGPTEKRVYLNSKLPSWA RAVVPKIFYYTEKANNYYPYTTENTCSPLPKFSYHLETKYEEN KOSNDTIFDNEAKDVERSVCPJDIACDGPTEKRYKESEDPKHFK SEKTGRGQLREGWRDSHQPIMCSYKLVTVKFEWGELDTRVGDFV HVVRDILLIGHRQAFAWVDGWYDTMTMDDVRFYKNMHEQTNIK VCNQHSSPVDDIESRAGTST 1444 PPRPQGELUVSLATUTFVASQKALSVESKAVIKQCLESVSNGWT VXTLARQASRAMINDHAKELYQSLLTVOAKSHFYFWLINSLKEPS HAEQCLTGLQEENYSSALSCLAESLKFYHKGIASLTAASTPLNF LSFQCEFVKLRIDLLQAFSOLICTCNSLAFPPALATILAMTL GRDLQRGGRISNQMKQSMEEFRSLASRYGDLYQASPDADSATLR NVELQQQSCLLISHATERALLLDFSBASFQCYSGTTATAADSSPLF RRMMSVYNHVLEEVESLINGKYTPVSYHTATCLCMAITALKVPL SSQRYFFQKLQSTSIKLALSPSPRRPAEPTAQVGNQALLKVEG VQYGGSKPGLFFKKLGSVCINVSSTLGSKSGOPKIFDIDMTNEM EGRVEPHNDYFSTOPLLNFAILGTHITVESSVKOANGIVWKTG PPTTIFVKSLEDPYSQGLTXQCOAQOQDCANNYTEF EGRAGSLINKLIFSRILVNSTLGSKSGOPKIFDIDMTNEM EGRVEPHNDYFSTOPLLNAFDHOLQOAQOQCHNAYTER CREADAGSLINKLIFSRILVNTROAVVKTNANAKTDEEKE BERAAGSLINKLIFSRILVNTROAVVKTNANAKTDEEKE REPRAAGSLINKLIFSRILVNTROAVVKTNANAKTDEEKE REPRAAGSLINKLIFSRILVNTROAVVKTNANAKTDEEKE REPRAAGSLINKLIFSRILVNTROAVVKTNANAKTDEEKE BERAAGSLINKLIFSRILVNTROAVVFRUARSTUBERGUNTE RIKHVESUVKFAQKVVPDNVIKKREEETLDTIKGYTVICSSR DEKRQALCULNGADTIAQGGQGTTAQAACKRUBDVIT TAELKKYESGLRDLERGSCRUTTROAGRIPAGRATUTGKRLDYI TAELKKYESGLRDLERGSCROCATAQAGCARAGAPG KA 6257 210 615 APTPAMAELIQKKLQGEVEKYQOLQKDLSKSMSGRQLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAELKKYESGLRDLERGSCROCRETAQOCARRAGAPG KA 6258 210 615 APTPAMAELIQKKL				AVAQNRWLHIYDNQGIELHCIRRCDRVTRLEFLPFHFLLATASE
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TGKTAAFVLAMLSQVEPANKYPQCLCLSPTYELALQTGKVIEQM GKFYPELKLAYAVRGNKLERGQKISEQIVIGTPGTVLDWCSKLK FIDPKKIKVFVLDEADVMIATQGHQDQSIRIQRMLPRNCQMLLF SATFEDSVWKFAQKVVPDPDVIKLKREEETLDTIKQYYVLCSSR DEKFQALCNLYGAITIAQAMIFCHTRKTASWLAAELSKEGHQVA LLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVV INFDLPVDKDGNPDNETYLHRIGRTGRFGKRGLAVNMVDSKHSM NILNRIQEHFNKKIERLDTDDLDEIEKIAN 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6258 210 615 AFIPAMAELIQKKLQGEVBKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA KA	1	1		
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FIDPKKIKVFVLDEADVMIATQGHQDQSIRIQRMLPRNCQMLLF SATFEDSVWKFAQKVVPDPNVIKLKREEETLDTIKQYYVLCSSR DEKFQALCNLYGAITIAQAMIFCHTRKTASWLAAELSKEGHQVA LLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVV INFDLPVDKDGNPDNETTLHRIGRTGRFGKRGLAVNMVDSKHSM NILNRIQEHFNKKIERLDTDDLDEIEKIAN 6257 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSBQQRETLAQLQQEFQRAQAAKAGAPG KA KA KA				
SATFEDSVWKFAQKVVPDPNVIKLKREEETLDTIKQYYVLCSSR DEKFQALCRLYGAITIAQAMIFCHTRKTASWLAAELSKEGHQVA LLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVV INFDLPVDKDGNPDNETYLHRIGRTGRFGKRGLAVNMVDSKHSM NILNRIQEHFNKKIERLDTDDLDEIEKIAN 6257 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA KA	1			
DEKFQALCNLYGAITIAQAMIFCHTRKTASWLAAELSKEGHQVA LLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVV INFDLPVDKDGNPDNETYLHRIGRTGRFGKRGLAVNMVDSKHSM NILNRIQEHFNKKIERLDTDDLDEIEKIAN 6257 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA	1]		
LLSGEMMVEQRAAVIERFREGKEKVLVTTNVCARGIDVEQVSVV INFDLPVDKDGNPDNETYLHRIGRTGRFGKRGLAVNMVDSKHSM NILNRIQEHFNKKIERLDTDDLDEIEKIAN 6257 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA	1	1		
INFDLPVDKDGNPDNETYLHRIGRTGRFGKRGLAVNMVDSKHSM NILNRIQEHFNKKIERLDTDDLDEIEKIAN 6257 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6258 210 615 AFIPAMAELIQKKLQGEVBKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA	1	1	İ	
NILNRIQEHFNKKIERLDTDDLDEIEKIAN 6257 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVPKLLGPVLVKQEIGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6258 210 615 AFIPAMAELIQKKLQGEVBKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSBQQRETLAQLQQEFQRAQAAKAGAPG KA	1	1		
6257 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA	1	1	1	I I
NNIVKEELALLDGSNVVPKLLGPVLVKQEIGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSBQQRETLAQLQQEFQRAQAAKAGAPG KA		L		1
TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA 6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA	6257	210	615	
KA 6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSBQQRETLAQLQQEFQRAQAAKAGAPG KA	1			NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI
6258 210 615 AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAQLTE NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA	1			TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG
NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSEQQRETLAQLQQEFQRAQAAKAGAPG KA	1	1		KA
NNIVKEELALLDGSNVVFKLLGPVLVKQELGEARATVGKRLDYI TAEIKRYESQLRDLERQSBQQRETLAQLQQEFQRAQAAKAGAPG KA	6258	210	615	AFIPAMAELIQKKLQGEVEKYQQLQKDLSKSMSGRQKLEAOLTE
TAEIKRYESQLRDLERQSBQQRETLAQLQQEFQRAQAAKAGAPG KA	1			
KA	1	1		
		1		
	6259	2	1540	ILEKGFPSQCHPERKWKVDDVLESSQENEDDHFWELLFHNNKTV
SVENGDRGSKTFNLGTDPVSLRNYPYKICDSCEMNLKNISGLII		1		
SKKNCSRKKPDEFNVCEKLLLDIRHEKIPIGEKSYKYDOKRNAI	1			
]	1		
NYHQDLSQPSFGQSFEYSKNGQGFHDEAAFFTNKRSQIGETVCK	1			
YNECGRIFIESLKLNISQRPHLEMEPYGCSICGKSFCMNLRFGH		İ		1
QRALTKDNPYEYNEYGEIFCDNSAFIIHQGAYTRKILREYKVSD		1		_
KTWEKSALLKHQIVHMGGKSYDYNENGSNFSKKSHLTQLRRAHT	1	1		
GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCQ	L	<u> </u>		GEKTFECGECGKTFWEKSNLTQHQRTHTGEKPYECTECGKAFCQ

SEQ Predicted Predicted end Amino acid segment containing	signal peptide
ID beginning nucleotide (A=Alanine, C=Cysteine, D=Aspa	
NO: nucleotide location Glutamic Acid, F=Phenylalanine	, G=Glycine,
location corresponding H=Histidine, I=Isoleucine, K=I	ysine,
corresponding to first L=Leucine, M=Methionine, N=Asp	aragine,
to first amino acid P=Proline, Q=Glutamine, R=Argi	nine,
amino acid residue of S=Serine, T=Threonine, V=Valin	
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Ur	•
amino acid sequence Codon, /=possible nucleotide d	
sequence \=possible nucleotide insertic	
KPHLTNHQRTHTGEKPYECKQCGKTFCVKS	
YECNACGKSFCHRSALTVHORTHTGEKPF1	
IVHQRTHTGEKPYKCNECGKTFCEKSALTE	
ACGKTFSQRSVLTKHQRIHTRVKALSTS	arginia about
6260 2081 1436 GTGPEIHACAHASARAPGSRAMALRELKVO	T.T.GDTGVGKSSTVW
RFVEDSFDPNINPTIGASFMTKTVQYQNEI	
RALAPMYYRGSAAAIIVYDITKEETFSTLE	-
VVAIAGNKCDLIDVREVMERDAKDYADSIF	-
NELFIEISRRIPSTDANLPSGGKGFKLRRQ	-
6261 3 1188 FWYRLGPGTRSRWPRRGSWAASLVPRGPSI	
SPACEPCRPDFAPRPALLLRSGPRSAPAVI	_
MAEVSIDQSKLPGVKEVCRDFAVLEDHTLF	
NVQRNRLVQHDLQVAKQLQEEDLKAQAQLQ	
QEIQEKLAIEAERRRIQEKKDEDIARLLQE	
EFPATRAYADSYYYEDGGMKPRVMKEAVST	_
EIARKLQEEELLATQVDMRAAQVAQDEEIA	
KEREKSSLDKRKQDPEWKPKTAKAANSKSF	
RPPPPIMTDGEDADYTHFTNQQSSTRHFSF	
6262 2 1759 PECHSQGLCSVHRPGKVPQARMSGLVLGQF	
GSTRLVSQGLEALRSBHQAVLQSLSQTIEG	
ARQLRRSMENIELGLSEAQVMLALASHLST	
LCQENQWLRDELAGTQQRLQRSEQAVAQLE	EBEKKHLEFLGQLRQ
YDEDGHTSEEKEGDATKDSLDDLFPNEEER	EDPSNGLSRGQGATA
AQQGGYEIPARLRTLHNLVIQYAAQGRYEV	/AVPLCKQALEDLER
TSGRGHPDVATMLNILALVYRDQNKYKEAF	AHLLNDALSIRESTL
GPDHPAVAATLNNLAVLYGKRGKYKEAEPI	CORALEIREKVLGT
NHPDVAKQLNNLALLCQNQGKYEAVERYYC	RALAIYEGQLGPDN
PNVARTKNNLASCYLKQGKYAEABTLYKE	LTRAHVQEFGSVDD
DHKPIWMHAEEREEMSKSRHHEGGTPYAES	/GGWYKACKVSSPTV
NTTLRNLGALYRRQGKLEAAETLEECALRS	RRQGTDPISQTKVA
ELLGESDGRRTSQEGPGDSVKFEGGEDASV	/AVEWSGDGSGTLQR
SGSLGKIRDVLRR	
6263 1 2408 RELDSLADLPERIKPPYANGLSTSHLRSSS	SVEDVKLIISEGRPT
IEVRRCSMPSVICEHTKQFQTISEESNQGS	
EVFSNVPERDLSNVSNIHSSFATSPTGASN	
APVNTVMDSPVHLEPSSQVGVIQNKSWEME	
PNSNIPDQESSLQSFCNSENKVLKENADFI	
DPASFMPPQQPCSFPSQSLSDAESISKHMS	-
KNAVQIISSALDTDNESTKDTENTFVLGDV	
IOEASPNFEKAYTLPVLPSEKDFNGSDAST	
SSSGHEVENSTTDTQVISHEKENKLESLVI	
AGMPKGNLNBQDPKHCPESEKCLLSIEDEE	
OSTOPEMHKYGQLVKVELEENAEDDKTENO	
NOSKOILASCTLLSEKDSESSSPRGRIRLI	
VSRVPQPVQVSPSLLQAKEKTQQSLAAIVI	-
ANPYFEYLHIRKKIEEKRKLLCSVIPQAPC	_
	=
DGNPLSKICIPTITPPPSLSDPLKELFRQC	* * *
REKLIVSNEQEVLRVHYRAARTLANQTLPE	
PLDSQSDDSKTSVRDRFNARQFMSWLQDVI	
QHEAAALNAVQRLEWQLKLQELDPATYKSI	STARIGELAADIAD
VNDDFELTPI	
6264 143 1960 KHRQENNALDMAPEIHMTGPMCLIENTNGE	
TQPVVVAIVGLYRTGKSYLMNKLAGKNKG	
WMWCVPHPKKPEHTLVLLDTEGLGDVKKGD	NONDSWIFTLAVLL
l	DNONDSWIFTLAVLL RSKSSPDENENEDS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
İ	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
		İ	ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
			INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
			LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQL
			DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
		•	YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
ŀ			QTDQILTEKEKEIEVECVKAESAQASAKMVEEMQIKYQQMMEEK
1			EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
1			CQGESTQLQNEIQKLQKTLKKKTKRYMSHKLKI
6265	143	1960	KHRQENNALDMAPEIHMTGPMCLIENTNGELVANPEALKILSAI
			TQPVVVVAIVGLYRTGKSYLMNKLAGKNKGFSLGSTVKSHTKGI
			wmwcvphpkkpehtlvlldteglgdvkkgdnqndswiftlavll
			SSTLVYNSMGTINQQAMDQLYYVTELTHRIRSKSSPDENENEDS
			ADFVSFFPDFVWTLRDFSLDLEADGQPLTPDEYLEYSLKLTQGT
-			SQKDKNFNLPRLCIRKFFPKKKCFVFDLPIHRRKLAQLEKLQDE
	1	1	ELDPEFVQQVADFCSYIFSNSKTKTLSGGIKVNGPRLESLVLTY
	1		INAISRGDLPCMENAVLALAQIENSAAVQKAIAHYDQQMGQKVQ
			LPAETLQELLDLHRVSEREATEVYMKNSFKDVDHLFQKKLAAQL
1			DKKRDDFCKQNQEASSDRCSALLQVIFSPLEEEVKAGIYSKPGG
			YCLFIQKLQDLEKKYYEEPRKGIQAEEILQTYLKSKESVTDAIL
			QTDQILTEKEKEIEVECVKABSAQASAKMVEEMQIKYQQMMEEK
ļ			EKSYQEHVKQLTEKMERERAQLLEEQEKTLTSKLQEQARVLKER
j			COGESTOLONEIOKLOKTLKKKTKRYMSHKLKI
6266	276	1421	GSHQKQMLVPCFLYSLQNRKPSLYGSLTCQGIGLDGIPEVTASE
1.			GFTVNEINKKSIHISCPKENASSKFLAPYTTFSRIHTKSITCLD
	i	1	ISSRGGLGVSSSTDGTMKIWQASNGELRRVLEGHVFDVNCCRFF
		1	
1			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL
6267	3	622	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFSQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFTASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK
6267	3	622	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFFQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS
6267	3	622	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDCNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA
6267	3	622	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDCMIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC
6268	160	622	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFSQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGFQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCONLPAGLSSAIIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSL HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATMEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRORAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEBPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPB
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATMEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTVWLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDCNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSPEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEBPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFRQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGFQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCONLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFSQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALTDNPLTLLLSTDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEBPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPB SQANSGALDTNQVLLHKIPPRKRRKRCDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIKKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCCKGFVQSSSLTQHQRVHS GERPFECQBCGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR
6268	160	1368	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFSQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSTDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKFTFSRSTKQITFFIRIKKGSQVCCCCSECGK IFNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQBCGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR
			PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATMEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYI9BKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRORAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEBPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL
6268	160	1368	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFSQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSTDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKFTFSRSTKQITFFIRIKKGSQVCCCCSECGK IFNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQBCGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR
6268	160	1368	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATMEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYI9BKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRORAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEBPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL
6268	160	1368	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATMEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYWLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPB SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSLTQHQRVHS GEPFECQECGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT
6268	160	1368	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDCNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCCKGFVQSSSLTQHQRVHS GEPFECQBCGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKELDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN
6268	160	1368	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFSQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISEKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEBPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKFTFSRSTKQITFIRIKKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQBCGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKSLDLAVKTMVEISRTQPLTRREQLHVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSINP TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY
6268	160	1368	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYI9BKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEBPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPB SQANSGALDTNQVLLHKIPPRKRLRKRDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQBCGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKELDLAVKTNVEISRTQPLTRREQLHVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSINP TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY WHWALYLIEKGEYEAALTIYDTHILPSLQANDAMLDVVDSCSML
6268	160	1368	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATMEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYISBKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRDRAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEBPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPB SQANSGALDTNQVLLHKIPPRKRLRKDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQBCGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKELDLAVKTNVEISRTQPLTRREQLHVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYGEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKBALSINP TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY WHWALYLIEKGEYEAALTIYDTHILPSLQANDAMLDVVDSCSML YRLQMEGVSVGQRWQDVLPVARKHSRDHILLFNDAHFLMASLGA
6268	160	1368	PSGLVVLSGGMDAQLKIWSAEDASCVVTFKGHKGGILDTAIVDR GRNVVSASRDGTARLWDCGRSACLGVLADCGSSINGVAVGAADN SINLGSFEQMPSEREVGTEAKMLLLAREDKKLQCLGLQSRQLVF LFIGSDAFNCCTFLSGFLLLAGTQDGNIYQLDVRSPRAPVQVIH RSGAPVLSLLSVRDGFIASQGDGSCFIVQQDLDYVTELTGADCD PVYKVATWEKQIYTCCRDGLVRRYQLSDL LGMMKKNNSAKRGPQDGNQQPAPPEKVGWVRKFCGKGIFREIWK NRYVVLKGDQLYI9BKEVKDEKNIQEVFDLSDYEKCEELRKSKS RSKKNHSKFTLAHSKQPGNTAPNLIFLAVSPEEKESWINALNSA ITRAKNRILDEVTVEEDSYLAHPTRORAKIQHSRRPPTRGHLMA VASTSTSDGMLTLDLIQEEDPSPEEPTSLC HRELCQNLPAGLSSALIDNPLTLLLSIDTYVMLQEPVTFQDVAV DFSREEWGLLGPTQRTEYRDVMLETFGHLVSVGWETTLENKELA PNSDIPEEBPAPSLKVQESSRDCALSSTLEDTLQGGVQEVQDTV LKQMESAQBKDLPQKKHFDNRESQANSGALDTNQVSLQKIDNPE SQANSGALDTNQVLLHKIPPRKRLRKDSQVKSMKHNSRVKIHQ KSCERQKAKEGNGCRKTFSRSTKQITFIRIHKGSQVCRCSECGK IFRNPRYFSVHKKIHTGERPYVCQDCGKGFVQSSSLTQHQRVHS GERPFECQBCGRTFNDRSAISQHLRTHTGAKPYKCQDCGKAFRQ SSHLIRHQRTHTGERPYACNKCGKAFTQSSHLIGHQRTHNRTKR KKKQPTS HASAPTRRNMAAASPLRDCHAWKDARLPLSTTSNEACKLFDATL TQYVKWTNDKSLGGIEGCLSKLKAADPTFVMGHAMATGLVLIGT GSSVKLDKELDLAVKTMVEISRTQPLTREQLHVSAVETFANGN FPKACELWEQILQDHPTDMLALKFSHDAYFYLGYQEQMRDSVAR IYPFWTPDIPLSSYVKGIYSFGLMETNFYDQAEKLAKEALSINP TDAWSVHTVAHIHEMKAEIKDGLEFMQHSETLWKDSDMLACHNY WHWALYLIEKGEYEAALTIYDTHILPSLQANDAMLDVVDSCSML

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 -	\=possible nucleotide insertion)
			DGNPDRVLELLLPIRYRIVQLGGSNAQRDVFNQLLIHAALNCTS
			SVHKNVARSLLMERDALKPNSPLTERLIRKAATVHLMQ
6270	23	2086	SVTVTLGSEGDGRPPTYHLEEMEQEPQNGEPAEIKIIREAYKKA
			FLFVNKGLNTDELGQKEEAKNYYKQGIGHLLRGISISSKESEHT
			GPGWESAROMOOKMKETLONVRTRLEILEKGLATSLONDLOEVP
1			KLYPEFPPKDMCEKLPEPQSFSSAPQHAEVNGNTSTPSAGAVAA
ì			PASLSLPSQSCPAEAPPAYTPQAAEGHYTVSYGTDSGEFSSVGE
i			EFYRNHSQPPPLETLGLDADELILIPNGVQIFFVNPAGEVSAPS
1			YPGYLRIVRFLDNSLDTVLNRPPGFLQVCDWLYPLVPDRSPVLK
ļ			CTAGAYMFPDTMLQAAGCFVGVVLSSELPEDDRELFEDLLRQMS
Ì			DLRLQANWNRAEEENEFQIPGRTRPSSDQLKEASGTDVKQLDQG
			NKDVRHKGKRGKRAKDTSSEEVNLSHIVPCEPVPEEKPKELPEW
1			SEKVAHNILSGASWVSWGLVKGAEITGKAIQKGASKLRERIQPE
	Ì		EKPVEVSPAVTKGLYIAKQATGGAAKVSQFLVDGVCTVANCVGK
			ELAPHVKKHGSKLVPESLKKDKDGKSPLDGAMVVAASSVQGFST
1			VWQGLECAAKCIVNNVSAETVQTVRYKYGYNAGEATHHAVDSAV
		ì	NVGVTAYNINNIGIKAMVKKTATQTGHTLLEDYQIVDNSQRENQ
ì			EGAANVNVRGEKDEQTKEVKEAKKKDK
6271	32	1058	GCGVKTAGMVGREKELSIHFVPGSCRLVEEEVNIPNRRVLVTGA
			TGLLGRAVHKEFQQNNWHAVGCGFRRARPKFEQVNLLDSNAVHH
Į.		İ	IIHDFQPHVIVHCAAERRPDVVENQPDAASQLNVDASGNLAKEA
ł			AAVGAFLIYISSDYVFDGTNPPYREEDIPAPLNLYGKTKLDGEK
[AVLENNLGAAVLRIPILYGEVEKLEESAVTVMFDKVQFSNKSAN
ĺ			MDHWQQRFPTHVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQM
1			TKYEMACAIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKL
			ETLGIGQRTPFRIGIKESLWPFLIDKRWRQTVFH
6272	1136	528	GAVMEDAAAPGRTEGVLERQGAPPAAGQGGALVELTPTPGGLAL
1			VSPYHTHRAGDPLDLVALAEQVQKADEFIRANATNKLTVIAEQI
İ			QHLQEQARKVLEDAHRDANLHHVACNIVKKPGNIYYLYKRESGQ
1			QYFSIISPKEWGTSCPHDFLGAYKLQHDLSWTPYEDIEKQDAKI
L			SMMDTLLSQSVALPPCTEPNFQGLTH
6273	256	843	SCPRVSPECRSLGCQVMFSLPLNCSPDHIRRGSCWGRPQDLKIA
1			SAAWNSKCHPGAGAAMARQHARTLWYDRPRYVFMEFCVEDSTDV
1			HVLIEDHRIVFSCKNADGVELYNEIEFYAKVNSKDSQDKRSSRS ITCFVRKWKEKVAWPRLTKEDIKPVWLSVDFDNWRDWEGDEEME
			LAHVEHYAEVRDNTYCVLPT
		1	LAHVEHYAEVRDNTYCVLPT AAAAMAAAAGGGAGAARSLSRFRGCLAGALLGDCVGSFYEAHDT
6274	56	1142	VDLTSVLRHVQSLEPDPGTPGSERTEALYYTDDTAMARALVQSL
1			LAKEAFDEVDMAHRFAQEYKKDPDRGYGAGVVTVFKKLLNPKCR
			DVFEPARAOFNGKGSYGNGGAMRVAGISLAYSSVQDVQKFARLS
1			AQLTHASSLGYNGAILQALAVHLALQGESSSKHFLKQLLGHMED
			LEGDAQSVLDARELGMEERPYSSRLKKIGELLDQASVTREEVVS
			ELGNGIAAFESVPTAIYCFLRCMEPDPEIPSAFNSLQRTLIYSI
			SLGGDTDTIATMAGAIAGAYYGMDQVPESWQQSCEGYEETDILA
	1		QSLHRVFQKS
6075	20	565	SRRGRARCLARGSRRPVPRPAKTMAFMVKTMVGGQLKNLTGSLG
6275	20	505	GGEDKGDGDKSAAEAQGMSREEYEEYQKQLVEEKMERDAQFTQR
			KAERATLRSHFRDKYRLPKNETDESQIQMAGGDVELPRELAKMI
			EEDTBEEEEKASVLGQLASLPGLNLGSLKDKAQATLGDLKQSAE
			KCHVM
6376	707	97	TLLPLPPLPDTEGMILLNTGLEGTVAENPVPIVHTPSGNILTLE
6276	797) 31	SCLOOLATHPGHWGIHLQIAEPAALRPSLALLARLSSLGLLHWP
	1		VWVGAKISHGSFSVPGHVAGRELLTAVAEVFPHVTVAPGWPEEV
			LGSGYREQLLTDMLELCQGLWQPVSFQMQAMLLGHSTAGAIGRL
			LASSPRATVTVEHNPAGGDYASVRTALLAARAVDRTRVYYRLPQ
			GYHKDLLAHVGRN
L		_l	

ID	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No. location corresponding to first amino acid residue of amino acid residue of amino acid residue of amino acid sequence 2744 Eventual S	_			
Cocation Corresponding Cofired to first State Commission Corresponding Cofired to first State Commission Corresponding Cofired to first State Commission Commis	I	, , ,		
corresponding to first amino acid amino acid residue of amino acid residue of amino acid residue of amino acid sequence sequence sequence company to the sequence sequence company to the sequence sequence company to the seq		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first amino acid residue of sequence 6277 4600 2744 WTYPODAM, Y=TYPODAM, Y=TYPODAM, Y=Stop COOM, /=possible nucleotide delectide delection 6277 4600 2744 MARTEMELYYSYFKTIVEAPSFLNGVMHNDKLTEYPLVIN LKRPNLYPSYLIASWYRITKINDLIGIOTKICWTVIIGEGISI TESCEGIGPACFYVAVIIINMALFFIGYTYLESSALVING LKRPNLYPSYLIASWYRITKINDLIGIOTKICWTVIIGEGISI TESCEGIGPACFYVAVIIINMALFFIGYTYLSSALVING LKRPNLYPSYLIASWYRITKINDLIGIOTKICWTVIIGEGISI TESCEGIGPACFYVAVIIINMALFFIGYTYLSSALVING LKRPNLYPSYLIASWYRITKINDLIGIOTKICWTVIIGEGISI TESCEGIGPACFYVAVIIINMOMPACFYULTGIASLEAVYVVO IDICKLEKIIVIMISLALCEVIMEOSMALITSYSLVIIM TKHYNGSLIALCISNVFFMLPWGPAGFYULTGIASLEAVYVVO HALQLLAYTALGILIMELKLEIPHENCMASIICISRQLFGMLP KWIPGALVVATILAAMSIGGSANLOTOMNIUGEFSNLOGEGII KWIPGALVVATILAAMSIGGSANLOTOMNIUGEFSNLOGEGII KWIYSMYSKRAAEEVKRELIKLKVNYYILEESWCVRSKPGGSP PEIMOVEDPANAGKTELCKLIVVGKSKPFFTTVFOKYVVULEV. KE 6278 3 823 ILFRIVLLSLYVLINSVATEERKPABVLIVEGGGYAVWGTVLIL IRTILEYCGGVNN FSYTTDMLTRISDLIKYFNSSCOLUGAN ALQVVGIKKITTKNILASSRCLQIVYGKSPFFTYFOKYVVULEV. KE 6278 4 823 ILFRIVLLSLYVLINSVATEERKPABVLIVEGGGYAVWGTVLIL IRTILEYCGGVNN FSYTTDMLTRISDLIKYFNSSCOLUGAN ALQVVGIKKITTKNILASSRCLQIVYGKSPFFTYFOKYVVLUEV. KE 6279 127 1687 GGARASDGARKÇFWKRSNSKLPGSIQHVYGAQHPFFDPLHGTI LKRATANPTTPVKARKVSTOFFESNTISAMDAGEDDDBLIAN ABSINSVVMETARNVLNENHSGORGSFTLIGEGFELIOKOKREBAE PPSPSGDLIRUKSVSSESHTSCPARSASDABLGRGSDLISHGEN ALSNSSVVMETARNVLNENHSGORGSFTLIGEGFELIOKOKREBAE PPSPSGDLIRUKSVSSESHTSCPARSASDABLGRGSCDLIBELGE LWSGIBKPVRPMTWKLLISGYLDANDRRATLGRKOKSYPTE ELYDSKNDEVHOPTTWTHILDJERGOVALVKKEELE LEWSLIBKPVRPMTWKLLISGYLDANDRRATLGRKOKSYPTE ELYDSKNDEVHOPTTWTHILDJERGOVALVKKEELE LEWSLIBKPVRPMTWKLLISGYLDANDRRATLGRKOKSYPTE ELYDSKNDEVHOPTTWTHILDJERGOVALVKKEELE LEWSLIBGYFRIBTYGGABATLOKYRKEELE LEWSLIBGYFRIBTYGGABATLOKYRKEELE LEWSLIBGYFRIBTYGGABATLOKYRKEELE LEWSLIBGYFRIBTYGGABATLOKYRKEELE LEWSLIBGYFRIBTYGGABATLOKYRKEELE LEWSLIBGYFRIBTYGGABATLOKYRKEELE LEWSLIBGYFRIBTYGGABATLOKYRKEELE LEWSLIBGYFRIBTYGGABATLOKYRKEELE LEWSLIBGYFRIBTYGGABATLOKYRKEELE LEWSLIBGYTHOMOTOTISTLDSCHARGEEEEEEE DUDLAQULAYLLRRGGVELISSSSSONGALERGARGEEEEEE DUDLAQ	l l	corresponding		
residue of amino acid sequence Codon, /=possible nucleotide deletion, codon, /=possible nucleotide deletion, codon, /=possible nucleotide insertion) 6277 46600 2744 MAPRTEMSUTYSTYTUSAPSELMGVMMIMMORLITEYPLVININ LRKPNLYPSVIJABNITYSAPSELMGVMMIMMORLITEYPLVININ LRKPNLYPSVIJABNITYSAPSELMGVMMIMMORLITEYPLVINING LAKENDLYPSVIJABNITYSAPSELMGVMMIMMORLITEYPLVINING LRKPNLYPSVIJABNITYSAPSELMGVMMIMMORLITEYPLVINING LRKPNLYPSVIJABNITYSAPSELMGVMMIMMORLITEYPLVINING LRKPNLYPSVIJABNITYSSVI	<u> </u>		amino acid	
residue of amino acid sequence Codon, /=possible nucleotide deletide sequence Codon, /=possible nucleotide deletide sequence Codon, /=possible nucleotide sinsertion) 6277 4660 2744 MARTEMSILYSYPKTIVEAPSFLNGVMHNDKLTEYPLVIN LKRYNLYSYLIASWYRIYKHDLIGIOTKICMTVTIGEGISI TESCEGIGPACFYVAVIFILNGLMMALFFIGTTYLESSFLDYLVGGUTUTUTUTUSEGISI TESCEGIGPACFYVAVIFILNGLMMALFFIGTTYLESSFLDYLVGGUTUTUTUTUSEGISI TESCEGIGPACFYVAVIFILNGLMMALFFIGTTYLSSFLOWIGH VTVLCFFFRHGEGFRWHMTPDLESSFSYPLUMGLUVTHILR THLYRGSLIALCISNVFFMLPMGPMGLTVTASLFOFM IN THE THE THIN SELECTION CONTROL OF THE THE THIN SELECTION CONTROL OF THE THIN SELECTION CO		amino acid		S=Serine, T=Threonine, V=Valine,
amino acid sequence Codom, /=possible nucleotide deletion, -possible nucleotide insertion -costible nucleotide insertion -c	}	residue of	amino acid	The state of the s
Sequence _possible nuclectide insertion		amino acid	sequence) · · · · · · · · · · · · · · · · · · ·
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VTULCFFFNIGSCTRUMMTPPLERSFSYPFLVLQMILUTHILER TKLYRGGSLIALCISNUFPMLDWCAPGPUTQLASILPAYVVVO) IDICKLRKI IYIHMI SLALCFVIMFGNSMLLTSYTASSLVI IM ILAMKPHFLKINVSELSIMVIQGCWILFGYVILKYITSKI FGI IN NAHIGKLIATKISFFSYKOFDTLIYTCAAFDFMEKSTFLRTKY LLLPVILVGFVA LVRKI ISDMWGULAKQOTHVRKHOFDIGSLUV HAIQKLIATALGILIMRIKLFITFPHCVMASLICSRQLEGGILFG KVHPGAIVFAILAMSI JGGSANLOTOMNIVGEFSNLEGGEILFE IKYSYK DAVAVFAAMPTALGSTLIMRIKLFITFPHCVMASLICSRQLEGGILFG KVHPGAIVFAILAMSI JGGSANLOTOMNIVGEFSNLEGGEILFE IKYSYK DAVAVFAAMPTALASYKISLARI JWHSPHYEDAALBARI KIVYSMYSRKAAEEVKRELIKLKVNYYI LEESWCVRRSKPGCSM PEIMOVEDPANAGKTPLCNILLVKDEKPHFTTVFQNSVYKVLEV. KE 6278 3 823 ILFRIVILLSLVYLLNSVATEERKPAEVLIVEGGQYAVVGTVLLIV. KE IRIILEYGCGVONIP SVYTMMLRISJBLIKKFNSRSCQLVLGAA ALQUVGLKTITTKNIALSSRCLQLIVHTIPVTRAHFEARLEPKK YSMLHRHPHITKNYHOHA EI SAKUVA BLEPPKLLSKYEVKA PVPSACFRNICKQMTKMHEAI FDLLPEGOTOMLFIRINASYKLE LKKQLSHLNVINDGGPQNGLVTADVAFYTONLQALKGIKDLDLIM ALGUSHLNVINDGGPQNGLVTADVAFYTONLQALKGIKDLDLIM ARSILNSEVVWETANRVLRNISGROGRPTLQAGGHPFDPLLHGTI LKSTAMMPTTPVWARKVSTFGFESNTSDANDAGEDDDBLLIAM ARSILNSEVVWETANRVLRNISGROGRPTLQAGGHPFDPLLHGTI LKSTAMMPTTPVWARKVSTFGFESNTSDANDAGEDDDBLLIAM ARSILNSEVVWETANRVLRNISGROGRPTLQAGGCLPHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELR LSWASGIPKPVREMTWKLLSGYLPANVDRRPATLGRKGYFPAFI EHYDSRNDEVNGDTYRGVHIND PREMSPEALILQFKVTEIFERI LEIMAIRHPASGYVQGINDLVTFFVVPICGYTLABEDDTTUDV GVPABVLCNLTBADTTWCRNSLLDGIGDNYTTAQPGIGMKVMLME ELVSRIDEGVHRHLDQHSVRYLLGFAFRMNNILLMREVPLRCTIR LEIMATRHPASGYVGGINDLVTTFFVVPICGYTLABEDDTTUDV GVPABVLCNLTBADTTWCARSLLDGIGDNYTTAQPGIGMKVMLME ELVSRIDEGVHRHLDQHSVRYLLGFAFRMNNILLMREVPLRCTIR LEIMATRHPASGYVGLVQCGGAANLQFIQALLDSEEEDDEA WORLGFRYNPEVDATPDTRELEFRE KTOYELANYGLGLIRRAA OKHISFFRININGREGALGRGSFSLEGGSFVISHFLDNILGGTTOS YSGKAFCGIYSKNGGIFMSACODOTIRLYDCRYGRFKFKSIKN RDWTANAVDAVDATPDONIBFLYSSMGSTYLTICHLTYGGGOTHMALD LRPDERRFAVFSIAVSSDGRFVLGGANDGCLYVFDREQNRRTLQ IRSHEDOVNAVAPADISSGILFSGGDATLISNSOCTIKLDGIRRAS BOMMASRQAATQUNADVTPDONIFLYSSMGSVIYNYOLLLGSHIVK LTINHKACVRDVSNHPPEKKIVSGGGAANLLGVVVYDLLGSHIVK LTINHKACVRDVSNHPPEKTREGOPTRELEFRE KTQVELANTQLGLGRAA WOR	į į			LKRFNLYPEVILASWYRIYTKIMDLIGIOTKICWTVTIGEGLSP
TKLYRGSLIALCISNVFMLPMCPAGPTULTQIASLPAYYVVOS LDICKLRKIYITHMISLALCYLMPGMULTSYXASSLVIIW ILAMKPHFLKINVSELSLWVIQGCWLFGTVILKYLTKKIFGIF NDAHLGNLLTSKFSYKDFDTLLYTCAAEPDPMEKETIRTTKY LLLPVVLWGVPAIVRKIJSDMWGULAKQOTHVRKHGFDHGELVS HALQLLAYTALGGILMRLKFLTFHHCVMASLICSRQLFGMLFC KWHPGAIJVFAILAMSIGSANLOTHWCBSPNLPGERLIBE IXYSTKPDAVFAGAMPTMASVKLSALRPIVMHPHYEDAGLARRI KIVYSMYSRKAAEVKRELIKLKVNYYILESWCVRSKPGCSB PEIWDVEDPAAAGKTPLCNLLVKDSKPHFTTVPGNSVKKULEV. KE 6278 3 623 ILFRIVLLSLVYLLNSVATEERKPASVLIVEGQQYAVVGTVLLI IRIILEYCQGYUNIPSVTTOMLTRLSDLLKYFNSRSCQLVLGAG ALQVVGLKTITTKNLALSSRCLQLIVHYIPVIRAHFEARLPPK YSMLRHPHTTKUYHDHTABISAKLVAIMDSLEPKLLSKKFEVKP PVPSACFRNICKQMTKMHBAIFDLDEEQTYMFFRINSYKLE LKKQLSHLNVINDGGGPGGLVTADVAFTLQALKGKEDLDL MAEIHEQKR GGMASDABARKOFWKRSNSKLPGSTQHVYGAQHPPFDPLLHGT LRSTAKMPTTPVKAKRVSTPGEFESNTSDANDAGEDDDELLAMA ABSLNSEVVMETANVLRNISGRGRPTLGARGKGVKPREAB PSPPSGDLKLVKSVSSSHTSCPASSADAJCRSQSLPHSAT VTLGGTSDPSTLSSSALSERBASRLDKKFQLLAGNNTDLEELRR LSWSGIPKPVRPMTWKLLGSYLPAVURAPLTQAKKGVYFAFI EHYYDSRNDEVHODTYRGIHDIPRNSPEALILQFKVTEIFBRF LETHMIRHPSGSYQGGINDLTVPFFVVZLYBABEVDTUVUS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVMLE ELVSRIDEQVHRHLDQHEVYYLQFAFRMMNNLLMREVPLRCTIR LETHMIRHPSGSYQGGINDLTVPFFVVZLYBABEVDTUTUS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVMLE ELVSRIDEQVHRHLDQHEVYYLQFAFRMMNNLLMREVPLRCTIR LETHMIRHPSGSYQGGINDLTVPFFVVZLYBABEVDTUTUS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVMLE ELVSRIDEQVHRHLDQHEVYYLQFAFRMMNNLLMREVPLRCTIR LDHTYGSPBFDGSHHTHYLVCARFLVMREVPLRCTIR LDHTYGSPBFDGSHHTYLVCARFLVMREVFREEBEEDDR WDGRLGGRYNPPVDATPDTRELEFNEIKTQVELATQGLGRAM WGRLGDRYNPPVDATPDTRELEFNEIKTQVELATQGLGRAM GKHSFFRMLHQRENGLCHGSSPSILEGSRVISHFLPNDLGGTTDS YSGKAFGGIYSKUGGIFFMSACQDOTIRLYDCRYGRRFKFSIKA RPVGMSVLUDWATPPDONBFLYSSMSDYLHICNIYGGGDTHTMALD LRPDBRRFAYFSIAVSBORBVLGGGANGCLYVFDREONRETU, ISBHEDDVANAPADISGJLFSGGGANGCLYVFDREONRETU, ISBHEDDVANAPADISGJLFSGGGANGCLYVFDREONRETU, ISBHEDDVANAPADISGJLFSGGGANGCLYVFDREONRETU, ISBHEDDVANAPADISGJLFSGGGANGCLYVFDREONRETU, ISBHEDDVANAPADISGJLFSGGGDANGLYGWDRTTMEDDER GWHLTIRCFSFBIHSGGPTSSBORGVVVYDLLGGHTVK LTINHKACVRDVSNHPPECHTRUTGGGTSS	l l			TESCEGLGDPACFYVAVIFILNGLMMALFFIYGTYLSGSRLGGL
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NDAHIGNILITSKFFSYKDPDTILITTCAAERDPMEKSTELRITKY LLLPVVLVGFVAIVRKIISDMMGVLAKQGTHVRKHQFDHGELVJ HALQLLATTALGILIMRLKFLTHEMHCVMASLICSRQLFGMLFK KVHPGAIVFAILAAMSIQGSANLQTQWNIVGEFSALLPQEELIE INYSTKPDAVFGAGMFTMASVUKLSHIVNIHPHYEDDGLIRAT KLVYSMYSRKAAEEVKRELIKLKVNYYILEESWCVRRSKPGGSS PEIMDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSYKYKULEV KE	į į			IDICKLRKIIYIHMISLALCFVLMFGNSMLLTSYYASSLVIIWG
LLLPVVLVGFVA IVRKII ISDMGVLAKQQTHVRKHQFDHGELUY HALQLLAYTALGI LIMRLKIFLTPHMCVMASLICSRQLFGWLFG KVHPGAIVFAILAAMSIQOSANLQTQMNIVGBFSMLPQEELIBE IKYSTKPDAVFAGAMFTMASVKLSALRPIVNHHYEDAGLRAR; KLYSMYSFRKAAEEVKREIL IKKUVHLESBKVVRSRKPQGSN PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVYKVLEVV KE 6278 3 823 ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLI IRIILEYCOGJOMI PSVTTDMLTKLSDLLKYFNSRSCQLVLGAA ALQVVGLKTITTKNLALSSRCLQLIVHYIPVTRAHFEARLPPK YSMLAHFPHITKUYHHHIAEISALUAIMDSEDDKLLSKYEVX PVPSACFRNICKOMTKMHBAI FDLLPBEQTQMLFLRINASYKLL LKKQLSHLNVINDGEQNGLVTADVAFYTONLQALKGLKDLDLM MAEIMEQXR 6279 127 1687 GGAMASDGARKOFWKRSNSKLPGSIQHYYGAQHPPFDPLLHGTI LSTAKMPTTPVKAKEVSTFOEFSSNTSDAWDAGEDDDELLAM ABSLNSEVVMETANRVLRNHSORGGRFTLQEGFGLQXPRPEAB PPSPPSGDLRLVXSVSSSTHSCPARSDAAPLCRSOSLPHSAT VTLGGTSDPSTLSSSALSERBASRLDKFKQLLAGPNTDLEELRR LSWGIFKPVRTWKLLISGYLPANVDRRPATLGRKQKEYPATI EHYYDSRNDEVHODTTRQHIDIPTRAMPEALLQRKVEYTEREL LFIWAIRHPASGTVQGINDLVTPFFVVPICEYIBAEEVDTVDUS GVPAEVLCNIBADTYWGNSLLDGLOTYFAQPGIQHKVMMLB ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIR LMDTYGSEPDGFSHFHLIVYCAAFLVRNKKS LIBERDFQELLLET UNLFTHAHDDEDISLLLABAYRLKFAFADAPHNYKK OKUSFFRNLHQRERGLCHRGSFSLGEGSRVIDCHTGPGLLLET UNLFTHAHDDEDISLLLABAYRLKFAFADAPHNYKK ROUGHSVLDVAAFTPDONHFLYSSWSDYIHLCHIYGEGDTHTALD LRPDERFFAVFSIAVSSGGFSUGGSRTVLCHRGQGGATLQFIQALGRERAB OKHSFFRNLHQRERGLCHRGSFSLGEGSRVIDCHTFKFSIKA RDVGKSULDVAAFTPDONHFLYSSWSDYIHLCHIYGEGDTHTALD LRPDERFFAVFSIAVSSGGFVIGGANDCLYVFDREQNRTIT GRANGSGGATAQDANDYRRQOPKKRLKLEPGDSSLMTYRGH GVLHTLIRCRFSPIHSTQQFIYSGCSTGKVVVYDLLSGHIVKK LITNHKACVRDVSNHFPERKIVSSSMOCNLRIMGYRQABKFINGEDDE PVGALAGHQDGITFIDSKGDARYLISSSKOGTKRAGLRRSEEBEEDE GMEASRQAATQCMNDYRRQOPKKRLKLLEPGGSBLTTYRGH GVLHTLIRCRFSPIHSTQQFIYSGCSTGKVVVYDLLSGHIVKK LITNHKACVRDVSNHFPERKIVSSSMOCNLRIMGYRQABKFODDM PSSECAAPAPPQSSTFFSSFG BOMBASRGAAPAPPQSSTFFSSFG BOMBASRGAAPAPPQSSTFFSSFG BOMBASRGAAPAPPQSSTFFSSFG BOMBASRGAAPAPPQSSTFFSSFG BOMBASRGAAPAPPQSSTFFSSFG BOMBASRGAAPAPPQSSTFFSSFG BOMBASRGAAPAPPQSSTFFSSFG BOMBASRGAAPAPPGSSTFFSSFG BOMBASRGAAPAPPGSSTFFSSFG BOMBASRGAAPAPPGSSTFFSSFG BOMBASRGAAPAPPGSSTFFSSFG BOMBASRGAAPAPPGSSTFFSS	İ			ILAMKPHFLKINVSELSLWVIQGCFWLFGTVILKYLTSKIFGIA
HALQLLAYTAIG ILIMELKI PITPIMCVMASILICSRQLFGRLFY KVHPGAIVPAILAAMSI QGSANLQTQWNIVGEFSNLPQEELIE INYSTKPDAVPAGAMPTMASVLISALR PIVNHEHYEDAGIRARI KIVYSMYSRKAAREVKRELI KLKVNYYI LEESKUVRRSKPGCSP PEIWDVEDPANAGKTELKLKVNYYI LEESKUVRRSKPGCSP PEIWDVEDPANAGKTELKLKVNYYI LEESKUVRRSKPGCSP PEIWDVEDPANAGKTELKLKVNYYI LEESKUVRSKPGCSP PEIWDVEDPANAGKTELKLKVNYYI LEESKUVRSKPGCSP PEIWDVEDPANAGKTELKLKVNYYI LEESKUVRSKPGCSP PEIWDVEDPANAGKTELKLKVNYYI LEESKUVRSKPGCSP REIWDVEDPANAGKTELKLKVNYYI LEESKUVRSKVEVKX KE 6278 3 823 ILFRLVLLSLVYLLINSVATEERKPAEVLIVEGQQYAVVGTVLLI IRIILEYCQGVDNI PSVTTDMLTRISSLLKYTNSKSCQLVLGAC ALQVVGLKTTITKNLALSSRCLGLIVHYIPUTRAHFERALPPK, YSMLRHFDHTTKYSHVHIABSLPKULKSKYEVKX PVPSACFRNICKQMTKMHEAIFDLLDEEQTQMLFLRINASYKLE LKKQLSHLNVINDGGPQNGLVTADVAFYTGNLFAKRICALKGLKDLDLK MAEINEQKR PVPSACFRNICKQMTKMHEAIFDLLDEEQTQMLFLRINASYKLE LKKQLSHLNVINDGGPQNGLVTADVAFYTGALGAKGKLDLDLK MAEINEQKR PPSPSGDLRLVKSVSESHTSCDARDAGGEDDELLAMM AESLNSEVVMETANRVLRNHSQRQRFTLQEGPGLQXFPREAE PPSPSGDLRLVKSVSESHTSCPAESASDAAPLRGSQLPHSAT VTLGGTSDPSTLSSSALSERRASLDKFKQLLAGPNTDLEELRR LSWSGIPKPVWFMTWKLLSGYLPANVDRRPATLQRKQKEYPAFI EHYYDSRDBEVHGTVRQHIDTGNIT HTGRKQKEYPAFI EHYYDSRDBEVHGTVRQHTUNGTHID IFRBAELILQRKVUTETERRI LSWSGIPKPWFMTWKLLSGYLPANVDRRPATLQRKQKEYPAFI EHYYDSRDBEVHGTHUNDHUTSULDTHIDTELERR PEALILQRKVUTETERRI LPIWAIRHPASGYVQGINDLVTPFVVFICEYIEAEEVDTVDVS GVPARVLCNLEADTYNCMSKLLDGIQDNTTFAOPGIOMKVMKL EELVSRIDEQVHRHLUDHEVRYLOFAFRWINNLLMREVYLERGT LWBDTQSSPDGFSHFHLIYCCAAFLVRRKSILEERDFCELLEFI QNOLTAAHDDEDISLLLAAPRULKPADAPHNYKK LDMTYQSSPDGFSHFHLIYCCAAFLVRRKSILEERDFCELLEFI QNOLTAAHDDEDISLLLLAAPRULKPRIVVELATQUGLGRRAA QKHSFPRNLHGGRRGLCHRGSFSLGEGSRVISHLDPNLGFTDS YSGAFCGIYSKGOGJFMSACQDGTLRLYDCRYGRGTHTALD LRPDERRTAYFSILAYSSDGREVLGGANDGCLVYDFRCHNRTTUL GREMDDVNAVAPADISSGILFSGGANALGVFORGMTTURGDDP PVGALAGHODGITFIDSKGDARYLISNSKOOTIKLMOTRFSSR BGMEASGAAPAPVORDYRNOVPRVAVYPORGUNRTIVRGDDP PVGALAGHODGITFIDSKGDARYLISNSKOOTIKLMOTRFSSR BGMEASGAAPAPVORSTFSSEG BGMEASGAAPAPVORSTFSSEG BGMEASGAAPAPVORSTFSSEG BGMEASGAAPAPVORSTFSSEG BCMEASGAAPAPVORSTFSSEG BCMEASGAAPAPVORSTFSSTFSSEGDDRRGAGLRRSEEEEEDE BV	1			NDAHIGNLLTSKFFSYKDFDTLLYTCAAEFDFMEKETPLRYTKT
KVIPGAIVFAILAMSIOGSANLQTOWNIVGEFSNLPGEELIEW IKYSTKPDAVFAGAMPTMASVKLSALRPIVNHPHYEDAGLRATI KIVYSMYSRKAAEEVKRELIKLKWNYYLLEESWCVRRSKPOGS PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVPQNSVYKVLEV KE 6278 3 823 ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLIJ IRIILEYCGGVDNIPSVTTDMLTRLSDLLKYHSPASSCQLVLGAG ALQVVGLKTITTKNLALSSSRCLQLIVHYYPUTRAHFEARLPPK, YSMLRHFDHITKDVHDHIARISAKLVAINDSLPOKLLSKYEVX PVPSACFFRICKQMTKMHBAIFAKLLOGLUVHYTPUTRAHFEARLPPK, YSMLRHFDHITKDVHDHIARISAKLVAINDSLPOKLLSKYEVX PVPSACFRNICKQMTKMHBAIFAKLLOGLUVHYTPUTRAHFEARLPPK, YSMLRHFDHITKDVHDHIARISAKLVAINDAGFTGNLQALKGIKDLDLM MAEIWEQKR 6279 127 1687 GGMARADGARKOFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTI LRSTAKMPTTPVKAKRVSTFQEFESNTSDANDAGEDDDELLAMA ABSLNSEVVMETANRVLRNISORQGRPTLQEGPCLQOKPREAE PSPPSEGOLRILVSVSSESHTSCASASDAAPLGRSQSLPHSAT VTLGGTSDPSTLSSSALSBERASRLDKFKQLLAGPNTDLEBLRR LWSGTSDPSTLSSSALSBERASRLDKFKQLLAGPNTDLEBLRR LWSGTSDPSTLSSSALSBERASRLDKFKQLLAGPNTDLEBLRR LEWARIPAGSGYQGINDLVTPFFVVTICEYIBABEVDTVDVS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTPAQPSIQMKVMML ELVSRIDEQVRRHLDQHEVYYLOFAFRWMINLLMREVPLRCTIR LWDTYQSEPDGFSHFHLIYCCAFLVWRKEILBEKDFQOKLVENGE ELVSRIDEGVRRHLDQHEVYYLOFAFRWMINLLMREVPLRCTIR LWDTYQSEPDGFSHFHLIYCCAFLVWRKEILBEKDFQELLFLFL QNLPTAHNDEDISLLLAEAYRLKFAPADANNHYKK 6280 857 2515 ECCDQKMGSNSSSAGGGGDFSEGLPRRGAGLRRSEEBEEEDE MDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATQQLGLRRAA QKHSFFRNHLNGREGQUFLVGGOTIRLYDCRYGFRFKFSIKA RDVGNSVLDVAFTPDGNHFLYSSWSDYHICNIYGEGDTHTALD LRPDERFAVFSIAVSSDGREVLGGANDGCLYYFDREONRATLOF 1ESHEDDVNAVAFADISSQILFSGGDDAICKVWRRTMREDDDF PVGALAGHQDGITFIDSKGDAFYLISNSKDTIKLMDIRRFSSR BGMEASRQAATQQMDWYNGQOYKKMWRKLKLEGSSIMTYGRH GVLHTLIRCRFSPHSTQQFTYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSHHPPEBKIVSSSMDGALRKWQKROAEYPQDDM PSSECASAPAPVPQSSTPFSSGD FSCECASAPAPVPQSSTPFSSGD FSCECASAPAPVPQSSTPFSSGD FSCECASAPAPVPQSSTPFSSGD FSCECASAPAPVPGSSTPFSGGD FSCECASAPAPVPGSSTPFSGGD FSCECASAPAPVPGSSTPFSGGD FSCECASAPAPVPGSSTPFSGGD FSSECASAPAPVPGSSTPFSGGD FSCECASAPAPVPGSSTPFSGGD FSCECASAPAPVPGSSTPFSGG FSCECASAPAPVPGSSTPFSGGD FSCECASAPAPVGGSTGANLOFTQALLDGEDENDRA WGGRLGDRYNPVDATPDTRELEFREIKTQVELLATGGLGLGRRAA FGCECASAPAPVGGS	{			LLLPVVLVGFVAIVRKIISDMWGVLAKQQTHVRKHQFDHGELVY
IKYSTKPDAVFAGAMPTIMASVKI.SALRPIVNIPHYEDAGILARAR KIVYSMYSRKAAEEVKRELIKLKVNYYILBESWCVRRSKPGGS PEIMOVEDPANAGKTPI.CNILVKDSKPHFTTVPQNSVYKVLEV KE 6278 3 823 ILFRLVLISLVYLINSVATEERKPAEVLIVEGQQYAVVGTVLILI IRI ILEYCQGVDNIPSVTTDMITRI.SDLIKYFNSRSCQLVIGAG ALQVVGLKTITTKNIAISSRCLQLIVHYIPVTRAHFEARLPPK YSMLRHPHHITKDHDHIARISSRCLQLIVHYIPVTRAHFEARLPPK YSMLRHPHHITKDHDHIARISSRCLQLIVHYIPVTRAHFEARLPPK YSMLRHPHHITKDHDHIARISSRCLQLIVHYIPVTRAHFEARLPPK YSMLRHPHHITKDHDHIARISSRCLQLIVHYIPVTRAHFEARLPPK YSMLRHPHHITKDHDHIARISSRCLQLIVHYIPVTRAHFEARLPPK LKKQLSHLNVINDGGPQNGLVTADVAFYTGNIQALKGIKCHLDLN MASIHEGKR 6279 127 1687 GGAMASDGARKQFWKRSNSKLPGGIQHVYGAQHPPFDELLHGTI LRSTARMPTTPVKAKRVSTFQEFESNTSDAWDAGEDDDELLAMA ASSLNSEVVMTEMAVVLRNISQRQGRPTUQBGPGLQQKPPREAE PPSPPSGDLRLVKSVSSESHTSCPASSASDAAPLQRSQSLPISAT VTLGGTSDPSTLSSSALSEREASRLDKFRQLLAGPNTDLEELRR LSWSGIPKPVRPMTWKLLSGYJPANVDRRPATLQRKQKEYPAFI EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQPKVTEIFERI LFIWAIRHPASGYVQGINDLVTPFVYITCEYIBAEEVDTYDVS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE ELVSRIDEQVURHLDQHEVYILQFAFRMMINLLMREVPLRCTIR LEMDTYGSEPDGFSHHJYVCAR-FVVFICEYIBAEEVDTELDELT QNLPTAHMDDEDISLLLARAYRLKFAFADAPNHYKK ELVSRIDEQVURHLDQHEVYILQFAFRMMINLLMREVPLRCTIR LWDTYGSEPDGFSHHJYVCAR-FWRKEILLEGENDFQELLTIT QNLPTAHMDEDISLLLLARAYRLKFAFADAPNHYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGSGDFSEGLPRRGAGLRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGANNLQFIQALLDSEEENDERA WOGRIGDRYNPPVDATPDTRELEFREIKTQVELATGLGUGRRAA QKHSFFRMLHQREBGLCHRGSPSLGGSRVISHFLPDLGFTDS YSQKAFGGIYSKDGQIFMSAGQDQTIRLYDCRYGFRRFKSIRA RDVGMSVLDVAFTDGMHFLYSSWSDYHHICNIYGGGDTTTALD LRPDERRFRAYSIANSAGGSGDMSGCLYVFOREONRATIQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPR PVGALAGHQDGITFIDSKGDAYLIISNSKDTIKMDIRRFSSR GMEASRQAATQQMDVNRQQVPKAWRKLKLPGDSIMTYGMG GVHTTLIR.GRFSPTHSTGQQFTYSGCSTIKVVVYDLLSGHIVKK LTNNKACVRDVSWHPPEKIVSSSWDGHKAWRIKLIFDGSIMTYGMG GVHTTLIR.GRFSPTHSTGQQFTYSGCSTIKVVVYDLLSGHIVK LTNNKACVRDVSWHPPEKIVSSSWDGARGGRRSSEEBEEEE DVDLAQVLAYLLRGQVRLVQGGGAANLQFTQALLDSBEENDRA WGGRLGDRYNPVDATPDTRELEFREIKTQVELATGGLGRRSEE				HALQLLAYTALGILIMRLKLFLTPHMCVMASLICSRQLFGWLFC
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6278 3 823 ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLI IRRILEYCGGVDNIPSVTTDMLTRLSDLLKYFNSRSCQLVLGAG ALQVVGLKTITYRNLALSSRCLQLIVHYIPVIRAHFERALPPK YSMLRHFDHITKDYHDHIAEISAKLVAIMDSLPDKLLSKYEVKA PVPSACFRRICKQMTKMHBAIFDLLEEQTQMLFLRINASYKLE LKKQLSHLNVINDGGPQNGLVTADVAFYTGNLQALKGLKDLDLN MABIWEQKR 6279 127 1687 GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHFPFDFLLHGTI LRSTARMPTTPVKAKRVSTFQFESNTSDAWDAGEDDDELLAMM ABSLNSEVVMETANRVLRNHSQRQGRPTLQGGGLQCKPREBAE PPSPPSGDLRLVKSVSSSHTSCPAESASDAAPLQRSQSLPHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELER LSWSGIPKPVRPMTWKLLSGYLPANVDRRPATLGRKQKEYPATI EHYYDSRNDEVHQDTVRQHIDIPFRVPFICEYIEAEEVDTVDVS GVPAEVLCNIEADTYWCMSKLLDGIQDNTTFAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEWYLQFAFRWMNNLLMREVPLRCTIR LWDTYQSEPDGFSHFHLYVCAAFLVRWKEILEEKDFQELLFI QQLLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK 6280 857 2515 ECCDQKMGSRNSSAGSGDPSEGLPRRAGGLRRASEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFIELKTQVELATGQLGLRRAA QKHSFFRMLMQREGGLGHAGGLRASEEEEEEDE DVDLAQVLAYLLRRGGVFLVGGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRRTLQ LRPDERFFAVFSIAVSDGGFVLGGANDCCLYVFDREQNRTTQ LRSHEDDVAVAFADISSQILFSGGGDATCKWDGTLKWDGRFSSK GGMEASRQAATQQNMDYRMQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSFIHSTGQQFTYSGGSTGKVVVYDLLSGHIVKK LTINKACVRDVSWHPPEEKIVSSWBGDIRLWQYRQAEYFQDDM PBSECASAFAPVPQSSTFFSSFQ 6281 857 2515 ECCDQKWGSRNSSAGGSGDPSEGLGRRGAGLRRSEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSBEENDRA WDGRLGDRYNPPVDATPDTRELEFREIKTQVELARGLGLRRAA				PEIWDVEDPANAGKTPLCNLLVKDSKPHFTTVFQNSVYKVLEVV
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ALQVVGLKTITTKNLALSSRCLQLIVHYIPVIRAHFEARLPPKÇ YSMLRHFDHITKNJAHDSISAKLAIMDSEJPKLLSKYEVKY, PVPSACFRIICKQMTKMHEAIFOLLPEGOTOMLFILTINAGYKLE LKKQLSHLNVINDGGPQNGLVTADVAFYTGNLQALKGLKDLDLN MAEIWBQKR 6279 127 1687 GGAMASDGARKQFWKRSNSKLPGSIQHVYGAQHPPFDPLLHGTI LRSTAKMPTTPVKAKRVSTFQEFESNTSDAWDAGEDDDELLAMA ABELNSEVVMETANRVLRHHSQRQGPFLLGEGGLQCKPRPBAE PPSPPSGDLRLVKSVSSSHTSCPAESASDAAPLQRSQSLPHSAT VTLGGTSDPSTLSSSALSEREASRLDKFKQLLAGPNTDLEELER LSWSGIPKPVRPMTWKILSGYLPANVDRRPATLGRKÇKEYPAFI EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQPKVTEIFERI LFIWAIRHPASGYVQGINDLVTFFFVVFICEYIEAEEVDTVDVS GVPAEVLCNIEADTYWCMSKLLDGIQDNTYFAQPGIQMKVKMLE ELVSRIDEQVHRHLDQHEVRYLQFAFRWMNNLLMREVPLRCTIT LWDTYQSEPGFSFHFHLYVCARFLVXWKKSILEEKDPGELLFI QNLPTAHWDDEDISLLLAEAYRLKFAFADAPNHYKK 6280 857 2515 ECCDQKMGSRNSSSAGSGSDDFSEGLPRGAGCLRRSEEEEEEEDE DVDLAQVLAYLLRGQVGLVLQGGGANLQFIQALLDSEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFFRMLHQRERGLCHRGSFSLEGSKVISHFLENDLGFTTDS YSQKAFCGIYSKDGQIFMSACQDQTTRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDONHFLYSSWSDLYHICNIYGEGDTHTALD LRPDERFFAVFSIAVSDGREVLGGANDGCLYVFDREQNRRTLQ UESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKQTIKLMQYRCABYPQDDM PSEECASAPAPVPQSSTPFSSFQ GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYVLLSGHIVKK LTINHKACVKDVSWHPPEEKIVSSSWDGNLRLMQYRQABYPQDDM PBSEECASAPAPVPQSSTPFSSFQ 6281 857 2515 ECCDQKMGSRNSSSAGGSGDDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRGGGGAANLQFIQALLDSBEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA	6278	3	823	ILFRLVLLSLVYLLNSVATEERKPAEVLIVEGQQYAVVGTVLLL
YSMLRHPDHITKDYHDHIAEISAKLVAIMDSLFDKLLSKYEVEA PVPSACFRNICKOMTKHHEAITDLIPEEQTQMLFIR.INASYKLE LKKQLSHLNVINDGGPQNGLVTADVAFYTGNLQALKGLKDLDLN MAEIWEQKR 6279 127 1687 GGAMASDGAKQFWKRSNSKLPGSIQHYYGAQHPPFDPLHHGTI LRSTAKMPTTPVKAKRVSTFQEFESNTSDAMDAGEDDDELLAM AESLNSEVVMETANRVLRNHSQRQGRPTLQEGPGLQQXPRPEAE PPSPPSGDLKLVKSVSESHTSCPARSASDAAPLQRSQSLPHSAT VTLGGTSDPSTLSSSALPERASABLAKFKQLLAGENTDLEELER LSWSGIPKPVRPMTWKLLSGYLPANVDRRPATLQRKQKEYFAFI EHYYDSRNDEVHQDTYRQIHIDIPRMSPEALILQPKVTEIFREI LFHWAIRHPASGYVQGINDLVTPFFVVPICEYIEABEVDTVDVS GVPAEVLCNIEADTYWCMSKLLDGIQDNYTFAQPGIQMKVKMLE ELVSRIDEQVHRHLDQMEVRYLQFAFRWMNNLLMREVPLRCTIR LWDTYQSEPDGFSHFHLYVCAAFLVRWRKEILEEKDFQELLLFI QNLPTAHWDDEDISLLLAEAYRLKFAFADAPMYKK ELVSRIDEQVHRHLDQMEVRYLQGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATQLGLRRAA QKHSFPRMLHQRERGLCHRGSPSLGEQSRVISHFLPNDLGFTDS VSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKKSIKA QKHSFPRMLHQRERGLCHRGSPSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYHHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLVVFDREQNRRTLQ LRPDERRFAVFSIAVSSDGREVLGGANDGCLVVFDREQNRRTLQ LRPDERRFAVFSIAVSSDGREVLGGANDGCLVVFDREQNRRTLQ ESHEDDVNAVAFADISQILFSGGDDAICKVWDRRTMEEDDFK PVGALAGHQDGITFIDSKGDARYLISNSKDGTIKLMDIRRFSSS EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVHTLIRCRFSFIHSTQQQFIYSGGSTGKVVVYDLLSGHIVKK LTMKKACVRDVSNHPPPERKIVSSSWDGAIRLMQYRQAEYFQDDM PBSEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGGSGSDBSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAVLAVLRRGQVQRVLVQGGGAANLQFIQALLDSBEENDRA WDGRLGDRYNPPVDATPDTRELEFILKTQVELATGQLGLRRAE				IRIILEYCQGVDNIPSVTTDMLTRLSDLLKYFNSRSCQLVLGAG
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DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGGFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWGDIRLWQYRQAEYFQDDM PESECCASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSBEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA				1
WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR BGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWGDIRLWQYRQAEYFQDDM PESEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGGSGGDPSEGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSBEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA	6280	857	2515	
QKHSFPRMLHQRERGLCHRGSFSLGEQSRVISHFLPNDLGFTDS YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PESSECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGGSGSGDPSEGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSBEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA	1			
YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR BGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTMHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PBSEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSGLPRRGAGLRRSEEREEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA		1		
RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR BGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PBSEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSGLPRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA				'
LRPDERFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR RGMEASRQAATQQNWDVRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PBSEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGGGSGDPSEGLPRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA	[İ	
IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR BGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PBSECCASAFAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSAGGGSGDPSEGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSBEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA				
PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR BGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPIHSTQQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWGDIRLWQYRQAEYFQDDM PESEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKWGSRNSSSAGGGGGDPSGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSBEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA	1			· ·
BGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH GVLHTLIRCRFSPHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQABYFQDDM PBSEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGGGSGDPSFGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSBEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA	İ			
GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PBSEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA				_
LTNHKACVRDVSWHPPEEKIVSSSWDGNLRLWQYRQAEYFQDDM PBSEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEBEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA	}	}		
PESEECASAPAPVPQSSTPFSSPQ 6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEREEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQF1QALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA]			1 1
6281 857 2515 ECCDQKMGSRNSSSAGSGSGDPSEGLPRRGAGLRRSEEEEEEDE DVDLAQVLAYLLRRGQVRLVQGGGAANLQF1QALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA				- - -
DVDLAQVLAYLLRRGQVRLVQGGGAANLQFIQALLDSEEENDRA WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA				
WDGRLGDRYNPPVDATPDTRELEFNEIKTQVELATGQLGLRRAA	6281	857	2515	-
	1			
	1			
]	1		-
1	1			YSQKAFCGIYSKDGQIFMSACQDQTIRLYDCRYGRFRKFKSIKA
		ĺ		RDVGWSVLDVAFTPDGNHFLYSSWSDYIHICNIYGEGDTHTALD
				LRPDERRFAVFSIAVSSDGREVLGGANDGCLYVFDREQNRRTLQ
	1			IESHEDDVNAVAFADISSQILFSGGDDAICKVWDRRTMREDDPK
PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR	L	<u> </u>	L	PVGALAGHQDGITFIDSKGDARYLISNSKDQTIKLWDIRRFSSR

SEQ ID NO:	Predicted beginning nucleotide location corresponding	Predicted end nucleotide location corresponding	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=Glutamic Acid, F=Phenylalanine, G=Glycine,
, ,	nucleotide location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location		Glutamic Acid, F=Phenylalanine, G=Glvcine.
			Translation Translation
		to first	H=Histidine, I=Isoleucine, K=Lysine,
	to first		L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
1 1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
1 1			EGMEASRQAATQQNWDYRWQQVPKKAWRKLKLPGDSSLMTYRGH
			GVLHTLIRCRFSPIHSTGQQFIYSGCSTGKVVVYDLLSGHIVKK
1			LTNHKACVRDVSWHPFEEKIVSSSWDGNLRLWQYRQAEYFQDDM
			PESEECASAPAPVPQSSTPFSSPQ
6282	125	906	RMAACRALKAVLVDLSGTLHIEDAAVPGAQEALKRLRGASVIIR
}	!		FVTNTTKESKQDLLERLRKLEFDISEDEIFTSLTAARSLLERKQ
	:		VRPMLLVDDRALPDFKGIQTSDPNAVVMGLAPEHFHYQILNQAF
			RLLLDGAPLIAIHKARYYKRKDGLALGPGPFVTALEYATDTKAT
1			VVGKPEKTFFLEALRGTGCEPEEAVMIGDDCRDDVGGAQDVGML
1			GILVKTGKYRASDEEKINPPPYLTCESFPHAVDHILQHLL
6283	140	1043	LSLFGIHVMNPFWSMSTSSVRKRSEGEEKTLTGDVKTSPPRTAP
	-		KKQLPSIPKNALPITKPTSPAPAAQSTNGTHASYGPFYLEYSLL
1 1			AEFTLVVKQKLPGVYVQPSYRSALMWFGVIFIRHGLYQDGVFKF
1			TVYIPDNYPDGDCPRLVFDIPVFHPLVDPTSGELDVKRAFAKWR
i i			RNHNHIWQVLMYARRVFYKIDTASPLNPEAAVLYEKDIQLFKSK
			VVDSVKVCTARLFDQPKIEDPYAISFSPWNPSVHDEAREKMLTQ
			VVDSVAVCIARDFDQFAIEDFIAISFSPWNPSVHDEAREKMLTQ
6284	<u>1</u>	2879	KKKPEEQHNKSVHVAGLSWVKPGSVQPFSKEEKTVAT
0204	1	2079	RSVIPGSTISSRWPGLSRPRFMAAHEWDWFQREELIGQISDIRV
			QNLQVERENVQKRTFTRWINLHLEKCNPPLEVKDLFVDIQDGKI
1 . 1			LMALLEVLSGRNLLHEYKSSSHRIFRLNNIAKALKFLEDSNVKL
			VSIDAAEIADGNPSLVLGLIWNIILFFQIKELTGNLSRNSPSSS
1 1			LAPGSGGTDSDSSFPPTPTAERSVAISVKDQRKAIKALLAWVQR
ļ I			KTRKYGVAVQDFAGSWRSGLAFLAVIKAIDPSLVDMKQALENST
]			RENLEKAFSIAQDALHIPRLLEPEDIMVDTPDEQSIMTYVAQFL
1	i		ERFPELEAEDIFDSDKEVPIESTFVRIKETPSEQESKVFVLTEN
1 1			GERTYTVNHETSHPPPSKVFVCDKPESMKEFRLDGVSSHALSDS
1			STEFMHQIIDQVLQGGPGKTSDISEPSPESSILSSRKENGRSNS
1	İ		LPIKKTVHFEADTYKDPFCSKNLSLCFEGSPRVAKESLRQDGHV
1			LAVEVAEEKEQKQESSKIPESSSDKVAGDIFLVEGTNNNSQSSS
1			CNGALESTARHDEESHSLSPPGENTVMADSFQIKVNLMTVEALE
l			EGDYFEAIPLKASKFNSDLIDFASTSQAFNKVPSPHETKPDEDA
1 1			EAFENHAEKLGKRSIKSAHKKKDSPEPQVKMDKHEPHODSGEEA
ł			EGCPSAPEETPVDKKPEVHEKAKRKSTRPHYEEEGEDDDLQGVG
			EELSSSPPSSCVSLETLGSHSEEGLDFKPSPPLSKVSVIPHDLF
1 1			YFPHYEVPLAAVLEAYVEDPEDLKNEEMDLEEPEGYMPDLDSRE
1			EEADGSQSSSSSVPGESLPSASDQVLYLSRGGVGTTPASEPAP
[LAPHEDHQQRETKENDPMDSHQSQESPNLENIANPLEENVTKES
			ISSKKKEKRKHVDHVESSLFVAPGSVQSSDDLEEDSSDYSIPSR
			TSHSDSSIYLRRHTHRSSESDHFSLCSVEERSRSG
6285	2157	1331	SCKTENLLEMWWFQQGLSFLPSALVIWTSAAFIFSYITAVTLHH
			IDPALPYISDTGTVAPEKCLFGAMLNIAAVLCIATIYVRYKQVH
			ALSPEENVIIKLNKAGLVLGILSCLGLSIVANFQKTTLFAAHVS
		}	GAVLTFGMGSLYMFVQTILSYQMQPKIHGKQVFWIRLLLVIWCG
		i	VSALSMLTCSSVLHSGNFGTDLEQKLHWNPEDKGYVLHMITTAA
			EWSMSFSFFGFFLTYIRDFQKISLRVEANLHGLTLYDTAPCPIN
ļ .		}	NERTRLLSRDI
6286	1619	276	· ·
	2027	2/0	KAGASCCGSANPYVSVGKSCVLLAMAQLQTRFYTDNKKYAVDDV
			PFSIPAASEIADLSNIINKLLKDKNEFHKHVEFDFLIKGQFLRM
		,	PLDKHMEMENISSEEVVEIEYVEKYTAPQPEQCMFHDDWISSIK
1			GAEEWILTGSYDKTSRIWSLEGKSIMTIVGHTDVVKDVAWVKKD
†	1		SLSCLLLSASMDQTILLWEWNVERNKVKALHCCRGHAGSVDSIA
j			VDGSGTKFCSGSWDKMLKIWSTVPTDEEDEMEESTNRPRKKQKT
1			EQLGLTRTPIVTLSGHMEAVSSVLWSDAEEICSASWDHTIRVWD
	į		VESGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHIRLWDPRT
} I			KDGSLVSLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDT
<u> </u>			RSCKAPLYDLAAHEDKVLSVDWTDTGLLLSGGADNKLYSYRYSP
			VESGSLKSTLTGNKVFNCISYSPLCKRLASGSTDRHIRLWDPRT KDGSLVSLSLTSHTGWVTSVKWSPTHEQQLISGSLDNIVKLWDT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Cluberia Prid D Phandalantin Acid, Es
NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
}	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 -	\=possible nucleotide insertion)
	203200		TTSHVGA
6202	5.70		
6287	278	1482	MOFFFNFQIGLRSTSGKEKYSGDAGFLGDALQLFLQCLALDEDF
			APAKLQVQKILCDLLLPENLKEGLKESSWSSLPCTKNRPFDFHS
	1		VMEESQSLNEPSPKQSEEIPEVTSEPVKGSLNRAQSAQSINSTE
İ	Į		MPAREDCLKRVSSEPVLSVQEKGVLLKRKLSLLEQDVIVNEDGR
1	ì		NKLKKQGETPNEVCMFSLAYGDIPEELIDVSDFECSLCMRLFFE
			PVTTPCGHSFCKNCLERCLDHAPYCPLCKESLKEYLADRRYCVT
			QLLEELIVKYLPDELSERKKIYDEETAELSHLTKNVPIFVCTMA
	ļ .		YPTVPCPLHVFEPRYRLMIRRSIQTGTKQFGMCVSDTONSFADY
1	1		
1			GCMLQIRNVHFLPDGRSVVDTVGGKRFRVLKRGMKDGYCTADIE
	ļ		YLEDV
6288	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
Ī			MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
			HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM
1			KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM
1			PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM
}			RSEDPRSVINLLRNVCSEAAQKRSLDR
6289	1	743	VTLYPCRGLVGNLLLGASGMASGCKIGPSILNSDLANLGAECLR
0000	_	143	MLDSGADYLHLDVMDGHFVPNITFGHPVVESLRKQLGQDPFFDM
ì			
			HMMVSKPEQWVKPMAVAGANQYTFHLEATENPGALIKDIRENGM
			KVGLAIKPGTSVEYLAPWANQIDMALVMTVEPGFGGQKFMEDMM
1			PKVHWLRTQFPSLDIEVDGGVGPDTVHKCAEAGANMIVSGSAIM
			RSEDPRSVINLLRNVCSEAAQKRSLDR
6290	3	1856	TLGRWLLGVYETVAPTLACLPRPRLRRRRRRRRRRRRRRMISRYTRKA
			VPQSLELKGITKHALNHHPPPEKLEEISPTSDSHEKDTSSQSKS
1		}	DITRESSFTSADTGNSLSAFPSYTGAGISTEGSSDFSWGYGELD
			QNATEKVQTMFTAIDELLYEQKLSVHTKSLQEECQQWTASFPHL
1	•		RILGRQIITPSEGYRLYPRSPSAVSASYETTLSQERDSTIFGIR
			GKKLHFSSSYAHKASSIAKSSSFCSMERDEEDSIIVSEGIIEEY
			LAFDHIDIEEGFHGKKSEAATEKQKLGYPPIAPFYCMKEDVLAY
			VFDSVWCKVVSCMEQLTRSHWEGFASDDESNVAVTRPDSESSCV
İ	·		
			LSELHPLVLPRVPQSKVLYITSNPMSLCQASRHQPNVNDLLVHG
1			MPLQPRNLSLMDKLLDLDDKLLMRPGSSTILSTRNWPNRAVEFS
1			TSSLSYTVQSTRRNPPPRTLHPISTSHSCAETPRSVEEILRGA
1			RVPVAPDSLSSPSPTPLSRNNLLPPIGTAEVEHVSTVGPQRQMK
1			PHGDSSRAQSAVVDEPNYQQPQERLLLPDFFPRPNTTQSFLLDT
1			QYRRSCAVEYPHQARPGRGSAGPQLHGSTKSQSGGRPVSRTRQG
			P
6291	1732	602	LVAKMASSASARTPAGKRVINGEELRRLMKEKORLSTSRKRIES
1	1	*	PFAKYNRLGQLSCALCNTPVKSELLWQTHVLGKQHREKVAELKG
1			AKEASQGSSASSAPQSVKRKAPDADDQDVKRAKATLVPQVQPST
			SAWTTNFDKIGKEFIRATPSKPSGLSLLPDYEDEEEEEEEEGD
1			
			GERKRGDASKPLSDAQGKEHSVSSSREVTSSVLPNDFFSTNPPK
			APIIPHSGSIEKAEIHEKVVERRENTAEALPEGFFDDPEVDARV
1			RKVDAPKDQMDKEWDEFQKAMRQVNTISEAIVAEEDEEGRLDRQ
}			IGEIDEQIECYRRVEKLRNRQDEIKNKLKEILTIKELQKKEEEN
			ADSDDEGELQDLLSQDWRVKGALL
6292	1835	1142	TCPGAMKMVAPWTRFYSNSCCLCCHVRTGTILLGVWYLIINAVV
			LLILLSALADPDQYNFSSSELGGDFEFMDDANMCIAIAISLLMI
1			LICAMATYGAYKQRAAWIIPFFCYQIFDFALNMLVAITVLIYPN
1			SIQEYIRQLPPNFPYRDDVMSVNPTCLVLIILLFISIILTFKGY
			LISCVWNCYRYINGRNSSDVLVYVTSNDTTVLLPPYDDATVNGA
1	0000		AKEPPPPYVSA
6293	2382	1035	FWCTLGTVDVHPIGWCAINSKILVPPRTIHAKFTDWKGYLMKRL
1			VGSRTLPVDFHIKMVESMKYPFRQGMRLEVVDKSQVSRTRMAVV
1			DTVIGGRLRLLYEDGDSDDDFWCHMWSPLIHPVGWSRRVGHGIK

SEQ Predicted Predicted end Amino acid segment containing state of the segment containing stat	
	ignal peptide
	tic Acid, E=
distance including the state of	G=Glycine,
location corresponding H=Histidine, I=Isoleucine, K=Lys	sine,
corresponding to first L=Leucine, M=Methionine, N=Aspan	ragine,
to first amino acid P=Proline, Q=Glutamine, R=Argini	ine.
amino acid residue of S=Serine, T=Threonine, V=Valine,	,
residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unkr	,
amino acid sequence Codon, /=possible nucleotide del	lown, *=Stop
sequence Codon, *possible nucleotide dei	letion,
sequence \=possible nucleotide insertion)	1
MSERRSDMAHHPTFRKIYCDAVPYLFKKVRAV	/YTEGGWFEEGMK
LEAIDPLNLGNICVATVCKVLLDGYLMICVDG	GPSTDGLDWFCY
HASSHAIFPATFCQKNDIELTPPKGYEAQTFN	WENYLEKTKSKA
APSRLFNMDCPNHGFKVGMKLEAVDLMEPRLI	יים שלעגע אייינע אייינעריי.
LSIHFDGWDSEYDQWVDCBSPDIYPVGWCELT	CAULANDIA SUB
ATPLKAKEATKKKKKQFGKKRKRIPPTKTRPI	GIQLQPPVAALP
POCHAGO PRINCIPAL PRINCIPA	ROGSKKEPTEDD
PQGARKISSEPVPGEIIAVRVKEEHLDVASPD	OKASSPELPVSVE
NIKQETDD	
6294 354 1814 AQLTTRGRTVAGGVRWIPSPFPDLELYSCCLG	TDRGFPELSHHC
KNVIATASDYDMAEITNIRPSFDVSPVVAGLI	GASVLVVCVSVT
VFVWSCCHQQAEKKHKNPPYKFIHMLKGISIY	PETLSNKKKTTK
VRRDKDGPGREGGRRNLLVDAAEAGLLSRDKD	PRGPSSGSCTDA
LPIKMDYGEELRSPITSLTPGESKTTSPSSPE	EDIMITICS ABOUT
DYNFPKKALVVTIQEAHGLPVMDDQTQGSDPY	TEMMET POWER
DIMPHI DATE DE LA CONTROL DE L	IKMITTPDKKHK
VKTRVLRKTLDPVFDETFTFYGIPYSQLQDLV	LHFLVLSFDRFS
RDDVIGEVMVPLAGVDPSTGKVQLTRDIIKRN	IIQKCISRGELQV
SLSYQPVAQRMTVVVLKARHLQKMDIAGLSGN	PYVKV N VYYGRK
RIAKKKTHVKKCTLNPIFNESFIYDIPTDLLP	DISIEFLVIDED
RTTKNEVVGRLILGAHSVTASGAEHWREVCES	PRKPVAKWHSLS
EY	
6295 2795 617 VSSALLTGATSGSDAAKSEGASASPLSCTNAV	AMDEDDECEDAR
TRRLSSSESPQRDPPPPPPPLLRLPLPPPPQ	ODDDI ODDBOPPAK
OVI. A DMDGVGI CDA I DDDDDDVI BEGGIDAV	ANAL DEPOSITE
QVLADMRGVGLGPALPPPPPYVILEEGGIRAY	FTLGAECPGWDS
TIESGYGEAPPPTESLEALPTPEASGGSLEID	FQVVQSSSFGGE
GALETCSAVGWAPQRLVDPKSKEEAIIIVEDE	DEDERESMRSSR
RRRRRRRKQRKVKRESRERNAERMESILQAL	EDIQLDLEAVNI
KAGKAFLRLKRKFIQMRRPFLERRDLIIQHIP	GFWVKAFLNHPR
ISILINRRDEDIFRYLTNLQVQDLRHISMGYK	
NMVIVKEFQRNRSGRLVSHSTPIRWHRGQEPQ.	ARRHGNODASHS
FFSWFSNHSLPEADRIAEIIKNDLWVNPLRYY	עעמעד מסמקס.ד
QEMKKRKTRGRCEVVIMEDAPDYYAVEDIFSE	TODIDOGGIANA
TORONOMO TOR	TODIDELIHDIK
ISDFMETTDYFETTDNEITDINENICDSENPD	HNEVPNNETTON
NESADDHETTDNNESADDNNENPEDNNKNTDDI	NEENPNNNENTY
GNNFFKGGFWGSHGNNQDSSDSDNEADEASDDI	EDNDGNEGDNEG
SDDDGNEGDNEGSDDDDRDIEYYEKVIEDFDKI	DQADYEDVIEII
SDESVEEEGIEEGIQQDEDIYEEGNYEEEGSE	DVWEEGEDSDDS
DLEDVLQVPNGWANPGKRGKTG	1
6296 727 1199 RHCGCDAQGACDSLPPTGTSSPVTARNAIPEA	RCCVWLLDGTTV
EAVRPARERLARKELRQKRMQQFSRDSAYSSNI	KDSTCLLTEDOT
LGTSLQFPSPFSGTISFGSFSDSGIFPLGSQC	CI CECOECTORY
KWALIHKRVRLSVFGARWGRIYFGK	CTOLOGOE STROK
TCO-OCT TATE IN COLUMN TO THE TATE IN COLUMN TO THE TAIL TO	LLGSALLVGFLS
VIFALVWVLHYREGLGWDGSALEFNWHPVLMV	rgfvfiqgiaii
VYRLPWTWKCSKLLMKSIHAGLNAVAAILA113	
NIANMYSLHSWVGLIAVICYLLQLLSGFSVFLI	
MPIHVYSGIVIFGTVIATALMGLTEKLIFSLRI	PAYSTEPPEGV
FVNTLGLLILVFGALIFWIVTRPQWKRPKEPNS	
GARGSMPAYSGNNMDKSDSELNNEVAARKRNLA	T DEFCOROUR
6298 3 985 SVPLRRISISGTI OGAGTTT KMAVARI AVANA	TUDEAGOKSTM
O . I DI LO DE DE LE CONTE LE LA CONTE LE LA CONTE LE LA CONTE LE	VVPCRSWGWAAV
PFGPHRGLSVLLARIPQRAPRWLPACRQKTSLS	
YKKLKGKSPGIIFIPGYLSYMNGTKALAIEEFO	
YSGVGSSDGNSEESTLGKWRKDVLSIIDDLADG	
WLMLHAAIARPEKVVALIGVATAADTLVTKFNO	
KGVWSMPSKYSEEGVYNVQYSFIKEAEHHCLLH	
T HOMODATION DOVE CONTROL CONT	
LHGMKDDIVPWHTSMQVADRVLSTDVDVILRKF QLLVYTIDDLIDKLSTIVN	SURKMKEKAUI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
-	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide deletion,
6299	512	814	(=possible nucleotide insertion)
6299	512	014	BCDLEGIMPNVTISLSLPTNGSPLQDILVHPCVTSLDSAILTSS
			SIDAMDDSAFSGPYKFPFTPPLESFNLCFYTSQVPVPPILGFYQ
6300	121	692	MKEEEVQLRNNH
0300	121	692	AAPSCWSQRGVPAAGTPSSPRLLVSRAAAPSAGPWGAWRQGARA
l	1		AQSPFSIPNSSSVPYGSQDSVHSSPEDGGGGRDRPVGGSPGGPR
1			LVIGSLPAHLSPHMFGGFKCPVCSKFVSSDEMDLHLVMCLTKPR
			ITYNEDVLSKDAGECAICLEELQQGDTIARLPCLCIYHKGCIDE
6301	616	204	WFEVNRSCPEHPSD
6301	010	284	GKFVPVNWEPPQPLPFPKYLRCYRCLLETKBLGCLLGSDICLTP
1			AGSSCITLHKKNSSGSDVMVSDCRSKEQMSDCSNTRTSPVSGFW
6302	ļ		IFSQYCFLDFCNDPQNRGLYTP
6302	490	745	IFGFLHLFHMEHSFLLVCALFAHVFFSSSCGSSVALHSDPCLLS
			PVLLNCLPGDLRPLDELYAQKLKYKAISEELDHALNDMTSL
6303	2	1961	YWNEYGGGLLWQSWQEKHPGQALSSEPWNFPDTKEEWEQHYSQL
			YWYYLEQFQYWEAQGWTFDASQSCDTDTYTSKTEADDKNDEKCM
			KVDLVSFLSSPIMGDNDSSGTSDKDHSEILDGISNIKLNSEEVT
			QSQLDSCTSHDGHQQLSEVSSKRECPASGQSEPRNGGTNEESNS
			SGNTNTDPPAEDSQKSSGANTSKDRPHASGTDGDESEEDPPEHK
			PSKLKRSHELDIDENPASDFDDSGSLLGFKYGSGQKYGGIPNFS
1	1		HRQVRYLEKNVKLKSKYLDMRRQIKMKNKHIFFTKESEKPFFKK
			SKILSKVEKFLTWVNKPMDEEASQESSSHDNGHDASTSCDSEEQ
			DMSVKKGDDLLETNNPEPEKCQSVSSAGELETENYERDSLLATV
			PDEQDCVTQEVPDSRQAETEAEVKKKKKKKKKKKKKVNGLPPEIAA
			VPELAKYWAQRYRLFSRFDDGIKLDREGWFSVTPEKIAEHIAGR
			VSQSFKCDVVVDAFCGVGGNTIQFALTGMRVIAIDIDPVKIALA
			RNNAEVYGIADKIEFICGDFLLLASFLKADVVFLSPPWGGPDYA
			TAETFDIRTMMSPDGFEIFRLSKKITNNIVYFLPRNADIDQVAS
			LAGPGGQVEIEQNFLNNKLKTITAYFGDLIRRPASET
6304	1	1438	HRARVDRSRESPGGDLRHPGRVRRDITLSGHPRLSTQHVVLLRE
]		DEVGDPGTKDLGHPQHGSPIQETQSEVVTLVSPLPGSDMAALPA
ì			WRATSGLTLWPHTAEGRDLLGAENRALTGGQQAEDPTLASGAYQ
	1		WPGSVEKLQGSVWCDAETLLSSSRTGGQAPPWLTDHDVQMLRLL
1			AQGEVVDKARVPAHGQVLQVGFSTEAALQDLSSPRLSQLCSQGL
			CGLIKRPGDLPEVLSFHVDRVLGLRRSLPAVARRFHSPLLPYRY
			TDGGARPVIWWAPDVQHLSDPDEDQNSLALGWLQYQALLAHSCN
1			WPGQAPCPGIHHTEWARLALFDFLLQVHDRLDRYCCGFEPEPSD
			PCVEERLREKCRNPAELRLVHILVRSSDPSHLVYIDNAGNLQHP
			EDKLNFRLLEGIDGFPESAVKVLASGCLQNMLLKSLQMDPVFWE
6205			SQGGAQGLKQVLQTLEQRGQVLLGHIQKHNLTLFRDEDP
6305	99	420	NMIWRGRSTYRPRPRRSVPPPELIGPMLEPGDEEPQQEEPPTES
			RDPAPGQEREEDQGAAETQVPDLEADLQELSQSKTGDECGDGPD
			VQGKILTKSEQFKMPEGR
6306	1	1874	PTRPSKVKVPHTFLIHSYTRPTVCQACKKLLKGLFRQGLQCKDC
			KFNCHKRCATRVPNDCLGEALINGDVPMEEATDFSEADKSALMD
			ESEDSGVIPGSHSENALHASEEEEGEGGKAQSSLGYIPLMRVVQ
			SVRHTTRKSSTTLREGWVVHYSNKDTLRKRHYWRLDCKCITLFQ
			NNTTNRYYKEIPLSEILTVESAQNFSLVPPGTNPHCFEIVTANA
			TYFVGEMPGGTPGGPSGQGAKAARGWETAIRQALMPVILQDAPS
			APGHAPHRQASLSISVSNSQIQENVDIATVYQIFPDBVLGSGQF
			GVVYGGKHRKTGRDVAVKVIDKLRFPTKQESQLRNEVAILQSLR
1			HPGIVNLECMFETPEKVFVVMEKLHGDMLEMILSSEKGRLPERL
-			TKFLITQILVALRHLHFKNIVHCDLKPENVLLASADPFPQVKLC
			DFGFARIIGEKSFRRSVVGTPAYLAPEVLLNQGYNRSLDMWSVG
			VIMYVSLSGTFPFNEDEDINDQIQNAAFMYPASPWSHISAGAID
	1		LINNLLQVKMRKRYSVDKSLSHPWLQEYQTWLDLRELEGKMGER
L			YITHESDDARWEQFAAEHPLPGSGLPTDRDLGGACPPQDHDMQG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	Debroline O Cluberine P Project
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
ſ	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1		sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6207	27.26		LAERISVL
6307	2136	589	CFLLPRGRDPEPPEAGAAAPCAPGAPDMSFRKVVRQSKFRHVFG
1			QPVKNDQCYEDIRVSRVTWDSTFCAVNPKFLAVIVEASGGGAFL
1			VLPLSKTGRIDKAYPTVCGHTGPVLDIDWCPHNDEVIASGSEDC
Ĭ			TVMVWQIPENGLTSPLTEPVVVLEGHTKRVGIIAWHPTARNVLL
			SAGCDNVVLIWNVGTAEELYRLDSLHPDLIYNVSWNHNGSLFCS
1			ACKDKSVRIIDPRRGTLVAEREKAHEGARPMRAIFLADGKVFTT
			GFSRMSERQLALWDPENLEEPMALQELDSSNGALLPFYDPDTSV
-			VYVCGKGDSSIRYFEITEEPPYIHFLNTFTSKEPQRGMGSMPKR
-			GLEVSKCEIARFYKLHERKCEPIVMTVPRKSDLFQDDLYPDTAG
	1		PEAALEAEEWVSGRDADPILISLREAYVPSKQRDLKISRRNVLS
			DSRPAMAPGSSHLGAPASTTTAADATPSGSLARAGEAGKLEEVM
			QELRALRALVKEQGDRICRLEEQLGRMENGDA
6308	2	1118	GRPTRPEKMLLSLVLHTYSMRYLLPSVVLLGTAPTYVLAWGVWR
1			LLSAFLPARFYQALDDRLYCVYQSMVLFFFENYTGVQILLYGDL
ì			PKNKENIIYLANHQSTVDWIVADILAIRQNALGHVRYVLKEGLK
ļ			WLPLYGWYFAQHGGIYVKRSAKFNEKEMRNKLQSYVDAGTPMYL
Į.			VIFPEGTRYNPEQTKVLSASQAFAAQRGLAVLKHVLTPRIKATH
			VAFDCMKNYLDAIYDVTVVYEGKDDGGQRRESPTMTEFLCKECP
			KIHIHIDRIDKKDVPEEQEHMRRWLHERFEIKDKMLIEFYESPD
			PERRKRFPGKSVNSKLSIKKTLPSMLILSGLTAGMLMTDAGRKL
			YVNTWIYGTLLGCLWVTIKA
6309	220	563	LVAEVKEPCSLPMLSVDMENKENGSVGVKNSMENGRPPDPADWA
1			VMDVVNYFRTVGFEEQASAFQEQEIDGKSLLLMTRNDVLTGLQL
			KLGPALKIYEYHVKPLQTKHLKNNSS
6310	36	979	GPRCWKFLILSSVNCETLRIGKAWPQSSGQERYWTPRTHSSASE
			AQRGSLAELNVAAAGLWADCDQPLYDCPMCGLICTNYHILQEHV
			DLHLEENSFQQGMDRVQCSGDLQLAHQLQQEEDRKRRSEESRQE
ļ			IEEFQKLQRQYGLDNSGGYKQQQLRNMEIEVNRGRMPPSEFHRR
			KADMMESLALGFDDGKTKTSGIIEALHRYYQNAATDVRRVWLSS
			VVDHFHSSLGDKGWGCGYRNFQMLLSSLLQNDAYNDCLKGMLIP
ļ			CIPKIQSMIEDAWKEGFDPQGASQLIIRLQGTKAWIGACEVYIL
			LTSLRV
6311	1	675	PVWWNSCEGPRLAAAARTGHGVGRRARLACLGEPRVKAAVMLTL
			ASKLKRDDGLKGSRTAATASDSTRRVSVRDKLLVKEVAELEANL
			PCTCKVHFPDPNKLHCFQLTVTPDEGYYQGGKFQFETEVPDAYN
			MVPPKVKCLTKIWHPNITETGEICLSLLREHSIDGTGWAPTRTL
1	1		KDVVWGLNSLFTDLLNFDDPLNIEAABHHLRDKEDFRNKVDDYI
			KRYAR
6312	213	1400	GDELVKREAGMKMLPGVGVFGTGSSARVLVPLLRAEGFTVEALW
	1		GKTEEEAKQLAEEMNIAFYTSRTDDILLHQDVDLVCISIPPPLT
			RQISVKALGIGKNVVCEKAATSVDAFRMVTASRYYPQLMSLVGN
			VLRFLPAFVRMKQLISEHYVGAVMICDARIYSGSLLSPSYGWIC
1			DELMGGGGLHTMGTYIVDLLTHLTGRRAEKVHGLLKTFVRQNAA
			IRGIRHVTSDDFCFFQMLMGGGVCSTVTLNFNMPGAFVHEVMVV
			GSAGRLVARGADLYGQKNSATQEELLLRDSLAVGAGLPEQGPQD
	1		VPLLYLKGMVYMVQALRQSFQGQGDRRTWDRTPVSMAASFEDGL
			YMQSVVDAIKRSSRSGEWEAVEVLTEEPDTNQNLCEALQRNNL
6313	2	2071	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
	1		FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD
	l i		RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
] .		TQEPLVEIBGVSKMAFRHLIEFTYTAKLMIQGEEEANDVWKAAE
	·		FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI
1			TESLPSAESEPVEIEVEIAEGTIEVEDEGIRTLEEVASAKQSVK
1			YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK
L			QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
	·		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	l .	nucleotide	
1	beginning		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
i	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		1	
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC
1			QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
1	i		LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK
1			PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVQ
1		1	TEPVTSMT1 IEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS
1			QVHDSHMSBLPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ
1			MPVEVQTELLEADLDHVTPEIMNQEERESSQADAAEAAREDHED
i			AEDLETKPTVDSEAEKAENEDRTALPVLE
6314	2	2071	QRSGAARLAFLPSPFSPACVHRSPLSFHGCWFYFVVVFMPLGVL
0514	-	2071	· ·
i			FHRRRAHGCTLSCSSFVEQPTAMEAEETMECLQEFPEHHKMILD
}	İ		RLNEQREQDRFTDITLIVDGHHFKAHKAVLAACSKFFYKFFQEF
}		1	TQEPLVEIEGVSKMAPRHLIEFTYTAKLMIQGEEEANDVWKAAE
		[FLQMLEAIKALEVRNKENSAPLEENTTGKNEAKKRKIAETSNVI
		1	TESLPSAESEPVEIEVBIAEGTIEVEDEGIETLEEVASAKOSVK
1			YIQSTGSSDDSALALLADITSKYRQGDRKGQIKEDGCPSDPTSK
1			QVEGIEIVELQLSHVKDLFHCEKCNRSFKLFYHFKEHMKSHSTE
1		1	
1			SFKCEICNKRYLRESAWKQHLNCYHLEEGGVSKKQRTGKKIHVC
1	1	1	QYCEKQFDHFGHFKEHLRKHTGEKPFECPNCHERFARNSTLKCH
]	1	1	LTACQTGVGAKKGRKKLYECQVCNSVFNSWDQFKDHLVIHTGDK
	1		PNHCTLCDLWFMQGNELRRHLSDAHNISERLVTEEVLSVETRVO
l			TEPVTSMTIIEQVGKVHVLPLLQVQVDSAQVTVEQVHPDLLQDS
Į.			QVHDSHMSELPEQVQVSYLEVGRIQTEEGTEVHVEELHVERVNQ
1			MPVEVQTELLEADLDHVTPEIMNOBERESSOADAAEAAREDHED
			AEDLETKPTVDSEAEKAENEDRTALPVLE
6315	1	1015	LGLAVNVVTTLVLISYCPTATERAPYWTYLLCALGLFIYQSLDA
	1	1	IDGKQARRINSCSPLGELFDHGCDSLSTVFMAVGASIAARLGTY
			PDWFFSCSFIGMFVFYCAHWQTYVSGMLRFGKVDVTEIOIALVI
			VFVLSAFGGATMWDYTIPILEIKLKILPVLGFLGGVIFSCSNYF
1			HVILHGGVGKNGSTIAGTSVLSPGLHIGLIIILAIMIYKKSATD
			VFEKHPCLYILMFGCVFAKVSQKLVVAHMTKSELYLQDTVFLGP
	†		
			GLLFLDQYFNNFIDEYVVLWMAMVISSFDMVIYFSALCLQISRH
		<u> </u>	LHLNIFKTACHQAPEQVQVLSSKSHQNNMD
6316	1503	792	VSAGAGTGIMGGTTSTRRVTFEADENENITVVKGIRLSENVIDR
			MKESSPSGSKSQRYSGAYGASVSDEELKRRVAEBLALEQAKKES
			EDQKRLKQAKELDRERAAANEQLTRAILRERICSEEERAKAKHL
1			ARQLEEKDRVLKKQDAFYKEQLARLEERSSEFYRVTTEQYQKAA
			EEVEAKFKRYESHPVCADLOAKILOCYRENTHOTLKCSALATOY
l			
<u></u>			MHCVNHAKQSMLEKGG
6317	102	839	PEAQTSAVLAREKGHLPTMRHEAPMQMASAQDARYGQKDSSDQN
[FDYMFKLLIIGNSSVGKTSFLFRYADDSFTSAFVSTVGIDFKVK
1			TVFKNEKRIKLQIWDTAGQERYRTITTAYYRGAMGFILMYDITN
1			EESFNAVQDWSTQIKTYSWDNAQVILVGNKCDMEDERVISTERG
1			QHLGEQLGFEFFETSAKDNINVKOTFERLVDIICDKMSESLETD
1			
L-22-2	ļ		PAITAAKQNTRLKETPPPPQPNCAC
6318	1765	733	PWHPLRTLPLHHPHPRPPRAEGREGADSMSHLPGLELRREAPPL
1	1		LGPLLSPFPLPAGSWHRQMLRSSLRFPITNSAGAPCKAAGRMNI
			LAPVRRDRVLAELPQCLRKEAALHGHKDFHPRVTCACQEHRTGT
ŀ			VGFKISKVIVVGDLSVGKTCLINRFCKDTFDKNYKATIGVDFEM
			ERFEVLGIPFSLQLWDTAGQERFKCIASTYYRGAQAIIIVFNLN
			DVASLEHTKQWLADALKENDPSSVLLFLVGSKKDLSTPAQYALM
			EKDALQVAQEMKAEYWAVSSLTGENVREFFFRVAALTFEANVLA
L			ELEKSGARRIGDVVRINSDDSNLYLTASKKKPTCCP
6319	88	717	AATMRLNONTLLLGKKVVLVPYTSEHVPSRYHEWMKSEELORLT
		1	ASEPLTLEQEYAMQCSWQEDADKCTFIVLDAEKWQAQPGATEES
ļ			CMVGDVNLFLTDLEDLTLGEIEVMIAEPSCRGKGLGTEAVLAML
L	l	<u> </u>	SYGVTTLGLTKFEAKIGQGNEPSIRMFQKLHFEQVATSSVFQEV
			· · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
į	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ļ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /*possible nucleotide deletion,
ļ	sequence	•	\=possible nucleotide insertion)
			TLRLTVSESEHQWLLEQTSHVEEKPYRDGSAEPC
6320	90	1111	RPRTGREKVAMAAVDSFYLLYREIARSCNCYMEALALVGAWYTA
5320			RKSITVICDFYSLIRLHFIPRLGSRADLIKQYGRWAVVSGATDG
	[{	IGKAYAEELASRGLNIILISRNEEKLQVVAKDIADTYKVETDII
			VADFSSGREIYLPIREALKDKDVGILVNNVGVFYPYPQYFTOLS
			EDKLWDIINVNIAAASLMVHVVLPGMVERKKGAIVTISSGSCCK
1			PTPQLAAFSASKAYLDHFSRALQYEYASKGIFVQSLIPFYVATS
į.	}		MTAPSNFLHRCSWLVPSPKVYAHHAVSTLGISKRTTGYWSHSIO
		1	FLFAQYMPEWLWVWGANILNRSLRKEALSCTA
6321	1418	341	HRKAALGALMAGRLLGKALAAVSLSLALASVTIRSSRCRGIOAF
		[RNSFSSSWFHLNTNVMSGSNGSKENSHNKARTSPYPGSKVERSO
			VPNEKVGWLVEWQDYKPVEYTAVSVLAGPRWADPQISESNFSPK
			FNEKDGHVERKSKNGLYEIENGRPRNPAGRTGLVGRGLLGRWGP
	1		NHAADPIITRWKRDSSGNKIMHPVSGKHILOFVAIKRKDCGEWA
	1		IPGGMVDPGEKISATLKREFGERALNSLQKTSAEKREIEEKLHK
			LFSQDHLVIYKGYVDDPRNTDNAWMETEAVNYHDETGEIMDNLM
			LEAGDDAGKVKWVDINDKLKLYASHSQFIKLVAEKRDAHWSEDS
1			EADCHAL
6322	2047	1083	NQEILKNVESSRTVQPHFLEFLLSLGWSVDVGRHPGWTGHVSTS
			WSINCCDDGEGSOOBEVISSEDIGASIFNGOKKVLYYADALTEI
İ			AFVVPSPVESLTDSLESNISDQDSDSNMDLMPGILKOPSLTLEL
}			FPNHTDNLNSSQRLSPSSRMRKLPQGRPVPPLGPETRVSVVWVE
ļ			RYDDIENFPLSELMTEISTGVETTANSSTSLRSTTLEKEVPVIF
			IHPLNTGLFRIKIQGATGKFNMVIPLVDGMIVSRRALGFLVRQT
			VINICRRKRLESDSYSPPHVRRKQKITDIVNKYRNKQLEPEFYT
i			SLFQEVGLKNCSS
6323	1	656	PASTTDGAQEARVPLDGAFWIPRPPAGSPKGCFACVSKPPALQA
•			PAAPAPEPSASPPMAPTLFPMESKSSKTDSVRAAGAPPACKHLA
			EKKTMTNPTTVIEVYPDTTEVNDYYLWSIFNFVYLNFCCLGFIA
}			LAYSLKVRDKKLLNDLNGAVEDAKTDRLINITRSGLAASCIMLW
		į	MALSVIATHRGLRSSASILVAEPHDWNTERPQVTFRERCPAL
6324	1	2061	EGAGMRRCPCRGSLNEAEAGALPAAARMGLEAPRGGRRRQPGQQ
			RPGPGAGAPAGRPEGGGPWARTEGSSLHSEPBRAGLGPAPGTES
			PQAEFWTDGQTEPAAAGLGVETERPKQKTEPDRSSLRTHLEWSW
			SELGTTCLWTETGTDGLWTDPHRSDLQFQPEBASPWTQPGVHGP
		İ	WTELETHGSQTQPERVKSWADNLWTHQNSSSLQTHPEGACPSKE
			PSADGSWKELYTDGSRTQQDIEGPWTEPYTDGSQKKQDTEAARK
			QPGTGGFQIQQDTDGSWTQPSTDGSQTAPGTDCLLGEPEDGPLE
			EPEPGELLTHLYSHLKCSPLCPVPRLIITPETPEPEAQPVGPPS
		1	RVEGGSGGFSSASSFDESEDDVVAGGGGASDPEDRSGSKPWKKL
			KTVLKYSPFVVSFRKHYPWVQLSGHAGNFQAGEDGRILKRFCQC
			EQRSLEQLMKDPLRPFVPAYYGMVLQDGQTFNQMEDLLADFEGP
			SIMDCKMGSRTYLEEELVKARERPRPRKDMYEKMVAVDPGAPTP
			EEHAQGAVTKPRYMQWRBTMSSTSTLGFRIEGIKKADGTCNTNF
			KKTQALEQVTKVLEDFVDGDHVILQKYVACLEELREALEISPFF
			KTHEVVGSSLLFVHDHTGLAKVWMIDFGKTVALPDHQTLSHRLP
	<u> </u>		WAEGNREDGYLWGLDNMICLLQGLAQS
6325	165	944	GLRDPFRRKRRLKPQVKMSNYVNDMWPGSPQEKDSPSTSRSGGS
		1	SRLSSRSRSFSRSSRSHSRVSSRFSSRSRRSKSRSRRRRHQ
		1	RKYRRYSRSYSRSRSRSRSRRYRERRYGFTRRYYRSPSRYRSRS
			RSRSRGRSYCGRAYAIARGQRYYGFGRTVYPEEHSRWRDRSR
1		!	TRSRSRTPFRLSEKDRMELLEIAKTNAAKALGTTNIDLPASLRT
L			VPSAKETSRGIGVSSNGAKPEVSILGLSEQNFQKANCQI
6326	238	680	GEPSPATQQKPSATGAGVLHQHFSSGHIYVLMGLLPPPWTISFT
			VQTTLQPPGGLPAAPVSGRMAFEPVGRDLARRMVPRAGKRTQTL
			GARRVAAQGARPLPEDRRPKSGERLHVTVAPCWEFVLPSVSLTA
		L	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	bequence	\=possible nucleotide insertion)
	sequence		
6337	ļ <u>,</u>		QAWGGVGQEASSGVP
6327	1	1337	SLARLAPAGGSVVMPTQQPAAPSTRAPKPSRSLSGSLCALFSDA
		J	DSGSGMKAELPPGPGAVGREMTKEEKLQLRKEKKQQKKKRKEEK
			GAEPETGSAVSAAQCQGPTRELPESGIQLGTPREKVPAGRSKAE
			LRAERRAKQEAERALKQARKGEQGGPPPKASPSTAGETPSGVKR
ł			LPEYPQVDDLLLRRLVKKPERQQVPTRKDYGSKVSLFSHLPQYS
1			RQNSLTQFMSIPSSVIHPAMVRLGLQYSQGLVRGSNARCIALLR
i			ALQQVIQDYTTPPNEELSRDLVNKLKPYMSFLTQCRPLSASMHN
l			AIKFLNKEITSVGSSKREEEAKSELRAAIDRYVQEKIVLAAQAI
			SRFAYQKISNGDVILVYGCSSLVSRILQEAWTEGRRFRVVVVDS
1			RPWLEGRHTLRSLVHAGVPASYLLIPAASYVLPEVSTEEKDSKV
1			GGEKV
6328	1030	276	HASAEVTTAAARGLGAMEEEMHTDAKIRAENGTGSSPRGPGCSL
			RHFACEQNLLSRPDGSASFLQGDTSVLAGVYGPAEVKVSKEIFN
			KATLEVILRPKIGLPGVAEKSRERLIRNTCEAVVLGTLHPRTSI
			TVVLQVVSDAGSLLACCLNAACMALVDAGVPMRALFCGVACALD
ł			SDGTLVLDPTSKQEKEARAVLTFALDSVERKLLMSSTKGLYSDT
			ELQQCLAAAQAASQHVFRFYRESLQRRYSKS
6329	3	2016	SSEVAAGGGTRSAMAEGSGEVVTVSATGAANGLNNGAGGTSATT
0329)	2010	
			SNPLSRKLHKILETRLDNDKEMLEALKALSTFFVENSLRTRRNL
1			RGDIERKSLAINEBFVSIFKEVKEELESISEDVQAMSNCCQDMT
1			SRLQAAKEQTQDLIVKTTKLQSESQKLEIRAQVADAFLSKFQLT
1			SDEMSLLRGTREGPITEDFFKALGRVKQIHNDVKVLLRTNQQTA
1			GLEIMEQMALLQETAYERLYRWAQSECRTLTQESCDVSPVLTQA
1			MEALQDRPVLYKYTLDEFGTARRSTVVRGFIDALTRGGPGGTPR
1			PIEMHSHDPLRYVGDMLAWLHQATASEKEHLEALLKHVTTQGVE
1			ENIQEVVGHITEGVCRPLKVRIEQVIVAEPGAVLLYKISNLLKF
			YHHTISGIVGNSATALLTTIEEMHLLSKKIFFNSLSLHASKLMD
}			KVELPPPDLGPSSALNQTLMLLREVLASHDSSVVPLDARQADFV
1			QVLSCVLDPLLQMCTVSASNLGTADMATFMVNSLYMMKTTLALF
			EFTDRRLEMLQFQIEAHLDTLINEQASYVLTRVGLSYIYNTVQQ
			HKPEQGSLANMPNLDSVTLKAAMVQFDRYLSAPDNLLIPQLNFL
}			LSATVKEQIVKQSTELVCRAYGEVYAAVMNPINEYKDPENILHR
	1		SPQQVQTLLS
6330	1151	333	FFYYTFYENKTFSRKMVAEKETLSLNKCPDKMPKRTKLLAQQPL
			PVHQPHSLVSEGFTVKAMMKNSVVRGPPAAGAFKERPTKPTAFR
			KFYERGDFPIALEHDSKGNKIAWKVEIEKLDYHHYLPLFFDGLC
			EMTFPYEFFARQGIHDMLEHGGNKILPVLPQLIIPIKNALNLRN
			RQVICVTLKVLQHLVVSAEMVGKALVPYYRQILPVLNIFKNMNV
			NSGDGIDYSQQKRENIGDLIQETLEAFERYGGENAFINIKYVVP
			TYESCLLN
6331	3	495	QQGQRVRTRGRRACASATPLEGCVDLSYPRTHAALLKVAQMVTL
~~~	1 -	]	LIAFICVRSSLWTNYSAYSYFEVVTICDLIMILAFYLVHLFRFY
	1		RVLTCISWPLSELLHYLIGTLLLLIASIVAASKSYNOSGLVAGA
		,	IFGFMATFLCMASIWLSYKISCVTQSTDAAV
6332	1	878	VTESNKFDLVSFIPLLRERIYSNNQYARQFIISWILVLESVPDI
0,3,2	1	0/0	
Į.			NLLDYLPEILDGLFQILGDNGKEIRKMCEVVLGEFLKEIKKNPS
			SVKFAEMANILVIHCQTTDDLIQLTAMCWMREFIQLAGRVMLPY
			SSGILTAVLPCLAYDDRKKSIKEVANVCNQSLMKLVTPEDDELD
!			ELRPGQRQAEPTPDDALPKQEGTASGEWTPSLHLTSCRGPREPD
			VIGVALGPHLSNQDYFMYVTHTIVAATQRSGSSGSPPFCRQDTG
			KLSTMATHSQLVKTGTGLEPRQAVSSSH
6333	3	1467	TRTPSEAEAGGESPQSCVSAAHSDWTAGKPVSLLAPLIPPRSAG
	1	Ì	QPLTFSPSGRQPLRSLLVGMCSGSGRRRSSLSPTMRPGTGAERG
			GLMMGHPGMHYAPMGMHPMGQRANMPPVPHGMMPQMMPPMGGPP
1			MGQMPGMMSSVMPGMMMSHMSQASMQPALPPGVNSMDVAAGTAS
		<u> </u>	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ	i		1
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			PALRKVYDQMPEPRYVVSMGSCANGGGYYHYSYSVVRGCDRIVP
Į.			VDIYIPGCPPTAEALLYGILQLQRKIKRERRLQIWYRR
6342	2	1191	DPRVRAMLATLARVAALRKTCLFSGRGGGRGLWTGRPQSDMNNI
00.12	1	"	KPLEGVKILDLTRVLAGPFATMNLGDLGAEVIKVERPGAGDDTR
	1	1	TWGPPFVGTESTYYLSVNRNKKSIAVNIKDPKGVKIIKELAAVC
	1		DVFVENYVPGKLSAMGLGYEDIDEIAPHIIYCSITGYGQTGPIS
ļ			-
<i>}</i>	l	1	QRAGYDAVASAVSGLMHITGPEVACLSHIAANYLIGQKEAKRWG
			TAHGSIVPYQAFKTKDGYIVVGAGNNQQPATVCKILDLPELIDN
			SKYKTNHLRVHNRKELIKILSERFEEELTSKWLYLFEGSGVPYG
			PINNMKNVFAEPQVLHNGLVMEMEHPTVGKISVPGPAVRYSKFK
1		<u> </u>	MSEARPPPLLGQHTTHILKEVLRYDDRAIGELLSAGVVDQHETH
6343	2	936	GTAMVSDEDELNLLVIVVDANPIWWGKQALKESQFTLSKCIDAV
	1	1	MVLGNSHLFMNRSNKLAVIASHIQESRFLYPGKNGRLGDFFGDP
		1	GNPPEFNPSGSKDGKYELLTSANEVIVEEIKDLMTKSDIKGQHT
			ETLLAGSLAKALCYIHRMNKEVKDNQEMKSRILVIKAAEDSALQ
			YMNFMNVIFAAQKQNILIDACVLDSDSGLLQQACDITGGLYLKV
		1	POMPSLLQYLLWVFLPDQDQRSQLILPPPVHVDYRAACFCHRNL
	}		IBIGYVCSVCLSIFCNFSPICTTCETAFKISLPPVLKAKKKKLK
-		1	VSA
6344	2508	147	TMPTATLGNLRGYGMASPGLAAPSLTPPQLATPNLQQFFPQATR
6344	2500	137	OSLLGPPPVGVPMNPSQFNLSGRNPQKQARTSSSTTPNRKDSSS
1			
		ŀ	QTMPVEDKSDPPEGSEEAAEPRMDTPEDQDLPPCPEDIAKEKRT
	1		PAPEPEPCEASELPAKRLRSSEEPTEKEPPGQLQVKAQPQARMT
i	}		VPKQTQTPDLLPEALEAQVLPRFQPRVLQVQAQVQSQTQPRIPS
			TDTQVQPKLQKQAQTQTSPEHLVLQQKQVQPQLQQEAEPQKQVQ
			POVOPQAHSQGPRQVQLQQEAEPLKQVQPQVQPQAHSQPPRQVQ
ļ			LQLQKQVQTQTYPQVHTQAQPSVQPQEHPPAQVSVQPPEQTHEQ
			PHTQPQVSLLAPEQTPVVVHVCGLEMPPDAVEAGGGMEKTLPEP
			VGTQVSMEEIQNESACGLDVGECENRAREMPGVWGAGGSLKVTI
			LQSSDSRAFSTVPLTPVPRPSDSVSSTPAATSTPSKQALQFFCY
1			ICKASCSSQQEFQDHMSEPQHQQRLGEIQHMSQACLLSLLPVPR
			DVLETEDEEPPPRRWCNTCQLYYMGDLIQHRRTQDHKIAKQSLR
			PFCTVCNRYFKTPRKFVEHVKSQGHKDKAKELKSLEKEIAGQDE
		ł	DHFITVDAVGCFEGDEEEEEDDEDEEEIEVEEBLCKQVRSRDIS
1			REEWKGSETYSPNTAYGVDFLVPVMGYICRICHKFYHSNSGAQL
			SHCKSLGHFENLOKYKAAKNPSPTTRPVSRRCAINARNALTALF
			TSSGRPPSQPNTQDKTPSKVTARPSQPPLPRRSTRLKT
7015	<del> </del>	1403 -	1
6345	2	3483	PRVRTKLILLVNDKKRYERVGGGPKRLGRDVEMEEMI EQLQEKV
			HELEKQNDTLKNRLISAKQQLQTQGYRQTPYNNVQSRINTGRRK
			ANENAGLQECPRKGIKFQDADVAETPHPMFTKYGNSLLEEARGE
			IRNLENVIQSQRGQIEELEHLAEILKTQLRRKENEIELSLLQLR
			EQQATDQRSNIRDNVEMIKLHKQLVEKSNALSAMEGKFIQLQEK
1			QRTLKISHDALMANGDELNMQLKEQRLKCCSLEKQLHSMKFSER
			RIEELQDRINDLEKERELLKENYDKLYDSAFSAAHEEQWKLKEQ
			QLKVQIAQLETALKSDLTDKTEILDRLKTERDQNEKLVQENREL
1			QLQYLEQKQQLDBLKKRIKLYNQENDINADELSEALLLIKAQKE
1			QKNGDLSFLVKVDSEINKDLERSMRELQATHAETVQELEKTRNM
}	1		LIMQHKINKDYQMEVEAVTRKMENLQQDYELKVEQYVHLLDIRA
1			ARIHKLEAOLKDIAYGTKOYKFKPEIMPDDSVDEFDETIHLERG
1			ENLFEIHINKVTFSSEVLQASGDKEPVTFCTYAFYDFELQTTPV
			VRGLHPEYNFTSOYLVHVNDLFLOYIQKNTITLEVHQAYSTEYE
		1	TIAACQLKFHEILEKSGRIFCTASLIGTKGDIPNFGTVEYWFRL
			RVPMDQAIRLYRERAKALGYITSNFKGPEHMQSLSQQAPKTAQL
			SSTDSTDGNLNELHITIRCCNHLQSRASHLQPHPYVVYKFFDFA
			DHDTAIIPSSNDPQFDDHMYFPVPMNMDLDRYLKSKSLSFYVFD
			DSDTQENIYIGKVNVPLISLAHDRCISGIFELTDHQKHPAGTIH
	<del></del>		

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P-Proline O-Clubanine, N=Asparagine,
	amino acid	residue of	P=Proline, Q=Glutamine, R=Arginine,
1	residue of	amino acid	S=Serine, T=Threonine, V=Valine,
ļ	amino acid	sequence	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	sequence	sequence	Codon, /=possible nucleotide deletion,
-	bequence		\=possible nucleotide insertion)
ļ			VILKWKFAYLPPSGSITTEDLGNFIRSEEPEVVQRLPPASSVST
ł			LVLAPRPKPRQRLTPVDKKVSFVDIMPHQSDVSQEGSVDEVKEN
			TEKMQQGKDDVSLLSEGQLAEQSLASSEDETEITEDLEPEVEED
			MSASDSDDCIIPGPISKNIKQPSEKIRIEIIALSLNDSQVTMDD
			TIQRLFVECRFYSLPAEETPVSLPKPKSGQWVYYNYSNVIYVDK
	}		ENNKAKRDILKAILQKQEMPNRSLRFTVVSDPPEDEQDLECEDI
1	i		GVAHVDLADMFQEGRDLIEQNIDVFDARADGEGIGKLRVTVEAL
6346			HALQSVYKQYRDDLEA
6346	2921	533	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
1			AKYTQKEESAEQPEFYYDEFGFRVYKEEGDEPGSSLLANSPLME
1			DAPQRLRWQAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
1			QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
1			TDQRVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
			DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
1			FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
			IADQGQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
			KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
			PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
			RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
			CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
1			ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW
6347	2921	533	DVDG
	-521	555	QDRRLLRLELQKTCQPTSTMSGSHTPACGPFSALTPSIWPQEIL
			AKYTQKEESAEQPEFYYDBFGFRVYKEEGDEPGSSLLANSPLME
j l			DAPORLRWOAHLEFTHNHDVGDLTWDKIAVSLPRSEKLRSLVLA
] ]			GIPHGMRPQLWMRLSGALQKKRNSELSYREIVKNSSNDETIAAK
			QIEKDLLRTMPSNACFASMGSIGVPRLRRVLRALAWLYPEIGYC
	i		QGTGMVAACLLLFLEEEDAFWMMSAIIEDLLPASYFSTTLLGVQ
			TDORVLRHLIVQYLPRLDKLLQEHDIELSLITLHWFLTAFASVV
			DIKLLLRIWDLFFYEGSRVLFQLTLGMLHLKEEELIQSENSASI
	[	ļ	FNTLSDIPSQMEDAELLLGVAMRLAGSLTDVAVETQRRKHLAYL
			IADQQQLLGAGTLTNLSQVVRRRTQRRKSTITALLFGEDDLEAL
	i		KAKNIKQTELVADLREAILRVARHFQCTDPKNCSVVSRQLPGLL
			PNTALTPPTPLVGLYSLWQELTPDYSMESHQRDHENYVACSRSH
			RRRAKALLDFERHDDDELGFRKNDIITIVSQKDEHCWVGELNGL
			RGWFPAKFVEVLDERSKEYSIAGDDSVTEGVTDLVRGTLCPALK
			ALFEHGLKKPSLLGGACHPWLFIEEAAGREVERDFASVYSRLVL
			CKTFRLDEDGKVLTPEELLYRAVQSVNVTHDAVHAQMDVKLRSL
			ICVGLNEQVLHLWLEVLCSSLPTVEKWYQPWSFLRSPGWVQIKC
1 1			ELRVLCCFAFSLSQDWELPAKREAQQPLKEGVRDMLVKHHLFSW
6348	3	2670	DVDG
""	١	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
]			KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
]			EHLQALLTPDEPDKSQGQDLQBQLAEGCRLAQHLVQKLSPENDN
		Į.	DDDEDVQVEVAEKVQKSSSPRBMQKAEEKEVPEDSLEECAITCS
			NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
			ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
			EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
	ŀ	İ	ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
			DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
L.—			LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE

PCT/US00/34263

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
l	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	eedneuce		BCAITCSNSHGPYDSNOPHRKTKITFEEDKVDSTLIGSSSHVEW
1			EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
}		Í	YSTLSIPPEMLASYKSYSSTFHSLEEQOVCMAVDIGRHRWDQVK
	1		KEDHEATGPRLSRELLDEKGPEVLODSLDRCYSTPSGCLELTDS
İ		1	COPYRSAFYVLEOORVGLAVNMDEIEKYOEVEEDODPSCPRLSR
			BLLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEB
1		[	QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD
l			SLDRCYSTPSSCLEOPDSCOPYGSSFYALBEKHVGFSLDVGEIE
1			KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG
			PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
			DMDEIEKYQEVEEDQDPSCPRLSGELLDEKBPEVLQESLDRCYS
1			TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
1			DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
1			PYSSAVYSLEEQYLGLALDVDRIKKDQEEEBDQGPPCPRLSREL
			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
1		1	VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
1			SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6349	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
			KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
		İ	EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
		,	DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
[		]	NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN
1			ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINEKLRPQLA
			EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
			ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
1			DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
1			LSPENDNDDDEDVQVEVAEKVQKSSAPREMPKAEEKEVPEDSLE ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
j	}		EDAVHIIPENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
			YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
			KEDHRATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
			COPYRSAFYVLEQORVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
			ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
			QYLGLALDVDRIKKDQEEBEDQGPPCPRLSRELLEVVEPEVLQD
		1	SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE
	1		KKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCPRLSRELLDEKG
		1	PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
			DMDEIEKYQEVERDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
1	'	}	TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDBIEKYQEVEE
			DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
			PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
1			LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
1	1		VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGBEDQNPPCP
1		1	RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSPQHYRSVFY
	<u> </u>		SFEERHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6350	3	3679	AGAEKCFVTLLACFLAKQQNKYKYEECKDLIKSMLRNELQFKEE
	1	•	KLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGRDASRSLN
[			EHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQKLSPENDN
]			DDDEDVQVEVAEKVQKSSSPREMQKAEEKEVPEDSLEECAITCS
1	1		NSHGPCDSNQPHKNIKITFEEDEVNSTLVVDRESSHDECQDALN ILPVPGPTSSATNVSMVVSAGPLSGEKAAINILEINBKLRPQLA
1	1		EKKQQFRNLKEKCFLTQLACFLANQQNKYKYEECKDLIKFMLRN
1			ERQFKEEKLAEQLKQAEELRQYKVLVHSQERELTQLREKLREGR
			DASRSLNEHLQALLTPDEPDKSQGQDLQEQLAEGCRLAQHLVQK
			LSPENDNDDDEDVOVEVAEKVQKSSAPREMPKAEEKEVPEDSLE
L	1	1	TO LEAD TO THE TANK AND VANCOUS VENERAL VARIABLE AS POSTE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			ECAITCSNSHGPYDSNQPHRKTKITFEEDKVDSTLIGSSSHVEW
ĺ			EDAVHII PENESDDEEEEEKGPVSPRNLQESEEEEVPQESWDEG
			YSTLSIPPEMLASYKSYSSTFHSLEEQQVCMAVDIGRHRWDQVK
			KEDHEATGPRLSRELLDEKGPEVLQDSLDRCYSTPSGCLELTDS
]			CQPYRSAFYVLEQQRVGLAVNMDEIEKYQEVEEDQDPSCPRLSR
			ELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQPYSSAVYSLEE
			QYLGLALDVDRIKKDQEEEEDQGPPCPRLSRELLEVVEPEVLQD
]			SLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKHVGFSLDVGEIE
			KKGKGKKRRGRRSKKERRRGRKEGEEDONPPCPRLSRELLDEKG
		<u> </u>	PEVLQDSLDRCYSTPSGCLELTDSCQPYRSAFYILEQQRVGLAV
			DMDEIEKYQEVEEDQDPSCPRLSGELLDEKEPEVLQESLDRCYS
	1	ł	TPSGCLELTDSCQPYRSAFYILEQQRVGLAVDMDEIEKYQEVEE
			DQDPSCPRLSRELLDEKEPEVLQDSLGRCYSTPSGYLELPDLGQ
			PYSSAVYSLEEQYLGLALDVDRIKKDQEEEEDQGPPCPRLSREL
	1		LEVVEPEVLQDSLDRCYSTPSSCLEQPDSCQPYGSSFYALEEKH
			VGFSLDVGEIEKKGKGKKRRGRRSKKERRRGRKEGEEDQNPPCP
			RLNSMLMEVEEPEVLQDSLDICYSTPSMYFELPDSFQHYRSVFY
			SFEEEHISFALYVDNRFFTLTVTSLHLVFQMGVIFPQ
6351	1291	319	REARRITERSQLGRMLVVEVANGRSLVWGAEAVQALRERLGVGG
			RTVGALPRGPRQNSRLGLPLLLMPEEARLLAEIGAVTLVSAPRP
			DSRHHSLALTSFKRQQEESFQEQSALAAEARETRRQELLEKITE
			GQAAKKQKLEQASGASSSQEAGSSQAAKEDETSDGQASGEQEEA
J		j	GPSSSQAGPSNGVAPLPRSALLVQLATARPRPVKARPLDWRVQS
			KDWPHAGRPAHELRYSIYRDLWERGFFLSAAGKFGGDFLVYPGD
	•		PLRFHAHYIAQCWAPEDTIPLQDLVAAGRLGTSVRKTLLLCSPQ
43			PDGKVVYTSLQWASLQ
6352	235	923	WSBWLSPCHAAKCKGLSMLRITMKTRAISLAADATEFVQGRSAP
ļ	1		AMARSLVHDTVFYCLSVYQVKISPTPQLGAASSAEGHVGQGAPG
			LMGNMNPEGGVNHENGMNRDGGMIPEGGGGNQEPRQQPQPPPEE
			PAQAAMEGPQPENMQPRTRRTKFTLLQVEELESVFRHTQYPDVP
			TRRELAENLGVTEDKVRVWFKNKRARCRRHQRELMLANELRADP
6353			DDCVYIVVD
6333	65	672	RFAGAGAIPEARARPPDVQAAEEEKEMDLPDSASRVFCGRILSM
	1		VNTDDVNAIILAQKNMLDRFEKTNEMLLNFNNLSSARLQQMSER
	}		FLHHTRTLVEMKRDLDSIFRRIRTLKGKLARQHPEAFSHIPEAS FLEEEDEDPIPPSTTTTIATSEQSTGSCDTSPDTVSPSLSPGFE
	1		DLSHVQPGSPAINGRSQTDDEEMTGE
6354	965	510	PSLRPMEPTRDCPLFGGAFSAILPMGAIDVSDLRPVPDNOEVFC
0354	,03	310	HPVTDQSLIVELLELQAHVRGEAAARYHFEDVGGVQGARAVHVE
			SVQPLSLENLALRGRCQEAWVLSGKQQIAKENQQVAKDVTLHQA
			LLRLPQYOTDLLLTFNOPP
6355	158	1662	RGSSAAFRGSGLRGAMIRRVLPHGMGRGLLTRRPGTRRGGFSLD
0333	***	1007	WDGKVSEIKKKIKSILPGRSCDLLQDTSHLPPBHSDVVIVGGGV
		İ	LGLSVAYWLKKLESRRGAIRVLVVERDHTYSQASTGLSVGGICO
			QFSLPENIQLSLFSASFLRNINEYLAVVDAPPLDLRFNPSGYLL
			LASEKDAAAMESNVKVQRQEGAKVSLMSPDQLRNKFPWINTEGV
			ALASYGMEDEGWFDPWCLLQGLRRKVQSLGVLFCQGEVTRFVSS
			SQRMLTTDDKAVVLKRIHEVHVKMDRSLEYQPVECAIVINAAGA
	1		WSAQIAALAGVGEGPPGTLQGTKLPVEPRKRYVYVWHCPQGPGL
			ETPLVADTSGAYFRREGLGSNYLGGRSPTEQEEPDPANLEVDHD
			FFQDKVWPHLALRVPAFETLKVQSAWAGYYDYNTFDQNGVVGPH
			PLVVNMYFATGFSGHGLQQAPGIGRAVAEMVLKGRFQTIDLSPF
			LFTRFYLGEKIOENNII
6356	354	633	TGLTSSCLPLQVMMTKRTKDMGKFSSVTVSTIDEBEEEIEAREV
	""		10010000FDQVINITACTADROATAGTTDBBBBBTEAREV
l		1	ADSVACNAKUTEKCI.ERKOMSKODI.ORI.ARI.RAKKAKMYOTI TO 📑
			ADSYAQNAKVIEKQLERKGMSKRRLQELABLEAKKAKMKGTLID NQFK

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	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6357	2	915	GLLRNMALLVRVLRNQTSISQWVPVCSRLIPVSPTQGQGDRALS
			RTSQWPQMSQSQACGGSEQIPGIDIQLNRKYHTTRKLSTTKDSP
			QPVEEKVGAFTKIIRAMGFTGPLKYSKWKIKIAALRMYTSCVEK
			TDFEEFFLRCQMPDTFNSWFLITLLHVWMCLVRMKQEGRSGKYM
1			CRIIVHFMWEDVQQRGRVMGVNPYILKKNMILMTNHFYAAILGY
1			DEGILSDDHGLAAALWRTFFNRKCEDPRHLELLVEYVRKQIQYL
1			DSMNGEDLLLTGEVSWRPLVEKNPQSILKPHSPTYNDEGL
6358	2009	1040	ASDALHSLSAPVLRLSSRSAARPATMTEQAISFAKDFLAGGIAA
			AISKTAVAPIERVKLLLQVQHASKQIAADKQYKGIVDCIVRIPK
1		į	EQGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGGVDKHT
			QFWRYFAGNLASGGAAGATSLCFVYPLDFARTRLAADVGKSGTE
			REFRGLGDCLVKITKSDGIRGLYQGFSVSVQGIIIYRAAYFGVY
			DTAKGMLPDPKNTHIVVSWMIAQTVTAVAGVVSYPFDTVRRRMM
			MQSGRKGADIMYTGTVDCWRKIFRDEGGKAFFKGAWSNVLRGMG
			GAFVLVLYDELKKVI
6359	98	1086	VCRQEEEKMKEDCLPSSHVPISDSKSIQKSELLGLLKTYNCYHE
		1	GKSFQLRHREEEGTLIIEGLLNIAWGLRRPIRLQMQDDREQVHL
	· ·		PSTSWMPRRPSCPLKEPSPQNGNITAQGPSIQPVHKABSSTDSS
			GPLEEAEEAPQLMRTKSDASCMSQRRPKCRAPGEAQRIRRHRFS
			INGHFYNHKTSVFTPAYGSVTNVRVNSTMTTLQVLTLLLNKFRV
	ļ		EDGPSEFALYIVHESGERTKLKDCEYPLISRILHGPCEKIARIF
1			LMEADLGVEVPHEVAQYIKFEMPVLDSFVEKLKEEEEREIIKLT
			MKFQALRLTMLQRLEQLVEAK
6360	1	345	GTRGAVPSTLEEVVLPPRSCRVFWIHSGTTMSKVSFKITLTSDP
1			RLPYKVLSVPESTPFTAVLKFAAEEFKVPAATSAIITNDGIGIN
			PAQTAGNVFLKHGSELRIIPRDRVGSC
6361	615	158	RPGLGQLQHCALAPQAGNRRCRFHGRLHALTRSTHRGKPMSIMQ
	Ì		FKDTLNTPLPDSSPVAVPLGAPIAVASTLSVEHNDGVETGIWAC
			APGRWRRQITSQEFCHFIQGRCTFTPDDGETLHIQAGDALMLPA
	350	1576	NSTGIWDIQETVRKTYVLIL
6362	350	1576	TTMDGSHSAALKLQQLPPTSSSSAVSEASFSYKENLIGALLAIF GHLVVSIALNLQKYCHIRLAGSKDPRAYFKTKTWWLGLFLMLLG
			ELGVFASYAFAPLSLIVPLSAVSVIASAIIGIIFIKEKWKPKDF
			LRRYVLSFVGCGLAVVGTYLLVTFAPNSHEKMTGENVTRHLVSW
			PFLLYMLVEIILFCLLLYFYKEKNANNIVVILLLVALLGSMTVV
			TVKAVAGMLVLSIQGNLQLDYPIFYVMFVCMVATAVYQAAFLSQ
			ASOMYDSSLIASVGYILSTTIAITAGAIFYLDFIGEDVLHICMF
			ALGCLIAFLGVFLITRNRKKPIPFEPYISMDAMPGMONMHDKGM
			TVOPELKASFSYGALENNDNISEIYAPATLPVMQEEHGSRSASG
			VPYRVLEHTKKB
6363	21	1201	RRTRLGSSFPRRRDSSAMESYDVIANOPVVIDNGSGVIKAGFAG
3333	1	]	DOIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI
}			RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL
1			NPRKNRERAAEVFFETFNVPALFISMOAVLSLYATGRTTGVVLD
		1	SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
			DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS
			TIEIGPSRFRAPELLFRPDLIGEESEGIHEVLVFAIQKSDMDLR
		1	RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE
1			RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
6364	21	1201	RRTRLGSSFPRRRDSSAMESYDVIANQPVVIDNGSGVIKAGFAG
	1		DOIPKYCFPNYVGRPKHVRVMAGALEGDIFIGPKAEEHRGLLSI
1			RYPMEHGIVKDWNDMERIWQYVYSKDQLQTFSEEHPVLLTEAPL
			NPRKNRERAAEVFFETFNVPALFISMQAVLSLYATGRTTGVVLD
			SGDGVTHAVPIYEGFAMPHSIMRIDIAGRDVSRFLRLYLRKEGY
			DFHSSSEFEIVKAIKERACYLSINPQKDETLETEKAQYYLPDGS
			TIEIGPSRFRAPBLLFRPDLIGEESEGIHEVLVFAIQKSDMDLR

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NO:		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
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1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
1		<del> </del>	RTLFSNIVLSGGSTLFKGFGDRLLSEVKKLAPKDVKIRISAPQE
1			
		ļ	RLYSTWIGGSILASLDTFKKMWVSKKEYEEDGARSIHRKTF
6365	234	1989	KHKSRASCAARAQAFGPSREREVHSRFRSGLRRLGESNSGCCTM
ľ			ASMGTLAFDEYGRPFLIIKDQDRKSRLMGLEALKSHIMAAKAVA
ŀ			NTMRTSLGPNGLDKMMVDKDGDVTVTNDGATILSMMDVDHQIAK
ľ	•		LMVELSKSQDDEIGDGTTGVVVLAGALLEEAEQLLDRGIHPIRI
ĺ			ADGYEQAARVAIEHLDKISDSVLVDIKDTEPLIQTAKTTLGSKV
1			VNSCHRQMAEIAVNAVLTVADMERRDVDFELIKVEGKVGGRLED
			TKLIKGVIVDKDFSHPQMPKKVEDAKIAILTCPFEPPKPKTKHK
	1		LDVTSVEDYKALQKYEKEKFEEMIQQIKETGANLAICQWGFDDE
	1		ANHLLLQNNLPAVRWVGGPEIELIAIATGGRIVPRFSELTAEKL
			GFAGLVQEISFGTTKDKMLVIEQCKNSRAVTIFIRGGNKMIIEE
			AKRSLHDALCVIRNLIRDNRVVYGGGAAEISCALAVSQEADKCP
			TLEQYAMRAFADALEVIPMALSENSGMNPIQTMTEVRARQVKEM
			NPALGIDCLHKGTNDMKQQHVIETLIGKKQQISLATQMVRMILK
			IDDIRKPGESEE
6366	257	1898	GNKEGAHSSTFWVLLSIFLGAVAMLCKEQGITVLGLNAVFDILV
	<b>!</b>	-	IGKFNVLEIVQKVLHKDKSLENLGMLRNGGLLFRMTLLTSGGAG
			MLYVRWRIMGTGPPAFTEVDNPASFADSMLVRAVNYNYYYSLNA
1			WLLLCPWWLCFDWSMGCIPLIKSISDWRVIALAALWFCLIGLIC
			QALCSEDGHKRRILTLGLGFLVIPFLPASNLFFRVGFVVAERVL
1			YLPSVGYCVLLTFGFGALSKHTKKKKLIAAVVLGILFINTLRCV
1			LRSGEWRSEEQLFRSALSVCPLNAKVHYNIGKNLADKGNQTAAI
1			RYYREAVRLNPKYVHAMNNIGNILKERNELQEAEELLSLAVQIO
			PDFAAAWMNLGIVQNSLKRFEAAEQSYRTAIKHRRKYPDCYYNL
1			GRLYADLNRHVDALNAWRNATVLKPEHSLAWNNMIILLDNTGNL
			AQAEAVGREALELIPNDHSLMFSLANVLGKSQKYKESEALFLKA
j			IKANPNAASYHGNLAVLYHRWGHLDLAKKHYEISLQLDPTASGT
			KENYGLLRRKLELMQKKAV
6367	287	1934	SIGFPVMLVLSILLYTCEMFQDSVAFEDVAVSFTQEEWALLDPS
			QKNLYRDVMQETFKNLTSVGKTWKVQNIEDEYKNPRRNLSLMRE
1			KLCESKESHHCGESFNQIADDMLNRKTLPGITPCESSVCGEVGT
			GHSSLNTHIRADTGHKSSEYQEYGENPYRNKECKKAFSYLDSFQ
			SHDKACTKEKPYDGKECTETFISHSCIQRHRVMHSGDGPYKCKF
			CGKAFYFLNLCLIHERIHTGVKPYKCKQCGKAFTRSTTLPVHER
	l i		THTGVNADECKECGNAFSFPSEIRRHKRSHTGEKPYECKOCGKV
1			
			FISFSSIQYHKMTHTGEKPYECKQCGKAFRCGSHLQKHGRTHTG
1			EKPYECRQCGKAFRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCA
1			SQLQIHERTHSGEKPHECKECGKVFKYFSSLRIHERTHTGEKPH
1			ECKQCGKAFRYFSSLHIHERTHTGDKPYECKVCGKAFTCSSSIR
1	}		YHERTHTGEKPYECKHCGKAFISNYIRYHERTHTGEKPYQCKQC
L			GKAFIRASSCREHERTHTINR
6368	1	327	RPVPAKLNPRSWPRTAGALPLRPPPLTMAVFHDEVEIEDFQYDE
1			DSETYFYPCPCGDNFSITKEDLENGEDVATCPSCSLIIKVIYDK
1			DQFVCGETVPAPSANKELVKC
6369	1	1745	AGCCRDTRFPTPRGPGSLCHNFCRSAACTVTRTIHGSPREDTGT
1			PRSREMMFQDSVAFEDVAVSFTQEEWALLDPSQKNLYRDVMOET
1			FKNLTSVGKTWKVQNIEDEYKNPRRNLSLMREKLCESKESHHCG
1			
			ESFNQIADDMLNRKTLPGITPCESSVCGEVGTGHSSLNTHIRAD
i			TGHKSSEYQEYGENPYRNKECKKAFSYLDSFQSHDKACTKEKPY
1			DGKECTETFISHSCIQRHRVMHSGDGPYKCKFCGKAFYFLNLCL
			IHERIHTGVKPYKCKQCGKAFTRSTTLPVHERTHTGVNADECKE
			CGNAFSFPSEIRRHKRSHTGEKPYECKQCGKVFISFSSIQYHKM
1			THTGEKPYECKQCGKAFRCGSHLQKHGRTHTGEKPYECRQCGKA
			FRCTSDLQRHEKTHTEDKPYGCKQCGKGFRCASQLQIHERTHSG
			EKPHECKECGKVFKYFSSLRIHERTHTGEKPHECKQCGKAFRYF

PCT/US00/34263

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	h .	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
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NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
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	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
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1		1	Codon, /=possible nucleotide deletion,
i	amino acid	sequence	
	sequence		\=possible nucleotide insertion)
			SSLHIHERTHTGDKPYECKVCGKAFTCSSSIRYHERTHTGEKPY
	1		ECKHCGKAFISNYIRYHERTHTGEKPYQCKQCGKAFIRASSCRE
		1	HERTHTINR
6370	1711	329	FVLSEQRLRTERTWPRSPGLGRGAAAAGARTAGAGLLRLLLGCG
63/0	1 1/11	1 323	ALVGGLRPVTMTTPANAQNASKTWELSLYELHRTPQEAIMDGTE
1		1	1
ŀ			IAVSPRSLHSELMCPICLDMLKNTMTTKECLHRFCSDCIVTALR
ļ	}		SGNKECPTCRKKLVSKRSLRPDPNFDALISKIYPSREEYEAHQD
i		1	RVLIRLSRLHNQQALSSSIEEGLRMQAMHRAQRVRRPIPGSDQT
	Į.	İ	TTMSGGEGEPGEGEGDGEDVSSDSAPDSAPGPAPKRPRGGGAGG
	1	ŀ	SSVGTGGGGTGGVGGGAGSEDSGDRGGTLGGGTLGPPSPPGAPS
1		ł	l I
1	1	1	PPEPGGEIELVFRPHPLLVEKGEYCQTRYVKTTGNATVDHLSKY
i			LALRIALERRQQQEAGEPGGPGGGASDTGGPDGCGGEGGGAGGG
1	<u> </u>		DGPEEPALPSLEGVSEKQYTIYIAPGGGAFTTLNGSLTLELVNE
	)	1	KFWKVSRPLELCYAPTKDPK
6371	3	288	GVANMSTAMNFGTKSFQPRPPDKGSFPLDHLGECKSFKEKFMKC
05/-	1		LHNNNFENALCRKESKEYLECRMERKLMLQEPLEKLGFGDLTSG
l .		1	KSEAKK
6372	2141	625	RVSAIASEGKAEERYKKLEDLLEKSFSLVKMPSLQPVVMCVMKH
1			LPKVPEKKLKLVMADKELYRACAVEVRRQIWQDNQALFGDEVSP
			LLKQYILEKESALFSTELSVLHNFFSPSPKTRRQGEVVQRLTRM
Į.	]	<b>,</b>	VGKNVKLYDMVLQFLRTLFLRTRNVHYCTLRAELLMSLHDLDVG
1			EICTVDPCHKFTWCLDACIRERFVDSKRARELQGFLDGVKKGQE
1			OVLGDLSMILCDPFAINTLALSTVRHLQELVGQETLPRDSPDLL
1		ļ	1 7
1			LLLRLLALGQGAWDMIDSQVFKEPKMEVELITRFLPMLMSFLVD
ļ.	1	•	DYTFNVDQKLPAEEKAPVSYPNTLPESFTKFLQEQRMACEVGLY
1	ĺ	1	YVLHITKQRNKNALLRLLPGLVETFGDLAFGDIFLHLLTGNLAL
			LADEFALEDFCSSLFDGFFLTASPRKENVHRHALRLLIHLHPRV
1	1		APSKLEALOKALEPTGQSGEAVKELYSQLGEKLEQLDHRKPSPA
1	1		QAAETPALELPLPSVPAPAPL
			PSRAARASPARLPAMVSWIISRLVVLIFGTLYPAYYSYKAVKSK
6373	67	711	
1	Ĭ	l	DIKEYVKWMMYWIIFALFTTAETFTDIFLCWPPFYYELKIAFVA
		1	WLLSPYTKGSSLLYRKFVHPTLSSKEKEIDDCLVQAKDRSYDAL
i			VHFGKRGLNVAATAAVMAASKGQGALSERLRSFSMQDLTTIRGD
1			GAPAPSGPPPPGSGRASGKHGQPKMSRSASESASSSGTA
6374	535	2105	HKLFCSYISTSEFPSSTRHHSCPTHTFCNYTSSTIFLSSTRDHS
63/4	235	2103	
1			CPTHTFCNYTSSTIFLSSTRDHSCPTHTSCNYTSSTIFLSSTRD
1			HSCPTHTSCNYTSSTIFLSSTRDHSCPTHTFCNYPRPIIRLSSC
			CPABLQTEGSNGKKEVLSGFQVVLEDTVLFPEGGGQPDDRGTIN
1			DISVLRVTRRGEQADHFTQTPLDPGSQVLVRVDWERRFDHMQQH
			SGOHLITAVADHLFKLKTTSWELGRFRSAIELDTPSMTAEQVAA
			IEOSVNEKIRDRLPVNVRELSLDDPEVEQVSGRGLPDDHAGPIR
1		,	_ = -
			VVNIEGVDSNMCCGTHVSNLSDLQVIKILGTEKGKKNRTNLIFL
1			SGNRVLKWMERSHGTEKALTALLKCGAEDHVEAVKKLQNSTKIL
			QKNNLNLLRDLAVHIAHSLRNSPDWGGVVILHRKEGDSEFMNII
Į.			ANEIGSEETLLFLTVGDEKGGGLFLLAGPPASVETLGPRVAEVL
1			EGKGAGKKGRFQGKATKMSRRMEAQALLQDYISTQSAKE
6375	<del> </del>	1535	AIMAAATRPVRLPEAGCEGRERCWNPSRSRSHSGEGGLAAWSRT
03/5	1	1232	
1			CPGRPRRPGQQVVRGPTMLVTAYLAFVGLLASCLGLELSRCRAK
1			PPGRACSNPSFLRFQLDFYQVYFLALAADWLQAPYLYKLYQHYY
		1 '	FLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLFSLTY
1			SLCCLTKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVER
1		1	HDFPAEWIPATFARAAFWNHVLAVVAGVAAEAVASWIGLGPVAP
1			FVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDR
I		1	1
1			RVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFSSFMAA
			SLLGSSLYRIATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSP
1		1	GQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPETEQAGVLN
	· · · · · · · · · · · · · · · · · · ·	A	<u></u>

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	eginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
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1 1	ocation	corresponding	
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1	esidue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
a	mino acid	sequence	Codon, /=possible nucleotide deletion,
s	equence		\=possible nucleotide insertion)
			WFRVPLHSLACLGLLVLHDSDRKTGTRNMFSICSAVMVMALLAV
			VGLFTVVRHDAELRVPSPTEEPYAPEL
6376	380	1437	ISSTDIDHYRFSFLVNSKMPSKESWSGRKTNRAAVHKSKQEGRQ
1			QDLLIAALGMKLGSPKSSVTIWQPLKLFAYSQLTSLVRRATLKE
1			NEQIPKYEKIHNFKVHTFRGPHWCEYCANFMWGLIAQGVKCADC
			GLNVHKQCSKMVPNDCKPDLKHVKKVYSCDLTTLVKAHTTKRPM
			VVDMCIREIESRGLNSEGLYRVSGFSDLIEDVKMAFDRDGEKAD
			ISVNMYEDINIITGALKLYFRDLPIPLITYDAYPKFIESAKIMD
1			
			PDEQLETLHEALKLLPPAHCETLRYLMAHLKRVTLHEKENLMNA
L			ENLGIVFGPTLMRSPELDAMAALNDIRYQRLVVELLIKNEDILF
6377	2311	1845	SRIRRRSSRRPRBPPGPSRRRRRRRPDPRTMPSEKTFKQRRTFE
1			QRVEDVRLIREQHPTKIPVIIERYKGBKQLPVLDKTKFLVPDHV
1			NMSELIKIIRRRLQLNANQAFFLLVNGHSMVSVSTPISEVYESE
Ll_			KDEDGFLYMVYASQETFGMKLSV
6378	686	191	GAGPWEAFPDGIGRRSRRARLPQYKRPPGRVGGGDSGRRNMAVA
1			DLALIPDVDIDSDGVFKYVLIRVHSAPRSGAPAAESKEIVRGYK
1			WAEYHADIYDKVSGDMQKQGCDCECLGGGRISHQSQDKKIHVYG
			YSMAYGPAQHAISTEKIKAKYPDYEVTWANDGY
6379	35	378	ERAGSPSPSRAALRRCAPORSQAPRWPDRAACRRSFQGSQGRAY
i l			LFNSVVNVGCGPAEERVLLTGLHAVADIYCENCKTTLGWKYEHA
			FESSQKYKEGKYIIELAHMIKDNGWD
6380	1414	462	PAVQGQRGAGPPTGRGSGNMARFALTVVRHGETRFNKEKIIOGO
""	2121	302	GVDEPLSETGFKQAAAAGIFLNNVKFTHAFSSDLMRTKQTMHGI
1			
			LERSKFCKDMTVKYDSRLRERKYGVVEGKALSELRAMAKAAREE
			CPVFTPPGGETLDQVKMRGIDFFEFLCQLILKEADQKEQFSQGS
			PSNCLETSLAEIFPLGKNHSSKVNSDSGIPGLAASVLVVSHGAY
i l			MRSLFDYFLTDLKCSLPATLSRSELMSVTPNTGMSLFIINFEEG
			REVKPTVQCICMNLQDHLNGLTENSLGLNLPSKSNHFEPLKGVP
			LALFTSLLC
6381	1668	218	AVVRAQGSRGFSGAGWRPRQAAAMNFSEVFKLSSLLCKFSPDGK
1 1			YLASCVQYRLVVRDVNTLQILQLYTCLDQIQHIEWSADSLFILC
į į			AMYKRGLVQVWSLEQPEWHCKIDEGSAGLVASCWSPDGRHILNT
		,	TEFHLRITVWSLCTKSVSYIKYPKACLQGITFTRDGRYMALAER
			RDCKDYVSIFVCSDWQLLRHFDTDTQDLTGIEWAPNGCVLAVWD
1			TCLEYKILLYSLDGRLLSTYSAYEWSLGIKSVAWSPSSQFLAVG
1			SYDGKVRILNHVTWKMITEFGHPAAINDPKIVVYKEAEKSPOLG
			LGCLSFPPPRAGAGPLPSSESKYEIASVPVSLQTLKPVTDRANP
			KIGIGMLAFSPDSYFLATRNDNIPNAVWVWDIQKLRLFAVLEQL
1			SPVRAFQWDPQQPRLAICTGGSRLYLWSPAGCMSVQVPGBGDFA
			VLSLCWHLSGDSMALLSKDHFCLCFLETEAVVGTACROLGGHT
6382	2	1062	FEEDEDRNLCLIAYPLKGDHGIVDIVDNSDCEPKSKLLRWTTNK
5552	-	1002	
1			KHHVLETEKTPKDWVRQHRKEEKMKSHKLEEEFEWLKKSBVLYY
			TVEKKGNISSQLKHYNPWSMKCHQQQLQRMKENAKHRNQYKFIL
j			LENLTSRYEVPCVLDLKMGTRQHGDDASEEKAANQIRKCQQSTS
			AVIGVRVCGMQVYQAGSGQLMFMNKYHGRKLSVQGFKEALFQFF
1			HNGRYLRRELLGPVLKKLTELKAVLERQESYRFYSSSLLVIYDG
1			KERPEVVLDSDAEDLEDLSEESADESAGAYAYKPIGASSVDVRM
1	j		IDFAHTTCRLYGEDTVVHEGQDAGYIFGLQSLIDIVTEISEESG
	i		E
6383	3159	1061	SPAPGRPSPHGSQPAARAAAPAMPSAKQRGSKGGHGAASPSEK
			GAHPSAARPLAAPTPAAPACRSPSPGGAPASFPGRAPRSLASQP
]			AARAAAPAMPSAKQRGSKGGHGAASPSEKGAHPSGGADDVAKK
1 1			PPPAPQQPPPPPAPHPQQHPQQHPQNQAHGKGGHRGGGGGGGKS
1 1			
			SSSSSASAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFG
	j		SSSSASAAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVOOVRRSHODFSROREELGOGLOGVEOKVOSLOA
			SSSSSASAAAAAAASSSASCSRRLGRALNFLFYLALVAAAAFS GWCVHHVLEEVQQVRRSHQDFSRQREELGQGLQGVEQKVQSLQA TFGTFESILRSSQHKQDLTEKAVKQGESEVSRISEVLQKLQNEI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine.
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
L	sequence		\=possible nucleotide insertion)
			LKDLSDGIHVVKDARERDFTSLENTVEERLTELTKSINDNIAIF
ì			TEVQKRSQKEINDMKAKVASLEESEGNKQDLKALKEAVKEIQTS
1		1	AKSREWDMEALRSTLQTMESDIYTEVRELVSLKQEQQAFKEAAD
ļ			TERLALQALTEKLLRSEESVSRLPEEIRRLEEELRQLKSDSHGP
			KEDGGFRHSEAFEALQQKSQGLDSRLQHVEDGVLSMQVASARQT
			ESLESLLSKSQEHEQRLAALQGRLEGLGSSEADQDGLASTVRSL
			GETQLVLYGDVEELKRSVGELPSTVESLQKVQEQVHTLLSQDQA
			QAARLPPQDFLDRLSSLDNLKASVSQVEADLKMLRTAVDSLVAY
			SVKIETNENNLESAKGLLDDLRNDLDRLFVKVEKIHEKV
6384	738	1904	IWEVPVCLTHLLHLQQANQPLPPPSSSINEEDADEANRAIGEKR
			AAPDSGKKPKTPKTKQQKDPNEPQKPVSAYALFFRDTQAAIKGO
			NPNATFGEVSQIVASMWDSLGEEQKQVYKRKTEAAKKEYLKALA
			AYRASLVSKAAAESAEAQTIRSVQQTLASTNLTSSLLLNTPLSQ
l			HGTVSASPQTLQQSLPRSIAPKPLTMRLPMNQIVTSVTIAANMP
	1		SNIGAPLISSMGTTMVGSAPSTQVSPSVQTQQHQMQLQQQQQQQ
			QQQMQQMQQQQLQQHQMHQQIQQQMQQQHFQHHMQQHLQQQQQH
			LQQQINQQQLQQQLQQRLQLQQLQHMQHQSQPSPRQHSPVASQI
			TSPIPAIGSPQPASQQHQSQIQSQTQTQVLSQVSIF
6385	2	1584	PRVRAADVAAGAQAVVSAGMAKSNGENGPRAPAAGESLSGTRES
ł	1	ļ	LAQGPDAATTDELSSLGSDSEANGFAERRIDKFGFIVGSQGAEG
			ALEEVPLEVLRQRESKWLDMLNNWDKWMAKKHKKIRLRCQKGIP
	1		PSLRGRAWQYLSGGKVKLQQNPGKFDELDMSPGDPKWLDVIERD
1			LHRQFPFHEMFVSRGGHGQQDLFRVLKAYTLYRPEEGYCQAQAP
İ			IAAVLLMHMPAEQAFWCLVQICEKYLPGYYSEKLEAIQLDGEIL
1			FSLLQKVSPVAHKHLSRQKIDPLLYMTEWFMCAFSRTLPWSSVL
l .	1		RVWDMFFCEGVKIIFRVGLVLLKHALGSPEKVKACQGQYETIER
			LRSLSPKIMQEAFLVQEVVELPVTERQIEREHLIQLRRWQETRG
			ELQCRSPPRLHGAKAILDAEPGPRPALQPSPSIRLPLDAPLPGS
l	·		KAKPKPPKQAQKEQRKQMKGRGQLEKPPAPNQAMVVAAAGDACP
6386	819	195	PQHVPPKDSAPKDSAPQDLAPQVSAHHRSQESLTSQESEDTYL
0300	63.9	133	TVCGSFYLGIMQRASRLKRELHMLATEPPPGITCWQDKDQMDDL
			RAQILGGANTPYEKGVFKLEVIIPERYPFEPPQIRFLTPIYHPN
			IDSAGRICLDVLKLPPKGAWRPSLNIATVLTSIQLLMSEPNPDD
			PLMADISSEFKYNKPAFLKNARQWTEKHARQKQKADEEEMLDNL PEAGDSRVHNSTQKRKASQLVGIEKKFHPDV
6387	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
550,	·	002	
	<b>!</b>		KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQK NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
			REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
			STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
6388	1	662	PGPTHASADAWADAWAQPNMAMHNKAAPPQIPDTRRELAELVKR
	_	552	KQELAETLANLERQIYAFEGSYLEDTQMYGNIIRGWDRYLTNQK
			NSNSKNDRRNRKFKEAERLFSKSSVTSAAAVSALAGVQDQLIEK
		l	REPGSGTESDTSPDFHNQENEPSQEDPEDLDGSVQGVKPQKAAS
			STSSGSHHSSHKKRKNKNRHSPSGMFDYDFEIDLKLNKKPRADY
6389	1074	497	AEPGDRMAGHRLVLVLGDLHIPHRCNSLPAKFKKLLVPGKIQHI
		=	LCTGNLCTKESYDYLKTLAGDVHIVRGDFDENLNYPEQKVVTVG
	-		QFKIGLIHGHQVIPWGDMASLALLQRQFDVDILISGHTHKFEAF
			EHENKFYINPGSATGAYNALETNIIPSFVLMDIQASTVVTYVYQ
			LIGDDVKVERIEYKKP
6390	158	535	GEERKEGRAPGKAFAPERNPAKMEKEETTRELLLPNWQGSGSHG
			LTIAQRDDGVFVQEVTQNSPAARTGVVKEGDQIVGATIYFDNLO
			SGEVTQLLNTMGHHTVGLKLHRKGDRFFPSLGQTWDP
6391	5386	2897	VRWNSKTECYLSIQTQENFPANLNELVNCIVISSLVTTQRKLKA
		1	MSLLGSRNQLARAVLNPNPMDFCTKDLLTTTSERIIAYLRDFNE
			DQKKAIETAYAMVKHSPSVAKICLIHGPPGTGKSKTIVGLLYRL
L	L		DOWNSTRIMIN KUSPSVAKICEIHGPPGTGKSKTIVGEFÄRE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
}	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ļ			LTENORKGHSDENSNAKIKONRVLVCAPSNAAVDELMKKIILEF
			KEKCKDKKNPLGNCGDINLVRLGPEKSINSEVLKFSLDSQVNHR
ľ			MKKELPSHVOAMHKRKEFLDYOLDELSRORALCRGGREIOROEL
		[	DENISKVSKEROELASKIKEVOGRPOKTOSIIILESHIICCTLS
l .		1	TSGGLLLESAFRGQGGVPFSCVIVDEAGQSCEIETLTPLIHRCN
ľ		1	KLILVGDPKQLPPTVISMKAQEYGYDOSMMARFCRLLEENVEHN
		Ì	MISRLPILQLTVQYRMHPDICLFPSNYVYNRNLKTNRQTEAIRC
			SSDWPFQPYLVFDVGDGSERRDNDSYINVQEIKLVMEIIKLIKD
1			KRKDVSFRNIGIITHYKAQKTMIQKDLDKEFDRKGPAEVDTVDA
			FQGRQKDCVIVTCVRANSIQGSIGFLASLQRLNVTITRAKYSLF
		1	ILGHLRTLMENOHWNOLIQDAQKRGAIIKTCDKNYRHDAVKILK
			LKPVLQRSLTHPPTIAPEGSRPQGGLPSSKLDSGFAKTSVAASL
			YHTPSDSKEITLTVTSKDPERPPVHDQLQDPRLLKRMGIEVKGG
1			IFLWDPQPSSPQHPGATPPTGEPGFPVVHQDLSHVQQPAAVVAA
ļ		1	LSSHKPPVRGEPPAASPEASTCQSKCDDPEEELCHRREARAFSE
			GEOEKCGSETHHTRRNSRWDKRTLEOEDSSSKKRKLL
6392	972	186	GRTGVDLASSMAHRLQIRLLTWDVKDTLLRLRHPLGEAYATKAR
			AHGLEVEPSALEQGFRQAYRAQSHSFPNYGLSHGLTSROWWLDV
			VLQTFHLAGVQDAQAVAPIAEQLYKDFSHPCTWQVLDGAEDTLR
			ECRTRGLRLAVISNFDRRLEGILGGLGLREHFDFVLTSEAAGWP
ſ		1	KPDPRIFQEALRLAHMEPVVAAHVGDNYLCDYQGPRAVGMHSFL
			VVGPQALDPVVRDSVPKEHILPSLAHLLPALDCLEGSTPGL
6393	2017	730	TGGSKMAAVATCGSVAASTGSAVATASKSNVTSFQRRGPRASVT
			NDSGPRLVSIAGTRPSVRNGQLLVSTGLPALDQLLGGGLAVGTV
			LLIEEDKYNIYSPLLFKYFLAEGIVNGHTLLVASAKEDPANILQ
İ		1	ELPAPLLDDKCKKEFDEDVYNHKTPESNIKMKIAWRYQLLPKME
1	1		IGPVSSSRFGHYYDASKRMPQELIEASNWHGFFLPEKISSTLKV
İ			EPCSLTPGYTKLLQFIQNIIYEEGFDGSNPQKKQRNILRIGIQN
i			LGSPLWGDDICCAENGGNSHSLTKFLYVLRGLLRTSLSACIITM
			PTHLIQNKAIIARVTTLSDVVVGLESFIGSERETNPLYKDYHGL
	Į.	ł	IHIRQIPRLNNLICDESDVKDLAFKLKRKLFTIERLHLPPDLSD
	1		TVSRSSKMDLAESAKRLGPGCGMMAGGKKHLDF
6394	1418	511	GAAAGGEGARRRPAAMATVMAATAAERAVLEBEFRWLLHDEVHA
		1	VLKQLQDILKEASLRFTLPGSGTEGPAKQENFILGSCGTDQVKG
			VLTLQGDALSQADVNLKMPRNNQLLHFAFREDKQWKLQQIQDAR
1	1	1	NHVSQAIYLLTSRDQSYQFKTGAEVLKLMDAVMLQLTRARNRLT
1			TPATLTLPEIAASGLTRMFAPALPSDLLVNVYINLNKLCLTVYQ
ł			LHALQPNSTKNFRPAGGAVLHSPGAMFEWGSQRLEVSHVHKVEC
	<u> </u>		VIPWLNDALVYFTVSLQLCQQLKDKISVFSSYWSYRPF
6395	13	658	PSGRPTRPLCCAARRGAARHGGSVSGWPAGRTPTETSNPGSSVM
	1		ESVTFEDVAVEFIQEWALLDSARRSLCKYRMLDQCRTLASRGTP
			PCKPSCVSQLGQRAEPKATERGILRATGVAWESQLKPEELPSMQ
			DLLEEASSRDMQMGPGLFLRMQLVPSIEERETPLTREDRPALQE
	<u> </u>		PPWSLGCTGLKAAMQIQRVVIPVPTLGHRNPWVARDSGE
6396	1	1221	ANILSSPSKRGQKGTLIGYSPEGTPLYNFMGDAFQHSSQSIPRF
	1		IKESLKQILEESDSRQIFYFLCLNLLFTFVELFYGVLTNSLGLI
	1		SDGFHMLFDCSALVMGLFAALMSRWKATRIFSYGYGRIEILSGF
			INGLFLIVIAFFVFMESVARLIDPPELDTHMLTPVSVGGLIVNL
	}		IGICAFSHAHSHAHGASQGSCHSSDHSHSHHMHGHSDHGHGHSH
			GSAGGGMNANMRGVFLHVLADTLGSIGVIVSTVLIEQFGWFIAD
		1	PLCSLFIAILIFLSVVPLIKDACQVLLLRLPPEYEKELHIALEK
		1	IQKIEGLISYRDPHFWRHSASIVAGTIHIQVTSDVLEQRIVQQV
			TGILKDAGVNNLTIQVEKEAYFQHMSGLSTGFHDVLAMTKQMES
6308	1 201		MKYCKDGTYIM
6397	391	122	GAGGVGRFEAIRAPARMIEVVCNDRLGKKVRVKCNTDDTIGDLK
	<u> </u>	l	KLIAAQTGTRWNKIVLKKWYTIFKDHVSLGDYEIHDGMNLELYY

Deginning   Cocation   Cortesponding   Cocation   Cortesponding   Cocation   Cortesponding   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   Coffice   C	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Sociation   Corresponding			i	(A=A)anine C-Cysteine D-Assertic A-id E
Cocresponding   Coffrest   amino acid   coffrest   corresponding   Coffrest   common acid   mmon   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   common   co				Glutamic Acid F-Dhenvlalanina C. Claria
L-Leucine, M-Methionine, N-Asparagine, proling of first amino acid residue of amino acid residue of amino acid sequence   S-Serine, T-Threonine, V-Valine, amino acid sequence   V-Tytopine, Y-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytopine, V-Tytop				W-Wishidine T-Tooleysine V-T
to first amino acid residue of amino acid amino acid amino acid amino acid sequence  5-Serien, T-Thirenoine, V-Valine, w-Tryptophan, Y-Tyrosine, K-Unknown, *-Stop coden, /-possible nucleotide deletion, \			, , ,	Laboration Manufacture, Name of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the Control of the
amino acid residue of amino acid sequence	1			Deproling O-Clutoming Reparaging,
residue of amino acid sequence				
amino acid sequence   Codon, /=possible nuclectide insertion)				Seserine, reinfeonine, vevaline,
Sequence   N-possible nucleotide insertion			1	w=liypcopnan, r=lyrosine, x=Unknown, *=Stop
6398  353  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1306  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1308  1		I	sequence	Codon, /=possible nucleotide deletion,
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DIEAQKNYFRWIGKARLLAWINGGKVLPONITTHAVAILFYTIN SNVHSDFTRAMASVARTPQGYERSHFKYLTYSAIQLIKKU SIMENGTLCYSVIYRTKDVIFNAYGATURPGGFLSTSLLKERA GEFONTLPTFTPTCGAPAVGYBELKEVLIPSAIQLIKEVA GEFONTLPTFTTPCGAPAVGYBELKEVLIPSAIGHEVALTHSPELST VITESKSRV  FILETYFGRCEKDSMNFTPTHTPVCRKRTVVSKRGVAVSGFTK RROMADSLESTPLPSFBERLAKLHESKELLEYYGKNAKEGEN EDLIKKLELIYKERAEGGGKHEDLOGKBEELAEGKALEDMOVC LFGEREHVIRLYSENDRARTRELEDKKKIQNILALVSTDAGEVT YFCKEPPHKVTILGKTIQAVGGEGSSSSFKHISKIRSKRPSK ERKESSBHYQRDIQTLILQVEALQAQLGEGTKLSRKDIGGLIED RRHHEETQVCHQRNONKIELTKNLHHTDELLTESTKDFLQLE SENQNEKSSMLEKDNIMSKIKQVRVQCKKKEDKIGKVLPVMHE SHHAGSEYIKWBLCKNEVYYSGRVEGIPKHISKRPSFBVL DINSVYFISLIDLQKNETLDHISLISGAVQLEHJSNNLEFTLKR DFLKLLPLESSPYLKWBLCKNEVYYSGRVEGIPKHISKRPSFBVL OTACKNLAWOTDEDSVODALHHKVYVLKALIRMKGLEKPEVY OTACKNLAWOTDEDSVODALHHKVYVLKALIRMKGLEKPEVY OTACKNLAWOTDEDSVODALHHKVYVLKALIRMKGLEKPEVY OTACKNLAWOTDEDSVODALHHKVYVLKALIRMKGLEKPEVY VLKKCKVKSLLHSPGDIVILLSGASPTVKVMALSAGTCHATLTCHTERWTKX VLKKCKVKSLLHSPGDIVILLSGASPTVKVMALSAGTCHATLTCHTERWTKX VLKKCKVKSLLHSPGDIVILLSGASPTVKVMALSAGTCHATLTCHTERWTKX VLKKCKVKSLLHSPGDIVILLSGASPTVKVMALSAGTCHATLTCHTERWTKX VLKKCKVKSLLHSPGDIVILLSGASPTVKVMALSAGTCHATLTCHTERWTKX VLKKCKVKSLLHSPGDIVILLSGASPTVKVMALSAGTCHATLTCHTERWTKX VLKKCKVKSLLHSPGDIVILLSGASPTVKVMALSAGTCHATLTCHTERWTKX VLKKCKVKSLLHSPGDIVILLSGASPTVKVMALSAGTCHATLTCHTERWTKX VLKKCKVKSLLHSPGDIVILLSGASPTVKVMALSAGTCHATLTCHTERWTXX VLKKCKSSLLGAGGAKNINGLOHNDTGLVFATSLISRNPLPEY RKSKGSSFLAGGASMINGLOHNDTGLVFATSULISRNPLPEY RKSKGSSFLAGGASMINGLOHNDTGLVFATSULISRNPLPEY RKSKGSSFLAGGASMINGLOHNDTGLVFATSULISRNPLPEY RKSKGSSFLAGGASMINGLOHNDTGLVFATSULISRNPLPEY RKSKGSSFLAGGASMINGLOHNDTGLVFATSULISRNPLPEY RKSKGSSFLAGGASMINGLOHNDTGLVFATSULISRNPLPEY RKSKGSSFLAGGASMINGLOHNDTGLVFATSULISRNPLPEY PAPTSCAGARAMINGLOHNDTGLVFATSULIDROMPTUL VDESSGAPGASSSSCAGGAGGAGKASPOCOPCROPTERMINGLOHNEN DEVERPERCOSSSATIVASMEFAAICLRNALLLLPEEGQODFOKON GANNSNQLGANTESSESSTCSSNAHMENDINITONGGRNLITING GANNSNQLGANTESSESSTCSSNAHMENDINITONGGRNLITING RXDDISGALHAGAMINGRATHARMINGHTUNGPOGGRNLITING PAPREGERGANGAGAGKASPOCHARPTTORT NINGERTYTON AANNSALAKANNOTILEDMOSQ	0396	353	1306	HAQMGPLIMACKKILLPTTVPPATMRIWLLGGLLPFLLLLSGLQ
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DKARKCLHQAASMIHPKEVPPEAILLAVYLELQNGNTQLALQII KRNQLLPAVKTHSEVRKKPVFQPVHPIQPIQMPAFTTVQRK  6403  2 1690 RGIHTSVLQGNLQNQMYSHNVVIMNLNNLNTUQVQRNLITNLQ RSVDDTSQAIQRIKNDFQNLQQVFLQAKKDTDWLKEKVQSLQTL AANNSALAKANNDTLEDMNSQLNSFTGQMENITISQANEQNLK DLQDLHKDAENRTAIKPNQLEERFQLFETDIVNIISNISYTAHH LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGP PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGPIG PAGPPGERGGKGSKGSQGFKGSRGSFGKPGPQGPSGDPGPP GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGP KGPPGPPGSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH WIGLTDSERRNEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL	1			
KRNQLLPAVKTHSEVRKKPVFQPVHPIQPIQMPAFTTVQRK  6403  2 1690  RGIHTSVLQGNLQNQMYSHNVVIMNLNNLNTQVQQRNLITNLQ RSVDDTSQAIQRIKNDFQNLQVFLQAKKDTDWLKEKVQSLQTL AANNSALAKANNDTLEDMNSQLNSFTGQMENITTISQANEQNIK DLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHH LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGP PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGPIG PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGP GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGP KGPPGPPGPSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH WIGLTDSERRNEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL				
RGIHTSVLQGNLQNQMYSHNVVIMNLNNLNTQVQQRNLITNLQ RSVDDTSQAIQRIKNDFQNLQQVFLQAKKDTDMLKEKVQSLQTL AANNSALAKANNDTLEBMNSQLNSFTGQMENITISQANEQNLK DLQDLHKDAENRTAIKFNQLEERFQLFETDIVNIISNISYTAHH LRTLTSNLNEVRTCTDTTLTKHTDDLTSLNNTLANIRLDSVSLR MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGP PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGPIG PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGP GKEGLPGPQGPPGFQGLQGTVGEPGVPGRGPGPLPGVPGMPGP KGPPGPPGPSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH WIGLTDSERRNEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL		1		DKARKCLHQAASMIHPKEVPPEAILLAVYLELQNGNTQLALQII
RSVDDTSQAIQRIKNDFONLQQVFLQAKKDTDMIKEKVQSLQTL AANNSALAKANNDTLEDMNSQLNSFTGQMENITTISQANEQNIK DLQDLHKDAENRTAIKPNQLEERFQLFETDIVNIISNISYTAHH LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNPTILQGP PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGBRGPIG PAGPPGERGGKGSGGPKGSRGSPGKPGPQGPSGDPGPPGPP GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGP KGPPGPPGSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY FSVEKEIPEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL	6463			
AANNSALAKANNDTLEDMNSQLNSFTGQMENITTISQANEQNLK DLQDLHKDAENRTAIKPNQLEERFQLFETDIVNIISNISYTAHH LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGP PGPRGPRGDRGSQGPPGPTGNKQQKGEKGEPGPPGPAGBRGPIG PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPP GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGP KGPPGPPGFSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH WIGLTDSERBNEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL	6403	2	1690	
DLQDLHKDAENRTAIKPNQLEERFQLFETDIVNIISNISYTAHH LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSVSLR MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNPTILQGP PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGPIG PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPP GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGVPGMPGP KGPPGPPGSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY FSVEKEIPEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL	1			
LRTLTSNLNEVRTTCTDTLTKHTDDLTSLNNTLANIRLDSV5IR MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNPTILQGP PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGPIG PAGPPGERGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPP GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGP KGPPGPPGSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY FSVEKEIPEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL				
MQQDLMRSRLDTEVANLSVIMEEMKLVDSKHGQLIKNFTILQGP PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGPIG PAGPPGERGGKGSKGSQGPKGSRGSFGKPGPQGPSGDPGPPGP GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGLPGVPGMPGP KGPPGPPGSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY FSVEKEIPEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL				
PGPRGPRGDRGSQGPPGPTGNKGQKGEKGEPGPPGPAGERGFIG PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPP GKEGLPGPQGPPGFQGLQGTVGEPGVPGPGGLPGVPGMPGP KGPPGPPGSGAVVPLALQNEPTPAPEDNSCPPHWKNFTVGCYY FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH WIGLTDSERZNEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL	1			
PAGPPGERGGKGSKGSQGPKGSRGSPGKPGPQGPSGDPGPPGPP GKEGLPGPQGPPGFPGFPGFQGLQGTVGEPGVPGPRGLPGVPGMPGP KGPPGPPGPSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL				
GKEGLPGPQGPPGFQGLQGTVGEPGVPGPRGLPGVPGMPGP KGPPGPPGFSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY FSVEKEIFEDAKLFCEDKSSHLVPINTREEQQWIKKQMVGRESH WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL				
KGPPGPPGFSGAVVPLALQNEPTPAPEDNSCPPHWKNFTDKCYY FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL	1	]		
FSVEKEIFEDAKLFCEDKSSHLVFINTREEQQWIKKQMVGRESH WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL				
WIGLTDSERENEWKWLDGTSPDYKNWKAGQPDNWGHGHGPGEDC AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL				
AGLIYAGQWNDFQCEDVNNFICEKDRETVLSSAL	1			
6404 1012 222 AAALAMAAPAPGLISVFSSSQELGAALAQLVAQRAACCLAGARA	-			
	6404	1012	222	AAALAMAAPAPGLISVFSSSQELGAALAQLVAQRAACCLAGARA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
		nucleotide	
ID	beginning		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		l .	
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sedneuce		\=possible nucleotide insertion)
			RFALGLSGGSLVSMLARELPAAVAPAGPASLARWTLGFCDERLV
	1		PFDHAESTYGLYRTHLLSRLPIPESQVITINPELPVEEAARDYA
			KKLROAFOGDSIPVFDLLILGVGPDGHTCSLFPDHPLLOEREKI
1			VAPISDSPKPPPQRVTLTLPVLNAARTVIFVATGBGKAAVLKRI
ł			
			LEDQEENPLPAALVQPHTGKLCWFLDBAAARLLTVPFEKHSPL
6405	1	1456	AALPRPTPRAPLGREGTGSDSEMAASMFYGRLVAVATLRNHRPR
(		1	TAQRAAAQVLGSSGLFNNHGLQVQQQQQRNLSLHEYMSMELLQE
			AGVSVPKGYVAKSPDEAYAIAKKLGSKDVVIKAQVLAGGRGKGT
1	1		FESGLKGGVKIVFSPEEAKAVSSQMIGKKLFTKQTGEKGRICNO
			VLVCERKYPRREYYFAITMERSFQGPVLIGSSHGGVNIEDVAAE
			TPEAIIKEPIDIEEGIKKEQALQLAQKMGFPPNIVESAAENMVK
1			LYSLFLKYDATMIBINPMVEDSDGAVLCMDAKINFDSNSAYRQK
}			KIFDLQDWTQEDERDKDAAKANLNYIGLDGNIGCLVNGAGLAMA
1			TMDIIKLHGGTPANFLDVGGGATVHQVTEAFKLITSDKKVLAIL
			VNIFGGIMRCDVIAQGIVMAVKDLEIKIPVVVRLQGTRVDDAKA
			LIADSGLKILACDDLDEAARMVVKLSEIVTLAKQAHVDVKFQLP
			I
	1036		<del>-</del>
6406	1036	167	HPROMRGEDTPEAPPYSSGRYDSIKTEVSGCPEDLTVGRAPTAD
•			DDDDDDDDDHEDNDKMNDSEGMDPERLKAFNMFVRLFVDENLDRM
	1		VPISKQPKEKIQAIIESCSRQFPEFQERARKRIRTYLKSCRRMK
			KNGMEMTRPTPPHLTSAMAENILAAACESETRKAAKRMRLEIYO
		1	SSQDEPIALDKQHSRDSAAITHSTYSLPASSYSQDPVYANGGLN
			YSYRGYGALSSNLQPPASLQTGNHSNGESGEARALASRPAPSWV
1			
L	<u> </u>		CRAALGSGMGRGKQRPVMERGCLTA
6407	492	150	VGLCLAVSQTVLAQLDALLVFPGQVAQLSCTLSPQHVTIRDYGV
	1		SWYQQRAGSAPRYLLYYRSEEDHHRPADIPDRFSAAKDEAHNAC
			VLTISPVQPEDDADYYCSVGYGFSP
6408	1458	903	RGCITSSQAWRLFGGVTRGFNMRIEKCYFCSGPIYPGHGMMFVR
			NDCKVFRFCKSKCHKNFKKKRNPRKVRWTKAFRKAAGKELTVDN
			SFEFEKRRNEPIKYQRELWNKTIDAMKRVEBIKQKRQAKFIMNR
1			
			LKKNKELQKVQDIKEVKQNIHLIRAPLAGKGKQLEEKMVQQLQE
L			DVDMEDAP
6409	150	446	NTALANLLRCFTCDRLCGGCTAPAPPAHQGIVLQPVMPSCDPGP
			GPACLPTKTFRSYLPRCHRTYSCVHCRAHLAKHDELISKSFOGS
			HGRAYLFNSV
6410	85	607	RGGTAGCVACLGCWGOSSSPKAAFPAGSACLPADSCPCLLFOAC
0.410	05	00/	
ŀ			AISGLFNCITIHPLNIAAGVWMIMNAFILLLCEAPFCCQFIEFA
ţ			NTVAEKVDRLRSWQKAVFYCGMAVVPIVISLTLTTLLGNAIAFA
l			TGVLYGLSALGKKGDAISYARIQQQRQQADEEKLAETLEGEL
6411	302	772	RLSIMASSLNEDPEGSRITYVKGDLFACPKTDSLAHCISEDCRM
			GAGIAVLFKKKFGGVQELLNQQKKSGEVAVLKRDGRYIYYLITK
ľ			KRASHKPTYENLQKSLEAMKSHCLKNGVTDLSMPRIGCGLDRLQ
<u></u>			WENVSAMIEEVFEATDIKITVYTL
6412	61	1709	RPVTSFSPLPGSCGGRLGTRTMLGRSLREVSAALKQGQITPTEL
ĺ			CQKCLSLIKKTKFLNAYITVSEEVALKQAEESEKRYKNGQSLGD
1			LDGIPIAVKDNFSTSGIBTTCASNMLKGYIPPYNATVVOKLLDO
1			GALLMGKTNLDEFAMGSGSTDGVFGPVKNPWSYSKQYREKRKON
l			
			PHSENEDSDWLITGGSSGGSAAAVSAFTCYAALGSDTGGSTRNP
1		•	AAHCGLVGFKPSYGLVSRHGLIPLVNSMDVPGILTRCVDDAAIV
1	1		IGALAGPDPRDSTTVHEPINKPFMLPSLADVSKLCIGIPKEYLV
1			PELSSEVQSLWSKAADLFESEGAKVIEVSLPHTSYSIVCYHVLC
1			TSEVASNMARFDGLQYGHRCDIDVSTEAMYAATRREGFNDVVRG
1			RILSGNFFLLKENYENYFVKAOKVRRLIANDFVNAFNSGVDVLL
1			· · · · · · · · · · · · · · · · · · ·
			TPTTLSEAVPYLEFIKEDNRTRSAQDDIFTQAVNMAGLPAVSIP
1		}	VALSNQGLPIGLQFIGRAFCDQQLLTVAKWFEKQVQFPVIQLQE
L			LMDDCSAVLENEKLASVSLKQ
	·	<del></del>	**************************************

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6413	2	885	HEPRCAGMAASLWMGDLEPYMDENFISRAFATMGETVMSVKIIR
			NRLTGIPAGYCFVEFADLATAEKCLHKINGKPLPGATPAKRFKL
			NYATYGKQPDNSPEYSLFVGDLTPDVDDGMLYEFFVKVYPSCRG
1			GKVVLDQTGVSKGYGFVKFTDELEQKRALTECQGAVGLGSKPVR
			LSVAIPKASRVKPVEYSQMYSYSYNQYYQQYONYYAQWGYDONT
I	[		GSYSYSYPQYGYTQSTMQTYEEVGDDALEDPMPQLDVTEANKEF
1			MEQSEELYDALMDCHWQPLDTVSSEIPAMM
6414	1	538	RGGRAALLPWRRFPCCRPRPQPARPSSRATPGPRSPGMATSIGV
			SFSVGDGVPEAEKNAGEPENTYILRPVFQQRFRPSVVKDCIHAV
	1		LKEELANAEYSPEEMPQLTKHLSENIKDKLKEMGFDRYKMVVQV
i			VIGEORGEGVFMASRCFWDADTDNYTHDVFMNDSLFCVVAAFGC
1			FYY
6415	2	1168	FVRQWQSSHRRACGLGCEARAGGGEEPRGRASSVAGWVGAFRAP
			FIEAAVAGLGAGSGKRRRGWKMPVHSRGDKKETNHHDEMEVDYA
ł			ENEGSSSEDEDTESSSVSEDGDSSEMDDEDCERRRMECLDEMSN
			LEKQFTDLKDQLYKERLSQVDAKLQEVIAGKAPEYLEPLATLQE
1			NMQIRTKVAGIYRELCLESVKNKYECEIQASRQHCESEKLLLYD
i			TVQSELEEKIRRLEEDRHSIDITSELWNDELQSRKKRKDPFWPD
			KKKPGVVSGPYIVYMLQDLDILEDWTTIRKAMATLGPHRVKTEP
1			PVKLEKHLHSARSEEGRLYYDGEWYIRGQTICIDKKDECPTSAV
			ITTINHDEVWFKRPDGSKSKLYISQLQKGKYSIKHS
6416	410	1519	EIAPADLEIPACAPVLLSRATSSTMSVTGGKMAPSLTQEILSHL
l	}		GLASKTAAWGTLGTLRTFLNFSVDKDAQRLLRAITGQGVDRSAI
			VDVLTNRSREQRQLISRNFQERTQQDLMKSLQAALSGNLERIVM
			ALLQPTAQFDAQELRTALKASDSAVDVAIBILATRTPPQLQECL
			AVYKHNFQVEAVDGITSETSGILQDLLLALAKGGRDSYSGIIDY
1			NLAEQDVQALQRAEGPSREETWVPVFTQRNPEHLIRVFDQYQRS
1		•	TGQELEEAVQNRFHGDAQVALLGLASVIKNTPLYFADKLHQALQ
1			ETEPNYQVLIRILISRCETDLLSIRAEFRKKFGKSLYSSLQDAV KGDCQSALLALCRAEDM
6417	1	845	RGESRVLWSELEGEAGGAGGWASSLNARMDNRFATAFVIACVLS
041,	1	043	LISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEFISDEAD
i .			EKTYNDALFRYNGTVGLWRRCITIPKNMHWYSPPERTESFDVVT
			KCVSFTLTEQFMEKFVDPGNHNSGIDLLRTYLWRCQFLLPFVSL
1			GLMCFGALIGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYV
1			AGIELLHQKLELPDNVSGEFGWSFCLACVSAPLQFMASALFIWA
			AHTNRKEYTLMKAYRVA
6418	2	662	TRTRPRRPPGLGAAVGKAGARSTSTPAGASPAAAYOADPPPPAH
	_		TPAPPPPPPCGGIACHGEPAKFYGYDNLQRQPIFTTQQBAELVQ
			YPDCKSSSGNIGEDPDHLNQSSSPSQMFPWMRPQAAPGRRRGRQ
			TYSRFQTLELEKEFLFNPYLTRKRRIEVSHALALTEROVKIWFO
			NRRMKWKKENNKDKFPVSRQEVKDGETKKEAQELEEDRAEGLIN
6419	1	973	PGRPRVRNFDLNSKSILQEFFCTRSIQIPANRSKTAMSKCPIFP
1			MARSISTSGPLDKEDTGRQKLISTGSLPATLQGATDSLGLEWHL
1			PSPDPVTVPYLSPLVVWKELESLLBNEGDHAITVADFVDHHPIV
			FWNLVWYFRRLDLPSNLPGLILSSBHCNKYSKIPRHCMSBDSKY
			VLIQMLWDNMKLHQDPGQPLYILWNAHTQKYPMVHLLQKSDNSF
			NQELLKSMVKSIKMNDVYGPMSQILETLNKCPHFKRQRSLYREI
			LFLSLVALGRENIDIDAFDKEYKMAYDRLTPSQVKSTHNCDRPP
	J		STGVMECRKTFGEPYL
6420	207	1187	RKMIDKNQTCGVGQDSVPYMICLIHILEEWFGVEQLEDYLNFAN
			YLLWVFTPLILLILPYFTIFLLYLTIIFLHIYKRKNVLKEAYSH
			NLWDGARKTVATLWDGHAAVWHGYEVHGMEKIPEDGPALIIFYH
1			GAIPIDFYYFMAKIFIHKGRTCRVVADHFVFKIPGFSLLLDVFC
			ALHGPREKCVEILRSGHLLAISPGGVREALISDETYNIVWGHRR
		·	GFAQVAIDAKVPIIPMFTQNIREGFRSLGGTRLFRWLYEKFRYP
	•	·	

	T = 11		
SEQ ID	Predicted	Predicted end	Amino acid segment containing signal peptide
NO:	beginning nucleotide	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	1	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding to first	to first	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	amino acid residue of	P=Proline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
	sequence	<del> </del>	\=possible nucleotide insertion)
			FAPMYGGFPVKLRTYLGDPIPYDPQITAEELAEKTKNAVQALID
			KHQRIPGNIMSALLERFH
6421	1844	362	WALSLRROPERMSNKLLSPHPHSVVLRSEFKMASSPAVLRASRL
1			YQWSLKSSAQFLGSPQLRQVGQIIRVPARMAATLILEPAGRCCW
1			DEPVRIAVRGLAPEQPVTLRASLRDEKGALFQAHARYRADTLGE
1			LDLERAPALGGSFAGLEPMGLLWALEPEKPLVRLVKRDVRTPLA
}	}	J	VELEVLDGHDPDPGRLLCQTRHERYFLPPGVRREPVRVGRVRGT
			LFLPPEPGPFPGIVDMFGTGGGLLEYRASLLAGKGFAVMALAYY
			NYEDLPKTMETLHLEYFEEAMNYLLSHPEVKGPGVGLLGISKGG
			ELCLSMASFLKGITAAVVINGSVANVGGTLRYKGETLPPVGVNR
			NRIKVTKDGYADIVDVLNSPLEGPDQKSFIPVERAESTFLFLVG
1	}	1	QDDHNWKSEFYANBACKRLQAHGRRKPQIICYPETGHYIEPPYF
1		1	PLCRASLHALVGSPIIWGGEPRAHAMAQVDAWKQLQTFFHKHLG
			GREGTIPSKV
6422	181	2133	EGENLSWFQEFWGDIAKEFYWKTPCPGPFLRYNFDVTKGKIFIE
1			WMKGATTNICYNVLDRNVHEKKLGDKVAFYWEGNEPGETTQITY
			HQLLVQVCQFSNVLRKQGIHKGDRVAIYMPMIPELVVAMLACAR
			IGALHSIVFAGFSSESLCERILDSSCSLLITTDAFYRGEKLVNL
			KELADEALQKCQEKGFPVRCCIVVKHLGRAELGMGDSTSQSPPI
	1		KRSCPDVQISWNQGIDLWWHELMQEAGDECEPEWCDAEDPLFIL
ļ	1		YTSGSTGKPKGVVHTVGGYMLYVATTFKYVFDFHAEDVFWCTAD
	l.		IGWITGHSYVTYGPLANGATSVLFEGIPTYPDVNRLWSIVDKYK
	ľ		VTKFYTAPTAIRLLMKFGDEPVTKHSRASLQVLGTVGEPINPEA
ŀ		ĺ	WLWYHRVVGAQRCPIVDTFWQTETGGHMLTPLPGATPMKPGSAT
		1	FPFFGVAPAILNESGEELEGEAEGYLVFKQPWPGIMRTVYGNHE
1		ĺ	RFETTYFKKFPGYYVTGDGCQRDQDGYYWITGRIDDMLNVSGHL
			LSTAEVESALVEHEAVAEAAVVGHPHPVKGECLYCFVTLCDGHT
			FSPKLTEELKKQIREKIGPIATPDYIQNAPGLPKTRSGKIMRRV
			LRKIAQNDHDLGDMSTVADPSVISHLFSHRCLTIQ
6423	614	1237	ANLKEIPRDLPPETVLLYLDSNQITSIPNFIFKDLHQLRVLNLS
]			KNGIEFIDEHAFKGVAETLQTLDLSDNRIQSVHKNAFNNLKARA
1			RIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRP
1			FLNAANDADLCNLPKKTTDYAMLVTMPGWFTMVISYVVYYVRQN
Į.			QEDARRHLEYLKSLPSRQKKADEPDDISTVV
6424	1	1188	KKVSWPVAAMVHCSCVLFRKYGNFIDKLRLFTRGGSGGMGYPRL
1			GGEGGKGGDVWVVAHNRMTLKQLKDRYPRKRFVAGVGANSKISA
			LKGSKGKDWEIPVPVGISVTDENGKIIGELNKENDRILVAQGGL
			GGKLLTNFLPLKGQKRIIHLDLKLIADVGLVGFPNAGKSSLLSC
1			VSHAKPAIADYAFTTLKPELGKIMYSDFKQISVADLPGLIEGAH
			MNKGMGHKFLKHIERTRQLLFVVDISGFQLSSHTQYRTAFETII
			LLTKELELYKEELQTKPALLAVNKMDLPDAODKFHELMSOLONP
			KDFLHLFEKNMIPERTVEFQHIIPISAVTGEGIEELKNCIRKSL
			DEQANQENDALHKKQLLNLWISDTMSSTEPPSKHAVTTSKMDII
6425	1850	1144	LAMBGGGGIPLETLKEESQSRHVLPASFEVNSLQKSNWGFLLTG
	1000	4177	LUCCTLUATIVATIVATIVATE EN LOCATIVATORIO DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DEL CONTRETA DEL CONTRETA DE LA CONTRETA DEL CONTRETA DEL CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DEL CONTRETA DE LA CONTRETA DEL CONTRETA DEL CONTRETA DE LA CONTRETA DEL CONTRETA DEL CONTRETA DE LA CONTRETA DEL CONTRETA DEL CONTRETA DE LA NTRETA DE LA CONTRETA DE LA CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONTRETA DEL CONT
1			LVGGTLVAVYAVATPFVTPALRKVCLPFVPATMKQIENVVKMLR
			CRRGSLVDIGSGDGRIVIAAAKKGPTAVGYELNPWLVWYSRYRA
			WREGVHGSAKFYISDLWKVTFSQYSNVVIFGVPQMMLQLEKKLE
			RELEDDARVIACRFPFPHWTPDHVTGEGIDTVWAYDASTFRGRE
6426	30	5.65	KRPCTSMHFQLPIQA
0120	30	565	SRGAAVGGMSVAGGEIRGDTGGEDTAAPGRFSFSPEPTLEDIRR
			LHAEFAAERDWEQFHQPRNLLLALVGEVGELAELFQWKTDGEPG
1	}		PQGWSPRERAALQEELSDVLIYLVALAARCRVDLPLAVLSKMDI
[			I NULVYVAKIADSSSEVVTDI.DUCATSSDANIGDADIDGDGGGGGGGGG
		İ	NRRRYPAHLARSSSRKYTELPHGAISEDQAVGPADIPCDSTGQT
CA 27	1,45	-	ST
6427	145	959	

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
10.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
İ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Bequence	\=possible nucleotide insertion)
<b></b>	sequence		WLLSPYTKGASLLYRKFVHPSLSRHEKEIDAYIVOAKERSYETV
İ	j		LSFGKRGLNIAASAAVQAATKSQGALAGRLRSFSMQDLRSISDA
		1	PAPAYHDPLYLEDQVSHRRPPIGYRAGGLQDSDTEDBCWSDTEA VPRAPARPREKPLIRSOSLRVVKRKPPVRBGTSRSLKVRTRKKT
	1	İ	1 2
			VPSDVDS
6428	1982	444	SGSGGKMEDHQHVPIDIQTSKLLDWLVDRRHCSLKWQSLVLTIR
			EKINAAIQDMPESEEIAQLLSGSYIHYFHCLRILDLLKGTEAST
			KNIFGRYSSQRMKDWQEIIALYEKDNTYLVELSSLLVRNVNYEI
			PSLKKQIAKCQQLQQEYSRKEEECQAGAAEMREQFYHSCKQYGI
	1		TGENVRGELLALVKDLPSQLAEIGAAAQQSLGEAIDVYQASVGF
1			VCESPTEQVLPMLRFVQKRGNSTVYEWRTGTEPSVVERPHLEEL
			PEQVAEDAIDWGDFGVEAVSEGTDSGISAEAAGIDWGIFPESDS
			KDPGGDGIDWGDDAVALQITVLEAGTQAPEGVARGPDALTLLEY
ľ			TETRNOFLDELMELEIFLAQRAVELSEEADVLSVSQFQLAPAIL
			QGQTKEKMVTMVSVLEDLIGKLTSLQLQHLFMILASPRYVDRVT
ļ			EFLQQKLKQSQLLALKKELMVQKQQEALEEQAALEPKLDLLLEK
			TKELQKLIEADISKRYSGRPVNLMGTSL
6429	3413	3442	EPSSWTAAPRGPLAAHPLEAAVQEDDRRALSFDSRIKVFANGTL
1			VVKSVTDKDAGDYLCVARNKVGDDYVVLKVDVVMKPAKIEHKEE
į			NDHKVFYGGDLKVDCVATGLPNPEISWSLPDGSLVNSFMQSDDS
			GGRTKRYVVFNNGTLYFNEVGMREEGDYTCFAENQVGKDEMRVR
			VKVVTAPATIRNKTCLAVQVPYGDVVTVACEAKGEPMPKVTWLS
-			PTNKVIPTSSEKYQIYQDGTLLIQKAQRSDSGNYTCLVRNSAGE
1			DRKTVWIHVNVQPPKINGNPNPITTVREIAAGGSRKLIDCKAEG
ļ			IPTPRVLWAPPEGVVLPAPYYGNRITVHGNGSLDIRSLRKSDSV
ł			QLVCMARNEGGEARLIVQLTVLEPMEKPIFHDPISEKITAMAGH
	<b>\</b>		TISLNCSAAGTPTPSLVWVLPNGTDLQSGQQLQRFYHKADGMLH
			ISGLSSVDAGAYRCVARNAAGHTERLVSLKVGLKPEANKQYHNL
1			VSIINGETLKLPCTPPGAGQGRFSWTLPNGMHLEGPQTLGRVSL
1			LDNGTLTVREASVFDRGTYVCRMETEYGPSVTSIPVIVIAYPPR
			ITSEPTPVIYTRPGNTVKLNCMAMGIPKADITWELPDKSHLKAG
			VQARLYGNRFLHPQGSLTIQHATQRDAGFYKCMAKNILGSDSKT
			TYIHVF
6430	1946	602	RTRVSTGLRRTLLWSEAVGASSTRGDTGIPGSGEGGAGPGGGEG
			AMLEAMAEPSPEDPPTTLKPETQPPEKRRRTIEDFNKFCSFVLA
1	1		YAGYIPPSKEESDWPASGSSSPLRGESAADSDGWDSAPSDLRTI
-			QTFVKKAKSSKRRAAQAGPTQPGPPRSTFSRLQAPDSATLLEKM
1			KLKDSLFDLDGPKVASPLSPTSLTHTSRPPAALTPVPLSQGDLS
			HPPRKKDRKNRKLGPGAGAGFGVLRRPRPTPGDGEKRSRIKKSK KRKLKKAERGDRLPPPGPPQAPPSDTDSEEEEEEEEEEEEE
1			TVVGGEAPVPVLPTPPEAPRPPATVHPEGVPPADSESKEVGSTE
			TSQDGDASSSEGEMRVMDEDIMVESGDDSWDLITCYCRKPFAGR
			PMIECSLCGTWIHLSCAKIKKTNVPDFFYCQKCKELRPEARRLG
	<del> </del>		GPPKSGEP
6431	3	605	WWNSSYNLPAYAPYLPCEACAMQDGRKGGAYAGKMEATTAGVGR
			LEEEALRRKERLKALREKTGRKDKEDGEPKTKHLREEEEEGEKH
			RELRIANYVPEDEDLKKRRVPQAKPVAVEEKVKEQLEAAKPEPV
}			IEEVDLANLAPRKPDWDLKRDVAKKLEKLKKRTQRAIAELIRER
			LKGQEDSLASAVDAATEQKTCDSD
6432	56	1692	GGLGTMGSRIKQNPETTFEVYVEVAYPRTGGTLSDPEVQRQFPE
1			DYSDQEVLQTLTKFCFPFYVDSLTVSQVGQNFTFVLTDIDSKQR
			FGFCRLSSGAKSCFCILSYLPWFEVFYKLLNILADYTTKRQENQ
		1	WNELLETLHKLPIPDPGVSVHLSVHSYFTVPDTRELPSIPENRN
			LTEYFVAVDVNNMLHLYASMLYERRILIICSKLSTLTACIHGSA
1			AMLYPMYWQHVYIPVLPPHLLDYCCAPMPYLIGIHLSLMEKVRN
1	1	1	MALDDVVILNVDTNTLETPFDDLQSLPNDVISSLKNRLKKVSTT

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	1	A=Aranine, C=Cysterne, D=Aspartic Acid, E=
NO.		location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K≈Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	2040000	\=possible nucleotide insertion)
	- Joquonec		/-possible nucleotide insertion;
			TGDGVARAFLKAQAAFFGSYRNALKIEPEBPITFCEEAFVSHYR
			SGAMRQFLQNATQLQLFKQFIDGRLDLLNSGEGFSDVFEEEINM
1			GEYAGSDKLYHQWLSTVRKGSGAILNTVKTKANPAMKTVYKFDI
	ſ		AENGCAPTPEEQLPKTAPSPLVEAKDPKLREDRRPITVHFGQVR
			PPRPHVVKRPKSNIAVEGRRTSVPSPEQNTIATPATLHILQKSI
1	İ	i	THFAAKFPTRGWTSSSH
6433	1524	484	APVTKRKEVFAKDSKGSALDAGRDPKRPALPETLCESGWASNTA
	1	'''	
ł			PTTPPQPGWCLCGKDFKSSCQTPGREKERRLATMHGSCSFLMLL
	j	i	LPLLLLLVATTGPVGALTDEEKRLMVELHNLYRAQVSPTASDML
		1	HMRWDEELAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDV
1	1		PLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCG
	i		SHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQCP
1			SGYHCKNSLCEPIGSPEDAQDLPYLVTEAPSFRATEASDSRKMG
			AEGPDKPSVVSGLNSGPGHVWGPLLGLLLLPPLVLAGIF
6434	40	2002	MPQLNFGMADPTQMGGLSMLLLAGEHALGTPEVFSGTCRPDVSE
			SPELRQKSPLFQFAEISSSTSHSDASTKQCQTSALFQFAEISSN
			TSQLGGAEPVKRCGKSALFQLAEMCLASEGMKMEESKLIKAKES
			DGGRIKELEKGKEEKEIKMEKTDETRLQKEAEFEKSAKENLRDS
1			KELRNFEALQIDDIMAIKMEDPKEIRKEELEEDHKCSHPPDFSY
1			SASSKIIISDVPSRKDHMCHPHGIMIIEDPAALNKPEKLKKKKK
			KSKMDRHGNDKSTPKKTCKKRQSSESDIESVIYTIEAVAKGDWG
1			IEKLGDTPRKKVRTSSSGKGSILDAKPPKKKVKSREKKMSKEKS
	f		SDTTKESRPPDFISISASKNISGETPEGIKAEPLTPMEDALPPS
			LSGQAKPEDSDCHRKIETCGSRKSERSCKGALYKTLVSEGMLTS
l			LRANVDRGKRSSGKGNSSDHEGCWNBESWTFSQSGTSGSKKFKK
İ			TKPKEDCLLGSAKLDEEFEKKFNSLPQYSPVTFDRKCVPVPRKK
l			KKTGNVSSEPTKTSKGSGDKWSNKQLFLDAIHPTEAIFSEDRNT
			MEDIUVIVIT DET ENIEDEDEEER DERGGONIDIGEERING
	į		MEPVHKVKNIPSIFNTPEPTTTARTFGGQPKEKSKENPDYSPCQ
6435	2227	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	DTQRAGYHHEEVLWMTNLMNNCGGVYLKQLRHTAMTNA
0433	2227	657	ALQRDAAAAYAHPEYEERFLQEETVSQQINSIELLQTRPLALPE
			VVKSQRPLQRQVHLRGRPASQPTVIRGITYYKAKVSEEENDIEE
			QQDEFFSGDNGVDLLIEDQLLRHNGLMTSVTRRPAATRQGHSTA
			VTSDLNARTAPWSSALPQPSTSDPSIANHASVGPTLQTTSVSPD
			PTRESVLQPSPQVPATTVAHTATQQPAAPAPPAVSPREALMEAM
			HTVPVPPTTVRTDSLGKDAPAGRGTTPASPTLSPEEEDDIRNVI
			GRCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDERIYVTNYYY
			GNTLVEFRNLENFKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNR
[			AFTRNIIKYDLKQRYVAAWAMLHDVAYEEATPWRWQGHSDVDFA
1			VDENGLWLIYPALDDEGFSQEVIVLSKLNAADLSTQKETTWRTG
1			LRENEYGNCFVICGVLYAVDSYNQRNANISYAFDTHTNTQIVPR
6436	1305	74.	LLFENEYFYTTQIDYNPKDRLLYAWDNGHQVTYHVIFAY
0436	1295	341	GACRPPVRQDPDSGPDYEALPAGATVTTHMVAGAVAGILEHCVM
]			YPIDCVKTRMQSLQPDPAARYRNVLEALWRIIRTEGLWRPMRGL
			NVTATGAGPAHALYFACYEKLKKTLSDVIHPGGNSHIANGAAGC
( !			VATLLHDAAMNPAEVVKQRMQMYNSPYHRVTDCVRAVWQNEGAG
			AFYRSYTTQLTMNVPFQAIHFMTYEFLQBHFNPQRRYNPSSHVL
.			SGACAGAVAAAATTPLDVCKTLLNTQESLALNSHITGHITGMAS
[ i			AFRTVYQVGGVTAYFRGVQARVIYQIPSTAIAWSVYEFFKYLIT
1			KROEEWRAGK
6437	1828	360	PPAPAPPAS PARHVTRTARGHLEGGSRAPPLLQAVFLQIKNMVK
1 1			
į .		İ	LIHTLADHGDDVNCCAFSFSLLATCSLDKTIRLYSLRDFTELPH
} [			SPLKFHTYAVHCCCFSPSGHILASCSTDGTTVLWNTENGQMLAV
			MEQPSGSPVRVCQFSPDSTCLASGAADGTVVLWNAQSYKLYRCG
į į			SVKDGSLAACAFSPNGSFFVTGSSCGDLTVWDDKMRCLHSEKAH
			DLGITCCDFSSQPVSDGEQGLQFFRLASCGQDCQVKIWIVSFTH
L			ILGFELKYKSTLSGHCAPVLACAFSHDGQMLVSGSVDKSVIVYD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	P=Ploline, Q=Glutamine, R=Arginine,
	residue of		S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
}			TNTENILHTLTQHTRYVTTCAFAPNTLLLATGSMDKTVNIWQFD
ŀ		•	LETLCQARSTEHQLKQFTEDWSEEDVSTWLCAQDLKDLVGIFKM
			NNIDGKELLNLTKESLADDLKIESLGLRSKVLRKIEELRTKVKS
			LSSGIPDEFICPITRELMKDPVIASDGYSYEKEAMENWDPAKRN
L	]		RTSPP
6438	109	901	EVQILRAKMFQTGGLIVFYGLLAQTMAQFGGLPVPLDQTLPLNV
ļ			NPALPLSPTGLAGSLTNALSNGLLSGGLLGILENLPLLDILKPG
1	1		GGTSGGLLGGLLGKVTSVIPGLNNIIDIKVTDPQLLELGLVQSP
-			DGHRLYVTIPLGIKLQVNTPLVGASLLRLAVKLDITAEILAVRD
ì	Ì		KQERIHLVLGDCTHSPGSLQISLLDGLGPLPIQGLLDSLTGILN
			KVLPELVQGNVCPLVNEVLRGLDITLVHDIVNMLIHGLQFVIKV
6439	23	412	SIQTASAITTEMASQSQGIQQLLQAEKRAAEKVADARKRKARRL
	}		KQAKEEAQMEVEQYRREREHEFQSKQQAAMGSQGNLSAEVEQAT
	1		RRQVQGMQSSQQRNRERVLAQLLGMVCDVRPQVHPNYRISA
6440	3	517	RARWINSDMGDLPGLVRLSIALRIQPNDGPVFYKVDGQRFGQNRT
	1	] ",	IKLLTGSSYKVEVKIKPSTLQVENISIGGVLVPLELKSKEPDGD
		·	RVVYTGTYDTEGVTPTKSGERQPIQITMPFTDIGTFETVWQVKF
6441	234	2.2.72	YNYHKRDHCQWGSPFSVIEYECKPNETRSLMWVNKESFL
0441	234	1373	KSGGLRRRQRPGRSAAVGEEELPPGMEKFKAAMLLGSVGDALGY
			RNVCKENSTVGMKIQEELQRSGGLDHLVLSPGEWPVSDNTIMHI
			ATARALTTDYWCLDDLYREMVRCYVEIVEKLPERRPDPATIEGC
			AQLKPNNYLLAWHTPFNEKGSGFGAATKAMCIGLRYWKPERLET
1			LIEVSVECGRMTHNHPTGFLGSLCTALFVSFAAQGKPLVQWGRD
			MLRAVPLAEEYCRKTIRHTAEYQEHWFYFEAKWQFYLEERKISK
			DSENKAIFPDNYDAEERBKTYRKWSSEGRGGRRGHDAPMIAYDA
			LLAAGNSWTELCHRAMFHGGESAATGTIAGCLFGLLYGLDLVPK
			GLYQDLEDKEKLEDLGAALYRLSTEEK
6442	34	796	AEDPAGGLAGQDTMFARGLKRKCVGHEEDVEGALAGLKTVSSYS
			LQRQSLLDMSLVKLQLCHMLVEPNLCRSVLIANTVRQIQEEMTQ
ì			DGTWRTVAPQAAERAPLDRLVSTEILCRAAWGQEGAHPASGLGD
1		l	GHTQGPVSDLCPVTSAQAPRHLQSSAWEMDGPRENRGSFHKSLD
1			QIFETLETKNPSCMEELFSDVDSPYYDLDTVLTGMMGGARPGPC
			EGLEGLAPATPGPSSSCKSDLGELDHVVEILVET
6443	2	555	MASPAASSVRPPRPKKEPQTLVIPKNAAEEQKLKLERLMKNPDK
1			AVPIPEKMSEWAPRPPPEFVRDVMGSSAGAGSGEFHVYRHLRRR
			EYQRQDYMDAMAEKQKLDAEFQKRLEKNKIAAEEQTAKRRKKRQ
1			KLKEKKLLAKKMKLEQKKQEGPGQPKEQGSSSAEASGTEEEEE
			VPSFTMGR
6444	390	899	GSTPRGKMRAPIPEPKPGDLIEIFRPFYRHWAIYVGDGYVVHLA
	3,0	099	
			PPSEVAGAGAASVMSALTDKAIVKKELLYDVAGSDKYQVNNKHD
			DKYSPLPCSKIIQRAEELVGQEVLYKLTSENCEHFVNELRYGVA
6445		753	RSDQVRDVIIAASVAGMGLAAMSLIGVMFSRNKRQKQ
0445	2	753	AGAAGAARSPRPQAHTKGVRGLPSRRRSPDCGRMELAAGSF
			SEEQFWEACAELQQPALAGADWQLLVETSGISIYRLLDKKTGLY
			EYKVFGVLEDCSPTLLADIYMDSDYRKQWDQYVKELYEQECNGB
			TVVYWEVKYPFPMSNRDYVYLRQRRDLDMEGRKIHVILARSTSM
		i	PQLGERSGVIRVKQYKQSLAIESDGKKGSKVFMYYFDNPGGQIP
			SWLINWAAKNGVPNFLKDMARACQNYLKKT
6446	1	1651	RCPTRSPPPDTPGSRGTTAMCSLASGATGGRGAVENEEDLPELS
			DSGDEAAWEDEDDADLPHGKQQTPCLFCNRLFTSAERTFSHCKS
1			EHQFNIDSMVHKHGLEFYGYIKLINFIRLKNPTVEYMNSIYNPV
1			PWEKEEYLKPVLEDDLLLQFDVEDLYEPVSVPFSYPNGLSENTS
			VVEKLKHMEARALSAEAALARAREDLQKMKQFAQDFVMHTDVRT
			CSSSTSVIADLQEDEDGVYFSSYGHYGIHEEMLKDKIRTESYRD
			FIYONPHIFKDKVVLDVGCGTGILSMFAAKAGAKKVLGVDQSEI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ļ	1 - 1 - 1 - 1 - 1	<del> </del>	LYQAMDIIRLNKLEDTITLIKGKIEEVHLPVEKVDVIISEWMGY
			FLLFESMLDSVLYAKNKYLAKGGSVYPDICTISLVAVSDVNKHA
			DRIAFWDDVYGFKMSCMKKAVIPEAVVEVLDPKTLISEPCGIKH
			IDCHTTSISDLEFSSDFTLKITRTSMCTAIAGYFDIYFEKNCHN
			RVVFSTGPQSTKTHWKQTVFLLEKPFSVKAGEALKGKVTVHKNK
1			KDPRSLTVTLTLNNSTQTYGLQ
6447	1554	1068	RLGPAEWHLSGPCHATLGAANRGRALGVRAAWRGAPLCORVMMP
	1	1000	SRTNLATGIPSSKVKYSRLSSTDDGYIDLQFKKTPPKIPYKAIA
ľ			LATVLFLIGAFLIIIGSLLLSGYISKGGADRAVPVLIIGILVFL
		ĺ	PGFYHLRIAYYASKGYRGYSYDDIPDFDD
6448	74	559	GOVLSHCYHYRSSRWRRGGLSRGRGAGVMALVPYEETTEFGLOK
1	/-	1	FHKPLATFSFANHTIQIRQDWRHLGVAAVVWDAAIVLSTYLEMG
			AVELRGRSAVELGAGTGLVGIVAALLACRIRYERDNNFLAMLER
			QFIVRKVHYDPEKDVHIYEAOKRNOKEDL
6449	597	1876	EYGVCENLRKLEITGVSCRDVYAKLLHRYRHILGLWOPDIGPYG
	]	1070	GLLNVVVDGLFIIGWMYLPPHDPHVDDPMRFKPLFRIHLMERKA
1			ATVECMYGHKGPHHGHIQIVKKDEFSTKCNQTDHHRMSGGROEE
		1	FRIWLREBWGRTLEDIFHEHMQELILMKFIYTSQYDNCLTYRRI
			YLPPSRPDDLIKPGLFKGTYGSHGLEIVMLSFHGRRARGTKITG
1			DPNIPAGQQTVEIDLRHRIQLPDLENQRNFNELSRIVLEVRERV
			RQEQQEGGHEAGEGRGRQGPRESQPSPAQPRAEAPSKGPDGTPG
			EDGGEPGDAVAAAEQPAQCGQGQPFVLPVGVSSRNEDYPRTCRM
1			CFYGTGLIAGHGFTSPERTPGVFILFDEDRFGFVWLELKSFSLY
1		ĺ	SRVQATFRNADAPSPQAFDEMLKNIQSLTS
6450	848	269	FVPAPRTVSGKRSLPGEWEERGEGEQRTGREFSGNGGRAVEAAR
			MRLLCGLWLWLSLLKVLQAQTPTPLPLPPPMQSFQGNQFQGEWF
			VLGLAGNSFRPEHRALLNAFTATFELSDDGRFEVWNAMTRGOHC
1	ļ		DTWSYVLIPAAQPGQFTVDHRVWTHEQAGRPQDQPAGQELVAAS
			RDAGPVHLPGQSSGPLG
6451	232	939	HSPTPPTSPRASTMEDVKLEFPSLPQCKEDAEEWTYPMRREMOE
		!	ILPGLFLGPYSSAMKSKLPVLQKHGITHIICIRQNIEANFIKPN
1			FQQLFRYLVLDIADNPVENIIRFFPMTKEFIDGSLQMGGKVLVH
1			GNAGISRSAAFVIAYIMETFGMKYRDAFAYVQERRFCINPNAGF
		İ	VHQLQEYEAIYLAKLTIQMMSPLQIERSLSVHSGTTGSLKRTHE
			EEDDFGTMQVATAQNG
6452	1	652	RTRGESSNMEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQ
	}	1	LKFLKPKINSFYAFEVKDAKGRTVSLEKYKGKVSLVVNVASDCO
	1		LTDRNYLGLKELHKEFGPSHFSVLAFPCNQFGBSEPRPSKEVES
			FARKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWK
	1		YLVNPEGQVVKFWRPEEPIEVIRPDIAALVRQVIIKKKEDL
6453	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
	1		RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
	1	}	DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
		1	FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT
L	1	[	PADSSGTAEGGSGVASPAQADKAEL
6454	827	223	HRRWLPGLSMSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSC
1			RDKKNCKVVFSQQELRKRLTPLQYHVTQEKGTESAFEGEYTHHK
	1		DPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITFTDD
			FSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFT
			PADSSGTAEGGSGVASPAQADKAEL
6455	1042	173	RVHLATVSASAAWDALGLPVRSHMQGSTRRMGVMTDVHRRFLQL
	†		LMTHGVLEEWDVKRLQTHCYKVHDRNATVDKLEDFINNINSVLE
			SLYIEIKRGVTEDDGRPIYALVNLATTSISKMATDFAENELDLF
	1		RKALELIIDSETGFASSTNILNLVDQLKGKKMRKKEAEQVLQKF
1			VQNKWLIEKEGEFTLHGRAILEMEQYIRETYPDAVKICNICHSL
	<del></del>	<del></del>	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
Ì			LIQGQSCBTCGIRMHLPCVAKYFQSNAEPRCPHCNDYWPHEIPK VFDPEKERESGVLKSNKKSLRSROH
6456	2	555	RPQSRSISMWRNSLLQVSSGLRWLRVCAMVDILGERHLVTCKGA
"""		333	TVEAEAALQNKVVALYFAAARCAPSRDFTPLLCDFYTALVAEAR
			RPAPFEVVFVSADGSSQEMLDFMRELHGAWLALPFHDPYRHELR
			KRYNVTAIPKLVIVKQNGEVITNKGRKQIRERGLACFQDWVEAA
			DIFONESV
6457	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
i			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEENICLDLKS
6458	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
İ			IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
ľ			DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
6459	23	000	SFLTLSSQLKPKPVGEENICLDLKS
0433	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
İ			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIFVFLND
			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
1		·	DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEBNICLDLKS
6460	23	892	PTTGFPVTNFPWNWPDGKPPIMILYVSKLNKIIHFPDFDKKIPV
			KLFPLPLLYVGNHISGLSSTSKLSLPMFTVLRKFTIPLTLLLET
		•	IILGKQYSLNIILSVFAIILGAFIAAGSDLAFNLEGYIPVFLND
1			IFTAANGVYTKQKMDPKELGKYGVLFYNACFMIIPTLIISVSTG
1		÷	DLQQATEFNQWKNVVFILQFLLSCFLGFLLMYSTVLCSYYNSAL
			TTAVVGAIKNVSVAYIGILIGGDYIFSLLNFVGLNICMAGGLRY
			SFLTLSSQLKPKPVGEENICLDLKS
6461	1653	360	LQQRTLRITAVGQTHPIAWMAWEPSLGAFYGPASFITFVNCMYF
			LSIFIQLKRHPERKYELKEPTEEQQRLAANENGEINHQDSMSLS
	1		LISTSALENEHTFHSQLLGASLTLLLYVALWMFGALAVSLYYPL
			DLVFSFVFGATSLSFSAFFVVHHCVNREDVRLAWIMTCCPGRSS
			YSVQVNVQPPNSNGTNGEAPKCPNSSAESSCTNKSASSFKNSSQ
1			GCKLTNLQAAAAQCHANSLPLNSTPQLDNSLTEHSMDNDIKMHV
1			APLEVQFRTNVHSSRHHKNRSKGHRASRLTVLREYAYDVPTSVE GSVQNGLPKSRLGNNEGHSRSRRAYLAYRERQYNPPQQDSSDAC
			STLPKSSRNFEKPVSTTSKKDALRKPAVVELENQQKSYGLNLAI
			QNGPIKSNGQEGPLLGTDSTGNVRTGLWKHETTV
6462	3	773	SEELDREKKLKEDSPRKTPNKESGVPSLPVSLTSIKEEPKEAKH
			PDSQSMEESKLKNDDRKTPVNWKDSRGTRVAVSSPMSQHQSYIQ
			YLHAYPYPQMYDPSHPAYRAVSPVLMHSYPGAYLSPGFHYPVYG
	j. · .		KMSGREETEKVNTSPSVNTKTTTESKALDLLQQHANQYRSKSPA
Í			PVEKATAEREREAERERDRHSPFGQRHLHTHHHTHVGMGYPLIP
			GQYDPFQGLTSAALVASQQVAAQASASGMFPGQRRE
6463	2	350	VILCILGGWIFKNADRSMBKKKGEPRTRAEARPWVDEDLKDSSD
			LHQAEEDADEWQESEENVEHIPFSHNHYPEKEMVKRSQEFYELL
	<u> </u>		NKRRSVRFISNEQVPMEVIDNVIRTAGL
6464	12	1154	GILROKEREERNRIHKKEILFLEHLLVVPSEMSSLSGKVQTVLG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine.
	corresponding	to first	
ľ	to first	amino acid	L=Leucine, M=Methionine, N=Asparagine,
	amino acid	l .	P=Proline, Q=Glutamine, R=Arginine,
		residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	l	į	LVEPSKLGRTLTHEHLAMTFDCCYCPPPPCQEAISKEPIVMKNL
1			YWIQKNAYSHKENLQLNQETEAIKEELLYFKANGGGALVENTTT
			GISRDTQTLKRLABETGVHIISGAGFYVDATHSSETRAMSVEQL
		•	TDVLMNEILHGADGTSIKCGIIGEIGCSWPLTESERKVLQATAH
	1		AQAQLGCPVIIHPGRSSRAPFQIIRILQEAGADISKTVMSHLDR
1			TILDKKELLEFAQLGCYLEYDLFGTELLHYQLGPDIDMPDDNKR
	ļ		IRRVRLLVEEGCEDRILVAHDIHTKTRLMKYGGHGYSHILTNVV
			PKMLLRGITENVLDKILIENPKQWLTFK
6465	126	1396	KMTVFFKTLRNHWKKTTAGLCLLTWGGHWLYGKHCDNLLRRAAC
Į.			QEAQVFGNQLIPPNAQVKKATVFLNPAACKGKARTLFEKNAAPI
1			LHLSGMDVTIVKTDYEGQAKKLLELMENTDVIIVAGGDGTLOEV
1			VTGVLRRTDEATFSKIPIGFIPLGETSSLSHTLFAESGNKVOHI
1		1	TDATLAIVKGETVPLDVLQIKGEKEQPVFAMTGLRWGSFRDAGV
			KVSKYWYLEPLKIKAAHFFSTLKEWPQTHQASISYTGPTERPPN
ł	1		EPEETPVQRPSLYRRILRRLASYWAQPQDALSQEVSPEVWKDVQ
			LSTIELSITTRNNQLDPTSKEDFLNICIEPDTISKGDFITIGSR
1			KVRNPKLHVEGTECLQASQCTLLIPEGAGGSFSIDSERYEAMPV
1	•		EVKLLPRKLQFFCDPRKREQMLTSPTQ
6466	1134	828	VARGTELSQLEKAHPPADMGRRKSKRKPPPKKKMTGTLETOFTC
1 0100	1.3.	020	PFCNHEKSCDVKMDRARNTGVISCTVCLEEFQTPITYLSEPVDV
1			YSDWIDACEAANO
6467	301	2571	GELRVLALAHGELACHAVLTASLLSLRSRLMDSDMDYERPNVET
1 0107	301	23/1	IKCVVVGDNAVGKTRLICARACNATLTOYOLLATHVPTVWAIDO
1	i		YRVCQEVLERSRDVVDDVSVSLRLWDTFGDHHKDRRFAYGRSDV
			VVLCFSIANPNSLHHVKTMWYPEIKHFCPRAPVILVGCQLDLRY
1	j		ADLEAVNRARRPLARPIKPNEILPPEKGREVAKELGIPYYETSV
1			
1			VAQFGIKDVFDNAIRAALISRRHLQFWKSHLRNVQRPLLQAPFL
1			PPKPPPPIIVVPDPPSSSEECPAHLLEDPLCADVILVLQERVRI
1	,		FAHKIYLSTSSSKFYDLFLMDLSEGELGGPSEPGGTHPEDHQGH
			SDQHHHHHHHHHGRDFLLRAASFDVCESVDEAGGSGPAGLRAST
			SDGILRGNGTGYLPGRGRVLSSWSRAFVSIQEEMAEDPLTYKSR
			LMVVVKMDSSIQPGPFRAVLKYLYTGELDENERDLMHIAHIAEL
i			LEVFDLRMMVANILNNEAFMNQEITKAFHVRRTNRVKECLAKGT
1			FSDVTFILDDGTISAHKPLLISSCDWMAAMFGGPFVESSTREVV
			FPYTSKSCMRAVLEYLYTGMFTSSPDLDDMKLIILANRLCLPHL
			VALTEQYTVTGLMEATQMMVDIDGDVLVFLELAQFHCAYQLADW
			CLHHICTNYNNVCRKFPRDMKAMSPENQEYFEKHRWPPVWYLKE
			EDHYQRARKEREKEDYLHLKRQPKRRWLFWNSPSSPSSSAASSS
C : 2 =	<u> </u>		SPSSSSAVV
6468	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
			LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
			KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
			SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
1		}	QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
			TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
ļ			GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL
			PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF
1	]		ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES
ļ			TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
			GKGKFSRAHFVLLSLL
6469	3	1374	DAWAGTNMAALAPVGSPASRGPRLAAGLRLLPMLGLLQLLAEPG
1			LGRVHHLALKDDVRHKVHLNTFGFFKDGYMVVNVSSLSLNEPED
1			KDVTIGFSLDRTKNDGFSSYLDEDVNYCILKKQSVSVTLLILDI
1			SRSEVRVKSPPEAGTQLPKIIFSRDEKVLGQSQEPNVNPASAGN
}			QTQKTQDGGKSKRSTVDSKAMGEKSFSVHNNGGAVSFQFFFNIS
			TDDQEGLYSLYFHKCLGKELPSDKFTFSLDIEITEKNPDSYLSA
	L	L	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
			L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	· · ·
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
		<del></del>	GEIPLPKLYISMAFFFFLSGTIWIHILRKRRNDVFKIHWLMAAL
	i	ĺ	PFTKSLSLVFHAIDYHYISSQGFPIEGWAVVYYITHLLKGALLF
		[	ITIALIGTGWAFIKHILSDKDKKIFMIVIPRRVLANVAYIIIES
		i	
			TEEGTTEYGLWKDSLFLVDLLCCGAILFPVVWSIRHLQEASATD
		}	GKGKFSRAHFVLLSLL
6470	2726	1437	AAASGVSSRADAPVLAQSPASAGNGRPSTPRVPGSRRHPSAPRS
			GPLPREDGCRTPGPQLLPLPGALLRPRTLLSSAAETGRSRHPDT
			OHPSSGGRCRGGTESPSSAAGRPASMAEAEEDCHSDTVRADDDE
		t .	ENESPAETDLQAQLOMFRAQWMFELAPGVSSSNLENRPCRAARG
	1	1	SLOKTSADTKGKOEQAKEEKARELFLKAVEEEQNGALYEAIKFY
	1	1	1
		l	RRAMQLVPDIEFKITYTRSPDGDGVGNSYIEDNDDDSKMADLLS
		1	YFQQQLTFQESVLKLCQPELESSQIHISVLPMEVLMYIFRWVVS
Į	1	1	SDLDLRSLEQLSLVCRGFYICARDPEIWRLACLKVWGRSCIKLV
	i	1	PYTSWREMFLERPRVRFDGVYISKTTYIRQGEQSLDGFYRAWHQ
		\$	VEYYRYIRFFPDGHVMMLTTPEEPQSIVPRLRTR
6471	1750	299	FFFDKMAAGGSGVGGKRSSKSDADSGFLGLRPTSVDPALRRRRR
04/1	1		GPRNKKRGWRRLAGEPLGLEVDQFLEDVRLQERTSGGLLSEAPN
		1	EKLFFVDTGSKEKGLTKKRTKVQKKSLLLKKPLRVDLILENTSK
ŧ	1	İ	_ ·
		1	VPAPKDVLAHQVPNAKKLRRKEQLWEKLAKQGELPREVRRAQAR
(	[	1	LLNPSATRAKPGPQDTVERPFYDLWASDNPLDRPLVGQDEFFLE
		1	QTKKKGVKRPARLHTKPSQAPAVEVAPAGASYNPSFEDHQTLLS
ļ	]		AAHEVELQRQKEAEKLERQLALPATEQAATQESTFQELCEGLLE
Ì			ESDGEGEPGQGEGPEAGDAEVCPTPARLATTEKKTEQQRRREKA
i	ł		VHRLRVQQAALRAARLRHQELFRLRGIKAQVALRLAELARRQRR
	1		ROARREAEADKPRRLGRLKYQAPDIDVQLSSELTDSLRTLKPEG
ļ	İ		NILRDRFKSFQRRNMIEPRERAKFKRKYKVKLVEKRAFREIQL
<u> </u>		897	SCGSDRAQWAMEFPFDVDALFPERITVLDQHLRPPARRPGTTTP
6472	3	697	_
Ì			ARVDLQQQIMTIIDELGKASAKAQNLSAPITSASRMQSNRHVVY
			ILKDSSARPAGKGAIIGFIKVGYKKLFVLDDREAHNEVEPLCIL
1	1	1	DFYIHESVORHGHGRELFQYMLQKERVEPHQLAIDRPSQKLLKF
İ	1		LNKHYNLETTVPQVNNFVIFEGFFAHQHRPPAPSLRATRHSRAA
l			AVDPTPAAPARKLPPKRAEGDIKPYSSSDREFLKVAVEPPWPLN
		1	RAPRRATPPAHPPPRSSSLGNSPERGPLRPFVP
6473	22	912	SSAVEFVWEGEKMAAEPNKTEIOTLFKRLRAVPTNKACFDCGAK
1 27,5	22	- ~~	NPSWASITYGVFLCIDCSGVHRSLGVHLSFIRSTELDSNWNWFQ
ļ.			LRCMQVGGNANATAFFRQHGCTANDANTKYNSRAAQMYREKIRQ
	1	[	
	1		LGSAALARHGTDLWIDNMSSAVPNHSPEKKDSDFFTEHTQPPAW
1			DAPATEPSGTQQPAPSTESSGLAQPEHGPNTDLLGTSPKASLEL
1			KSSIIGKKKPAAAKKGLGAKKGLGAQKVSSQSFSEIERQAQVAE
		L	KLREQQAADAKKQAEESMVASMRLAYQELQIDR
6474	3	462	LQRQRQHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS
			KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA
			KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP
			PSTLSVKGQIETVRVKGTEN
CA 35		1 - 452	LORGROHPAAAPAVPVRCFTFCFTDIVIMPKRKSPENTEGKDGS
6475	3	462	1
l .			KVTKQEPTRRSARLSAKPAPPKPEPKPRKTSAKKEPGAKISRGA
			KGKKEEKQEAGKEGTAPSENGETKAEEIHISRSTVNVSTSRGTP
			PSTLSVKGQIETVRVKGTEN
6476	106	1090	ARAMAQYKGTMREAGRAMHLLKKRERQREQMEVLKQRIAEETIL
			KSQVDKRFSAHYDAVEAELKSSTVGLVTLNDMKARQEALVRERE
ł	1		ROLAKROHLEEORLOGERGREGEORRERKRKISCLSFALDDLDD
1			QADAAEARRAGNLGKNPDVDTSFLPDRDREEEENRLREELRQEW
1			
			EAQREKVKDEEMEVTFSYWDGSGHRRTVRVRKGNTVQQFLKKAL
1	1	1	QGLRKDFLELRSAGVEQLMFIKEDLILPHYHTFYDFIIARARGK
	1	1	
			SGPLFSFDVHDDVRLLSDATMEKDESHAGKVVLRSWYEKNKHIF

SEQ   Predicted   Predicted end   Amino acid segment contains	ng signal peptide
ID beginning nucleotide (A=Alanine, C=Cysteine, D=A	
NO: nucleotide location Glutamic Acid, F=Phenylalar	
location corresponding H=Histidine, I=Isoleucine,	
	-
to first amino acid P=Proline, Q=Glutamine, R=J	
amino acid residue of S=Serine, T=Threonine, V=Va	
residue of amino acid W=Tryptophan, Y=Tyrosine, Y	
amino acid sequence Codon, /=possible nucleotic	
sequence   \=possible nucleotide inser	
6477 227 915 LQGHLMGIMAASRPLSRFWEWGKNIVO	VGRNYADHVREMRSAVL
SEPVLFLKPSTAYAPEGSPILMPAYTE	NLHHELELGVVMGKRCR
AVPEAAAMDYVGGYALCLDMTARDVQI	ECKKKGLPWTLAKSFTA
SCPVSAFVPKEKIPDPHKLKLWLKVNO	ELRQEGETSSMIFSIPY
IISYVSKIITLEEGDIILTGTPKGVGI	VKENDEIEAGIHGLVSM
TFKVEKPEY	
6478 2 1495 PVSSRILPESLASSEASTLEAMGRKEE	TOCSSWEEGTTNIPETP
1495 FVSSKIIFESIASSEASIIBEAMOKKEI	
BIAVLKKIKHENIVTLEDIYESTTHYY	
RGVYTEKDASLVIQQVLSAVKYLHENO	and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second s
ENSKIMITDFGLSKMEQNGIMSTACGT	
VDCWSIGVITYILLCGYPPFYEETES	
DDISESAKDFICHLLEKDPNERYTCE	
YPSVSLQIQKNFAKSKWRQAFNAAAVV	HHMRKLHMINLHSPGVRP
EVENRPPETQASETSRPSSPEITITE/	
QHGRRPTAPGGRSLNCLVNGSLHISS	SLVPMHQGSLAAGPCGCC
SSCLNIGSKGKSSYCSBPTLLKKANKI	QNFKSEVMVPVKASGSS
HCRAGQTGVCLIM	
6479 3 949 SCRGPGWHPAGGQAGAMELLSALSLGI	LALSFSRVPLFPVFDLS
YFIVSILYLKYEPGAVELSRRHPIASI	
IGEPLIDYFSNNSSILLASAVWYLIF1	
IFVAMKEVVRVRKIAVGIHHAHHHYH	
LMSNFEQLLRGVWKPETNEILHMSFP	
LPVSKASLIFIFTLFMVSCKVFLTATI	
FGSACGGDHHHDNHGGSHSGGGPGAQI	ISAMPARSKEELSBGSKK
KKAKKAD	
6480 192 514 DFMSIYFPIHCPDYLRSAKMTEVMMN	-
QIFPDPSDFDRCCKLKDRLPSIVVEP	REGEVESGELRWPPEEFL
VQEDEQDNCEETAKENKEQ	
6481 110 1131 KSRMDLDVVNMFVIAGGTLAIPILAF	/ASFLLWPSALIRIYYWY
WRRTLGMQVRYVHHEDYQFCYSFRGRI	PGHKPSILMLHGFSAHKD
MWLSVVKFLPKNLHLVCVDMPGHEGT"	rsslddlsidgqvkrih
QFVECLKLNKKPFHLVGTSMGGQVAGV	YAAYYPSDVSSLWLVCP
AGLQYSTDNQFVQRLKELQGSAAVEK	PLIPSTPEEMSEMLQLC
SYVRFKVPOOILOGLVDVRIPHNNFY	
NMDKIKVPTOIIWGKODOVLDVSGADN	
HSVVMERPRKTAKLIIDFLASVHNTDI	
6482 2517 568 EPVSKVSQSRRKAGVPTANIEESQAVI	
6482 251/ 568 EPVSKVSQSKRAGVPTANTEESQAVE	
RPEAEDGPGAGDHALGLPAEVVEPEGI	
NHIDTEELSAGEEHLVKCLRLLRRYRI	
LWSEREEIETAQAYLESSEALYNQYMI	
EKLTEQERSKRFEKVYTHNLYYLAQVY	
KRQLEHNAYHPIEWAINAATLSQFYII	
FGQTGKISATEDTPEAEGEVPELYHQF	
NAQLSMQDNIGELDLDKQSELRALRKI	(ELDEEESIRKKAVQFGT
GELCDAISAVEEKVSYLRPLDFEEAR	LFLLGQHYVFEAKEFFQ
IDGYVTDHIEVVQDHSALFKGLAFFE	DMERRCKMHKRRIAMLE
PLTVDLNPQYYLLVNRQIQFEIAHAYY	
SHIVKKINNLNKSALKYYQLFLDSLRI	
MLAKFRVARLYGKIITADPKKELENL	
RAAQEIEVELELSKEMVSLLPTKMERI	
6483 3 623 NSHLLCGLRARAPLSANGREARAMEQI	LABFRAARKRAGLAAQP
6483 3 623 NSHLLCGLRARAPLSANGREARAMEQI PAASQGAQTPGEKAEAAATLKAAPGWI	rlaefraarkraglaaqd Krplvwkprpasaraqd
6483 3 623 NSHLLCGLRARAPLSANGREARAMEQI	ilaefraarkraglaaop Krplvwkprpasaraop WDOSFLTNITFLKVLLW

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ı	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:			
ŀ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ļ	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	•	\=possible nucleotide insertion)
			VFNPGCEAIOGTLTAEOLERELOLRPLAGR
6484	201	965	QLAVKTKMSGLRPGTQVDPEIELFVKAGSDGESIGNCPFCORLF
0484	201	365	
		ļ	MILWLKGVKFNVTTVDMTRKPEELKDLAPGTNPPFLVYNKELKT
1			DFIKIEEFLEQTLAPPRYPHLSPKYKESFDVGCNLFAKFSAYIK
	ł	ì	NTQKEANKNFEKSLLKEFKRLDDYLNTPLLDEIDPDSAEEPPVS
			RRLFLDGDQLTLADCSLLPKLNIIKVAAKKYRDFDIPAEFSGVW
			RYLHNAYAREEFTHTCPEDKEIENTYANVAKQKS
6485	6	1091	FVDLVRAVEFLPCPDSQKLEKECQSSEESMGSNSMRSILEEDEE
1			DEEPPRVLLYHEPRSFEVGMLVWHKHKKYPFWPAVVKSVRORDK
ļ			KASVLYIEGHMNPKMKGFTVSLKSLKHFDCKEKQTLLNQAREDF
			NODIGWCVSLITDYRVRLGCGSFAGSFLEYYAADISYPVRKSIO
			1 -
Į.	1	1	QDVLGTKLPQLSKGSPEEPVVGCPLGQRQPCRKMLPDRSRAARD
			RANQKLVEYIGKAKGAESHLRAILKSRKPSRWLQTFLSSSQYVT
1		1	CVETYLEDEGQLDLVVKYLQGVYQEVGAKVLQRTNGDRIRFILD
			VLLPEAIICAISAGDEVDYKTABEKYIKGPSLSYREKEIFDNQL
	1	ļ	LEERNRRRR
6486	1.0	581	LVLQAGGAHLSPSRVTQGIYYMLAFSEMPKPPDYSELSDSLTLA
			GGTGRFSGPLHRAWRMMNFRORMGWIGVGLYLLASAAAFYYVFE
			ISETYNRLALEHIQQHPEEPLEGTTWTHSLKAQLLSLPFWVWTV
	1	j	IFLVPYLOMFLFLYSCTRADPKTVGYCIIPICLAVICNRHOAFV
			KASNQISRLQLIDT
6487	350	1	SFLKPLRGKMSVTLHTDVGDIKIEVFCERTPKTCENFLALCASN
648/	352	863	
	1	1	YYNGCIFHRNIKGFMVQTGDPTGTGRGGNSIWGKKFEDEYSEYL
	ł	1	KHNVRGVVSMANNGPNTNGSQFFITYGKQPHLDMKYTVFGKVID
	1	1	GLETLDELEKLPVNEKTYRPLNDVHIKDITIHANPFAQ
6488	878	241	TALQEFGTSGPPLSLRFALPSGTGRFKPLPGARGPSWPPSPRVP
			MEPPNLYPVKLYVYDLSKGLARRLSPIMLGKQLEGIWHTSIVVH
į			KDEFFFGSGGISSCPPGGTLLGPPDSVVDVGSTEVTEEIFLEYL
1			SSLGESLFRGEAYNLFEHNCNTFSNEVAQFLTGRKIPSYITDLP
	Ì	1	SEVLSTPFGQALRPLLDSIQIQPPGGSSVGRPNGQS
6489	1457	375	KVAKMATALSEEELDNEDYYSLLNVRREASSEELKAAYRRLCML
0105	1 2137	1 3.3	YHPDKHRDPELKSQAERLFNLVHQAYEVLSDPOTRAIYDIYGKR
J	1	ì	GLEMEGWEVVERRRTPABIREEFERLQREREERRLOORTNPKGT
1		1	
		1	ISVGVDATDLFDRYDEEYEDVSGSSFPQIEINKMHISQSIEAPL
		1	TATDTAILSGSLSTQNGNGGGSINFALRRVTSAKGWGELEFGAG
		1	DLQGPLFGLKLFRNLTPRCFVTTNCALQFSSRGIRPGLTTVLAR
	1		NLDKNTVGYLQWHCSSPLLQVQRPHRNTRACAPEPSFRPFLHVP
	1	1	TWDAECSGARTPSTAWTSAAVKLREACLSGPGSGSHQLLLLTPR
			SKRRTGGG
6490	3	1183	HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH
1			KDLIHDVSFDFHGRRMATCSSDOSVKVWDKSESGDWHCTASWKT
			HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEBIVGESNDKLRG
			OSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE
	1		APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
			1
			DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL
			GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
			NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL
			KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
6491	3	1183	HEAGCEVWLGYGPRAAAAAATVLFGGAGPTETMFVARSIAADH
1			KDLIHDVSFDFHGRRMATCSSDQSVKVWDKSESGDWHCTASWKT
1			HSGSVWRVTWAHPEFGQVLASCSFDRTAAVWEEIVGESNDKLRG
			QSHWVKRTTLVDSRTSVTDVKFAPKHMGLMLATCSADGIVRIYE
		J	APDVMNLSQWSLQHEISCKLSCSCISWNPSSSRAHSPMIAVGSD
1			
]		1	DSSPNAMAKVQIFEYNENTRKYAKAETLMTVTDPVHDIAFAPNL
		1	GRSFHILAIATKDVRIFTLKPVRKELTSSGGPTKFEIHIVAQFD
	<u></u>	L	NHNSQVWRVSWNITGTVLASSGDDGCVRLWKANYMDNWKCTGIL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
!	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	
1	amino acid		W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\-possible nucleotide insertion)
			KGNGSPVNGSSQQGTSNPSLGSNIPSLQNSLNGSSAGRKHS
6492	34	2573	IPFLKSCCCCCLFDFPPPPLDQVQEEECEVERVTEHGTPKPFRK
		<b>j</b>	PDSVAFGESQSEDEQFENDLETDPPNWQQLVSREVLLGLKPCEI
			KRQEVINELFYTERAHVRTLKVLDQVFYQRVSREGILSPSELRK
]			1FSNLEDILQLHIGLNEQMKAVRKRNETSVIDQIGEDLLTWFSG
ļ			PGEEKLKHAAATFCSNQPFALEMIKSRQKKDSRFQTFVQDAESN
	!	1	PLCRRLQLKDIIPTQMQRLTKYPLLLDNIATYTEWPTEREKVKK
			AADHCRQILNYVNQAVKEAENKQRLEDYQRRLDTSSLKLSEYPN
			VEELRNLDLTKRKMIHEGPLVWKVNRDKTIDLYTLLLEDILVLL
			QKQDDRLVLRCHSKILASTADSKHTFSPVIKLSTVLVRQVATDN
		1	KALFVISMSDNGAQIYELVAQTVSEKTVWQDLICRMAASVKEQS
	1		TKPIPLPQSTPGEGDNDEEDPSKLKEEQHGISVTGLQSPDRDLG
1			LESTLISSKPQSHSLSTSGKSEVRDLFVAERQFAKEQHTDGTLK
		[	EVGEDYQIAIPDSHLPVSEERWALDALRNLGLLKQLLVQQLGLT
			EKSVQEDWQHFPRYRTASQGPQTDSVIQNSENIKAYHSGEGHMP
ļ		}	FRTGTGDIATCYSPRTSTESFAPRDSVGLAPQDSQASNILVMDH
			MIMTPEMPTMEPEGGLDDSGEHFFDAREAHSDENPSEGDGAVNK
I			EEKDVNLRISGNYLILDGYDPVQESSTDEEVASSLTLQPMTGIP
ł			AVESTHOOOHSPONTHSDGAISPFTPEFLVOORWGAMEYSCFEI
ļ	İ	}	QSPSSCADSQSQIMEYIHKIEADLEHLKKVEESYTILCORLAGS
			ALTDKHSDKS
6493	557	1147	TPARMAYQGSSTSDCMSKTLDSASAHFAASAVVSAPVPSRSEVA
			KEQNTGHNNINGVVQPSGTSKTLYSTNMALSSSPGISAVQLVRT
l			VGHTTTNHLIPALCTSSPQTLPMNNSCLTNAVHLNNVSVVSPVN
			VHINTRTSAPSPTALKLATVAASMDRVPKVTPSSAISSIARENH
Į			EPERLGLNGIABTTVAMEVT
6494	2425	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
			LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG
			VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL
			EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL
		}	ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIBSVNLLVSAN
			GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS
			VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK
			PLIWIESVIEKHSHSRIEYMIKAKSQFKRRSTANNVEIHIPVPN
			DADSPKFKTTVGSVKWVPENSEIVWSIKSFPGGKEYLMRAHFGL
1			PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL
			PWVRYITQNGDYQLRTQ
6495	2425	1052	AVAGGARPCSTPSSPHRRCRRHRPRPLPRPPAAIMSASAVYVLD
1			LKGKVLICRNYRGDVDMSEVEHFMPILMEKEEEGMLSPILAHGG
			VRFMWIKHNNLYLVATSKKNACVSLVFSFLYKVVQVFSEYFKEL
			EEESIRDNFVIIYELLDELMDFGYPQTTDSKILQEYITQEGHKL
			ETGAPRPPATVTNAVSWRSEGIKYRKNEVFLDVIESVNLLVSAN
			GNVLRSEIVGSIKMRVFLSGMPELRLGLNDKVLFDNTGRGKSKS
			VELEDVKFHQCVRLSRFENDRTISFIPPDGEFELMSYRLNTHVK
			PLIWIESVIEKHSHSRIEYMIKAKSOFKRRSTANNVEIHIPVPN
1		1	DADSPKFKTTVGSVKWVPENSBIVWSIKSFPGGKEYLMRAHFGL
1			PSVEAEDKEGKPPISVKFEIPYFTTSGIQVRYLKIIEKSGYQAL
			PWVRYITQNGDYQLRTQ
6496	247	559	LRAVSLLPLQLVLPEYSIHSLFCIMFLCAOEWLTLGLNVPLLFY
			HFWRYFHCPADSSELAYDPPVVMNADTLSYCQKEAWCKLAFYLL
1	ļ		SFFYYLYCMIYTLVSS
6497	1053	352	ANTQICRLCPRRHLHPPCGAKMGNGTEEDYNFVFKVVLIGESGV
1		332	GKTNLLSRFTRNEFSHDSRTTIGVEFSTRTVMLGTAAVKAQIWD
			TAGLERYRAITSAYYRGAVGALLVFDLTKHQTYAVVERWLKELY
1			DHAEATIVVMLVGNKSDLSQAREVPTEEARMFAENNGLLFLETS
1	l		ALDSTNVELAFETVLKEIFAKVSKQRQNSIRTNAITLGSAQAGQ

ID	CEO T	Predicted	Predicted end	Amino acid segment containing signal peptide
NO: nucleotide location corresponding to first amino acid residue of amino acid amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se	SEQ	1		
location corresponding to first amino acid residue of amino acid sequence  6498  2636  272  SERICPWOTHLAGPTYMKLSSLLALIRPALPLIGISIGE LEVENINGE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORATIVE CORPORAT				
corresponding to first amino acid amino acid residue of amino acid amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	NO:	nucleotide	location	
to first amino acid residue of amino acid sequence  6498  2636  272  SERICPWGTHLAGPTTMRLSSLLALLRPALPLILGLSIGG LEVSNIGGEGEPPCVEAVGERGEPOPPDSRARLDQSDEDF VPYNDPNKPYKKVLRTRYICTBLGSRERLLVAVLISRAT AVANRTVAHFPRILLYPTGGRGARAPOLYSHEDEN KESSAFLSAFANHVYSEGTLMYLHKRESLLELLRALPLLPLLEGSREG  AVANRTVAUHFPRILLYPTGGRGARAPOLYSHEDEN KESSAFLSAFANHVYSEGTLMYLHKRESLLELRAYSH  BEPERGRAPVESTER  AVANRTVAUHFPRILLYPTGGRGARAPOLYSHEDEN KESSAFLSAFANHVYSEGTLMYLHKRESLLELRAYSE QAQINNLTVITPEGEGALSWEVLDAFPTPHISRFEVLGWD OHTFSCADGAPKCPLQGASRADVGDALETALEQINRRYOP QKORLLNAVREPSPAGEVYTLDHLEGGRGRAPPTPHISRFEVLGWD OHTFSCADGAPKCPLQGASRADVGDALETALEQINRRYOP QKORLLNAVREPSPAGEVYTLDHLEGGRGRAPPTHGWRAPABEL POTRIAMLAVRABAPSOYREGGRGRAPPHGFOXABABEL POTRIAMLAVRABAPSOYREGGRAPPHGFOXABABEL POTRIAMLAVRABAPSOYREGGRAPPHGFOXBABABEL POTRIAMLAVRABAPSOYREGGRAPPHGFOXBABABEL POTRIAMLAVRABABAPTE POTRIAMLAVRABAPSOYREGGRAPOLABAGETARAPEGUANST GRAPHCCHESTAGGAPKCPUGASRADVENTENTETTTV PEVLNRCRMAISGWAFFPVHRGERNALSPORSPGPP DPPSPPGAGRFORASABEGFYNADYLAARA ELAGGEEEALEGLEVMOVFLRFSGLHLERAVEPGUAVR CSPRISBELTHRCRISNLEGLGGRAQLAMALFEQCANNST GHAPWRDVYRQTWKLEGEALEQAIISQAPQVEKLIATTA PWYHSSLTREEABRKLYSGAQTTOKRLLRPRREGGTYALS KTVYHYLISODKAGKYCTPBGTKFDTLWGLWSTLKKADG LKRACPNSSANASGAAPATDPAHPSTLTHORRIDTHAN KTYSHYLISODKAGKYCTPBGTKFDTLWGLWSTLKKADG LKRACPNSSANASGAAPATDPAHPSTLTHORRIDTHAN KTYSHYLISODKAGKYCTPBGTKFDTLWGLWSTLKKADG LVGKREETPVSNVAGLHLGVSMMKYLEERNFVURINDLARR VNNHYAKISDFGLSKALGADDSYTTARAGGKPLKWTABE RKSSSSDVMSYGVTWMRALSYGGKPYKMMKGPEVMAFIE MRCPPBCPBELPGALAGDDSYTTARAGGKPLIKMTABE RKSSSSDVMSYGVTWMRALSTGGKPLKWTABE RKSSSSDVMSYGVTWMRALSTGGKPLKWTABE RKSSSSDVMSYGVTWMRALSTGGKPLKWTABE RKSSSSDVMSYGVTWMRALSTGGKPLKWTABE RKSSSSDVMSYGVTWMRALSTGGKPLKWTABE RKSSSSDVMSYGVTWMRALSTGGKPLKWTABE RKSSSSDVMSYGVTWMRALSTGGKPLKWTABE RKSSSSDVMSYGVTWMRALSTGGKPLKWTABE RKSSSSDVMSYGVTWMRALSTGGKPLKWTABE RKSSSSDVMSYGVTWMRALSTGGKPLKWTABE RKSSSSDVMSYGVTWMRALSTGGKPLKWTABE RKSSSSDVMSYGVTWMRALSTGGRYKMMKVLEENNFVTHILAGRACH SKURGERFSSSENVKYESINMDTNIMMLMMRANAYKY RNDCYNWFTLARDTTFAIIBHLKKYFLLKKDGSOPFYLGHT DLEYVGMEGGIVLSVSSMKRLINIELKINIEGCRGKMIMK YRDCYM		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first amino acid residue of amino acid sequence  6498  2636  272  SERICPWGTHLAGPTTMRLSSLLALLRPALPLILGISIGG LEVSNIGGEOEDCVEAVGERGOPONPDSRARLDQSDEDF VPYYRDPNKPYKKVLRTRYICTBLGSRERLLVAVLISRAT AVAVNRTVAHFPRILLYTGQRGARAPAGMQVVSHGDERP, SETLEHLHTHTGGAGARAPAGMQVVSHGDERP, SETLEHLHTHTGGAGARAPAGMQVVSHGDERP, SETLEHLHTHTGGAGARAPAGMQVVSHGDERP, SETLEHLHTHTGGAGARAPAGMQVVSHGDERP, SETLEHLHTHTGGAGARAPAGMQVVSHGDERP, SETLEHLHTHTGGAGARAPAGMQVVSHGDERP, SETLEHLHTHTGGADVMFFIMODDTVVQAPELAALGHLS LYUGRAEFFIOADGGARYCHGGPGYLLSRSLLLRPHLDD DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKN KBGSSAFLSAFAWHVVSEGTIMTKLHKKRSALELERAYSE QAQINNLTVLTPEGEAGLSWPCVLPAPFPHSRFEVLGMD QHTFSCANGAPKCPLQGASRADVGDALETALEQLNRRYQP QKQRLLNGVRRFDPARGEWFYLDLLLEGGRGRAPPHGVSKAABEL POTRLAWLAVRAEAPSQVRLMDVVSKARHVVSTLEFPLTVTW PEVLNRCRMMAISGMQAFFFVHFGEFNALSPQSCP DPSSPPGAGGFFOGASASGFYNADYLAARAB ELAGGEEEALBGLEVMDVFLRFSGLHLFRAVEPGLVQKP CSPRLSELYHRCRLSNLEGLGGRAQLAMALFGQEQANST GKAPHASCAGARACH CSPRLSELYHRCRLSNLEGLGGRAQLAMALFGQEANST GKAHGGPAELCEFYSRDPDGLPCNLEKPCNRPSGLEPGBG LRDAWRDVVRQTWKLEGGAALGAALTSQAPQVEKLIATTA PWYHSSLTREEABRKLYSGAQTTGKRLLRFRKEGGTYALST KTVYHYLISODKAGKYCIPBGTKFDTLWGLWFRIKKAGG LKRGCPNSSANASGAAAPTDPAHPSTLTHQRRIDTIANS PEPARITSPDKPR PMPMDTSVYSSPYSDPEELKOKKLFLK LIADIELGCNNGGSWCGVYMRKKKQLDVALKUKLGAGE KKRCPNSSANASGAAAPTDPAHPSTLTHQRRIDTIANS PEPARITSPDKPR PMPMDTSVYSSPYSDPEELKOKKLFLK LIADIELGCNNGGSWCGVYMRKKKQLDVALKUKLGAGTE EMMREAQIMHQLDNPYIVRLIGVCQAEALMLUMEMAGGGP LVCKREEI PVSNVAELLEQVSMMKKLEERNFVIRMLARAR VNSHYAKISPGLSKALGADDSYYTARASGKYRLINGLARR VNSHYAKISPGLSKALGADDSYYTARASGKYRLINGLARR VNSHYAKISPGLSKALGADDSYYTARASGKYRLINGLARR VNSHYAKISPGLSKALGADDSYYTARASGKYRLINGLARR VNSHYAKISPGLSKALGADDSYYTARASGKYRLINGLARR VNSHYAKISPGLSKALGADDSYYTARASGKYRLINGLARR VNSHYAKISPGLSKALGADDSYYTARASGKYRLINGLARR VNSHYAKISPGLSKALGADDSYYTARASGKYRLINGLARR VNSHYAKISDGGAGADDSYYTARASGKYRLINGLARR VNSHYAKISDGGAGADDSYYTARASGKYRLINGLARR VNSHYAKISDGGAGADDSYYTARASGKYRDYRCHAALSCH GAGDON THE MECOPECPECTURA THE MECOPECPEGGMIWK VRCHAKISPGSCHVYFISMORYFISMORYFISMORYSUNGLARRACYSIRAMAY VROCUKKFACVYSENKRUNGLINIPECCPGCGGMIWK VR		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	1		l .	P=Proline, O=Glutamine, R=Arginine,
residue of amino acid sequence				
amino acid sequence  Codon, /=possible nucleotide deletion,  #Popssible nucleotide insertion)  BROFGEKRACCISI  SURLCPWGTHLAGFTTMRLSSLALLRPALPLIIGLSGC.  LRYSMIGGEBDPCVERVAVERGRGPONPDSRARLDOSDEDF VPYYRDPNKPYKKVLRTRYIQTELGSRERLLVAVLTSRAT AVAVNRTVAHHFRELIYFTGGRGARAPAGMGVYSHODERP, SETLERLHTHFRGADYDWFIMDDTYVQARRLAALGHLS LYMGRAEBFIGAGBQARYCHGGFGYLLGRSLLGLRPHHLD DILSAR PDEWLGRCLIDSLGVGCOSYGGQQYRSFELANN KEGSSAFLSAPAVHPVSEGTLMYRLHKRFSALELERAYSE QAQIRNLTVLTPBGEAGLSWPVGLBAPFTHRSFEVLGWD QHTFSCAGGAKCPLQGASRAPUGDALETALEQLNRRYOP QKQRLLNGYRRPDPARGMSYTLDLLLECVTQRGHRRALAR LRPLSRVEILPMPYVTEATRVQLVPLLVABAAAPAFLE NVLEFREHALLTLLLYGPREGGRGAPDPFLGYKAAAAEL PGTRLAMLAVRAEAPSQVELMDVVSKKHPVDTLFFLTTW PEVLNRCRNAISGWAGPFFVHIGFPALSPGRSPGPP DPPSPPGADPSRGAPTGGRFDRQASAEGGYNADYLARAA ELAGGEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKF CSPRLSEELYHRCKLSNLBGLGGRAGLAMALFRQGRANST GRHDVVPQVGGGDGAMPTVULRRAAGAFTGSPLAJEPFTFV GKAHGGPAELGEFYSRDPDGLPCNLRKPCNRPSGLEPOPG GHPVVPQVGGGDGAMPDPAALIF PFYGSISRAEAECHLK ADGLPLLRCCLRSLGGYVLSUHDVRFHHPPIERQLNGTY GKAHGGPAELGEFYSRDPDGLPCNLRKPCNRPSGLEPOPG LRDAMMYDVRQTHKLEGGALGGAIISQAPQUEKLIATTA PWYHSSLTREBAERKLYSGAQTDGKFFLLRPRKSGGTYALS KTYYHYLISODKAGKYCIPEGYKFDUJEVIKLKLADG LKEACPNSSASNASGAAPTLPAHPSTLTHEQRRIDTINS PEPARI TSDDKRRMWGNITSVTESTYSDPEELDKKLIFLK LIADIELGCGNFGSVRGGYYRMKKRQLDVAIKVLKGGTEK EMMRRAQIMHGLDNPYIVLIIGVCQAEALMLVWRMGGGFP LVCKREET PVSNVAELHHOVSMMKKRQLDVAIKVLKGGTEK EMMRRAQIMHGLDNPYIVLIIGVCQAEALMLVWRMGGGFP LVCKREET PVSNVAELHHOVSMORKGLDKALLKKAPGE KRYSSRSDVMSYGYTMMEALSYGQXYKKKRGLDKALLKKAPGE KRYSSRSDVMSYGYTMMEALSYGQXYKKKRGLDKALLKKAPG SKVEGPPGSTGKARAACA TGYHKAGDLAHVSCHYKFEINANGLNPTLAVERDSCAPATL MLSESSSPLKGVMLGSIFCALITMLGHIRIGHGNRMHHE QAPNKEDILKISEDERMELSKSFRYCGLILVKRDVSLMA TMYKHGUKAFFFSSENVKYFESINDDTDMMILMMRKNYKY YRDQYNWFFLARPTTFAIIENLXYFLLKKDPSOPFYLGHT DLEYVGMEGGIVLSVESMKRLINSLINIPEKCPPGCGMIKK KQLAVCLKYAGVFARNAEDADGKDVPNTKSVGLSIKRANT DLEYVGMEGGIVLSVESMKRLINSLINIPEKCPPGCGMIKK KQLAVCLKYAGVFARNAEDADGKDVPNTKSVGLSILERAMT	,			
Appossible nucleotide insertion				
EPGGEKRACCISL  SIRLCPWGTHLAGPTTMRLSSLLALLRPALPLILGISIGG LRVSWIGGEGEDPCVEAVGERGGPQNPDSRARLDQSDEDF VPYYRDPKPYKKVLRTRYIGTBLGSRERILVAVAUTSRAT AVAVANTVAHIPPLLYPTGORGABAPGMOVSHGDER, SETLRHLHTHPGADYDWFFIMQDDTYVQAPRLAALAGHLS LYLGRAEFFIGAGGARYCHGGFGYLLSRSELLRAPHLD DIISARAPDEWIGRCILDSLGVGCVSQHGGQQYRSFELAKN KBGSSAPLSARAVHPVSEGTIMYRLHKKFSALBLERAYSE QAQIRNLTVLTPEGEAGLSWPVGLPAPFPHSRFEVLGWD QHTFSCADGARKCHLGSASRADVGALETALEQLNRRYQP QKQRLLNGYRFPDRAGMSYTLDLLLSCTYGOCHRRALLAR LRPLSRYSLIDMPYVTDATRYQLVLYLLVABAAAAPAFLE NVLEPREHALLTLLLVYGPREGGGADPDPLGWXAAAABL PGTRLAMLAVRAEAPSQVRLMDVVSKKHYDVTLFFLTTVW PPEVLNRCRMAISGWQAFFPVHFGFFNPALSPORSPFGPP DPPSPPGADPSRGAPTIGRFFDRQASAEGCFYNADYLAARA ELAGGEEBEALEGLEWDWVFLKFSGLYOFT CSPRLSEELYHRCRLSNLEGLGGRAQLAMALFEQEQANST GHDVURPVONSGPGAMPTVALRAAAGAFTISSFLALGPETFQV GKAHCGPABLCFFYSRDPDQLPCMLECTRISGELEPGPY GKAHCGPABLCFFYSRDPDQLPCMLECTRISGELEPGPY GKAHCGPABLCFFYSRDPDQLPCMLECTRISGELEPGPY GKAHCGPABLCFFYSRDPDQLPCMLECTRISGELEPGPY GKAHCGPABLCFFYSRDPDQLPCMLECTRISGELEPGPY GKAHCGPABLCFFYSRDPDQLPCMLECTRISGELEPGPY GKAHCGPABLCFFYSRDPDQLPCMLECTRISGELEPGPY GKAHCGPABLCFFYSRDPDQLPCMLECTRISGETTLAGFTEFOL LRDAWWRDYWRQTWKLEGGALEQAIISQAPQUEKLIATTA PMYHSSLTREEBERKLYSGAQTDGKFFLLWFRKGGTYALS KTYMYTLISGDKAKKVI PEGYKFDTLWOLUEVIKKKADG LKRACPNSSASNASGAAPTLPAHPSTLTHPQRRIDTINS PEPARITSPDKPRPMPDTSVYSSPYSDPEELKOKKKLFIKK EMPRRAQTMHGLDNPYIVELIGVCQAEALMLUVEMAGGGGP LUGKKEE IPVSNVAELHHQVSMMKYLESINFVHRLDLARR VNRHYAKISDFGLSKALGADDSYYTARSAGKWELKWADB RKYSSRSDVMSYGYTMWALSTGROPPTLTVSQRWRACY SKVEGPPGSTGKABAACA TGYHKGDELHGVSKAFFSSVRGYYKWRKQIDVTSVRGVPRARAY YRCDYNWFFLARADAGGLVRSVTRENGFRPPTTVSQRWRACY SKVEGPPGSTGKABAACA TGYHKABADAGGLURSSTBRCANVRGNPCAAALSCPQAUL MLSESSSPLKGVMLGSIFCALITMLGHIRIGHGNRMHHEH QAPNKEDILKSEDSRWELSKSFRWYCILLVKRDVSDGFFLIGH TMYKGUGEGVULSVESMKKLINSLINITEKCPDSCHGMIK MCCPPECCPPELYALMSDCMIYKWESTBLKGDFGOGMIKK KGLAVCLKYRGVPRAENAEDABGCDVPNTKSVGLSIKRANT THYKGUGKAFFSSENKYKVFESINDDTDMMLMMRXAYKY YRDQYNWFFLARPTTFAIIENLXYFLLKKOPSGOFFLIGHT DLEYVGMEGGIVLSVESMKRLINSLINITEKCPGGMIKK KGLAVCLKYRGVPRINERDABGCDVPNTKSVGLSIKRANT		amino acid	sequence	
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LRVSWICGEGEDPCVEAVGERGGPQNPDSRARLDQSDEDF VPYYRDPKKYLRTRYIQTBLGSRERLIVAVUTSRAT AVAVNTVHAHFPERLLYFTGGRGARAPAGMQVVSHGDER, SETLRHLHTHFGADYDWFFIMQDDTYVQARRLAALAGHLS, LYLGRAEFFIGAGGARYCHGGFGYLLSRSLLLRLRPHLD DILSARPDEWLGRCLIDSLGVGCVSOMCGGQYRSFELAKN KBGSSAFLSAFAVHPVSBGTLMYRLHKRFSALELERAYSE QAQIRNLTVLTPEGEAGLSWPVGLPAPFTPHSRFEVLGWD QHTFSCADGAPKCPLQGASRADVGDALETALEQLMRRYQP QKQRLLNGYRRFDPARGMEYTLDLLLECVTORGHRRALAR LRPLSRVEILPMPYUTEATRVQLPLDLWABAAAPAFLE PGTRLAWLAVRAEAPSQVTLMDVVSKCHPUTLFFLTTVW PEVLINKCRMANISGMOAFFPVHPOTLFFLTTVW PEVLINKCRMANISGMOAFFPVHPALSPORSFPGPP DPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAARA ELAGGEEEEALEGLEVMUVFLRFSGHLHFRAVEPGLVGKF CSPRLSEELYHRKCISNLEGLGGRQLAMALFEGEGANST GAHPVNPQVONGGPGAMPDDPAAHLPFFYGSILALFPAEPGLVGKY GKAHCGPAELCFYSRDPGLPCNLRRPCRRSGELEPOPG GRAHCGPAELCFYSRDPGLPCNLRRPCRRSGELEPOPG GRAHCGPAELCFYSRDPGLPCNLRRPCRRSGELEPOPG GRAHCGPAELCFYSRDPGLPCNLRRPCRRSGELEPOPG GRAHCGPAELCFYSRDPGLPCNLRRPCRRSGELEPOPG GRAHCGPAELCFYSRDPGLPCNLRRPCRRSGELEPOPG LRDAMVRDYVRQTWKLEGEALEQAIJSQAPOVEKLIATTA PWYHSSLTREEEERKLYSGAQTDCKFLLRRREKGQTYALS KTYYHYLISODKAGKYCIPEGTKFDTLWOLVEYLKLKADG GLKREGPNSSANSAGAAPTLPAPATSTTHPQRRIDTINS PEPARITSPDKPRPMPDTSVYESPYSDPEELKDKKLFLK LIADIELGGGNFGSVRGCVYRMRKKQIDVIKVLKGGTIEK MEGCPPSCPPELVALMSDCWIYKMRKQIDVIKVLKGGTIEK MEGCPPSCPPELVALMSDCWIYKMKKGTUKMAGGGP LVGKREEIPVSNVAELLHQVSMGMKYLEEKNFVHRDLAAR VNRHYAKISDFGLSKALGADDSYYTARSAGKKQLKWYABE RKFSSSDWSSGYTMMEALSYGKYKMKGETWAFIE MECPPSCPPELVALMSDCWIYKMCGPTCAAALSCPQAVL MLSESSPLKGVMLGSIFCALITHLGHIRTGHGNRHHHE MECPPSCPPELVALMSDCWIYKMCGPTCAAALSCPQAVL MLSESSSPLKGVMLGSIFCALITHLGHIRTGHGNRHHHE QAPNKEDILKISEDERMELSKSFRVYCILIVKPKDVSLMA TWYKHCDKAEFFSSSNVKVFESIMMDTNDMWLMMRKAYKY YRDQYNWFFLARPTTFALIENLKYFLLKKDPSOPFYLGHT DLEYVGMEGGIVLSVESNKRINGLINTPEKCPROGGMIKK KQLAVCLKYAGVYAENAEDADAGKDVPNTKSVGLSIKEAMT	C400	3636	272	ST.DT.CDWGTHI.AGDTTMPI.SSLI.ALI.PDALDI.ILGI.SIGCSI.SI.
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MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHE QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWA. TWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKY. YRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHT DLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWK KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMT				
QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWA. TWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKY. YRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHT DLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWK KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMT	6500	1773	726	
TWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKY. YRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHT DLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWK KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMT				MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHL
TWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKY. YRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHT DLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWK KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMT				QAPNKEDILKISEDERMELSKSFRVYCIILVKPKDVSLWAAVKE
YRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHT DLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWK KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMT				TWTKHCDKAEFFSSENVKVFESINMDTNDMWLMMRKAYKYAFDK
DLEYVGMEGGIVLSVESMKRLNSLLNIPEKCPEQGGMIWK KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMT				1
KQLAVCLKYAGVFAENAEDADGKDVFNTKSVGLSIKEAMT				
QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ				
			1	QVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGPYFQ
6501 1 570 LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIK	65'01	1	570	LVGMSGGGTETPVGCEAAPGGGSKKRDSLGTAGSAHLIIKDLGE
				IHSRLLDHRPVIQGETRYFVKEFEEKRGLREMRVLENLKNMIHE
		1		TNEHTLPKCRDTMRDSLSQVLQRLQAANDSVCRLQQREQERKKI
				HSDHLVASEKQHMLQWDNFMKEQPNKRAEVDEEHRKAMERLKEQ
		1	1	1
YAEMEKDLAKFSTF			<u> </u>	
	6502	213	1650	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE
KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLA				KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS
		1		SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
			i	AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLBEK
			1	
				KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ
	1			EQARRDALKQRAEQSISEEPGWEEEEEBLMGISPISPKEAKVPV
				AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETG				QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
l	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
<u> </u>	l .	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	residue of	1	
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
{	•		IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
			KSTPSNNGKKGSSTDISEDWEKDFDLDMTEEEVQMALSKVDASG
			EVSGPGGSEGSEPNGPGCESSPQPAQLSPQEGPCSCLR
6503	213	1650	AGNKPDPWAGRNRTAVLPDVSVFHREDVGWWRSWLQQSYQAVKE
			KSSEALEFMKRDLTEFTQVVQHDTACTIAATASVVKEKLATEGS
İ			SGATEKMKKGLSDFLGVISDTFAPSPDKTIDCDVITLMGTPSGT
			AEPYDGTKARLYSLQSDPATYCNEPDGPPELFDAWLSQFCLEEK
i			KGEISELLVGSPSIRALYTKMVPAAVSHSEFWHRYFYKVHQLEQ
	1		EQARRDALKQRAEQSISEEPGWEEEEEELMGISPISPKEAKVPV
			AKISTFPEGEPGPQSPCEENLVTSVEPPAEVTPSESSESISLVT
			QIANPATAPEARVLPKDLSQKLLEASLEEQGLAVDVGETGPSPP
1			IHSKPLTPAGHTGGPEPRPPARVETLREEAPTDLRVFELNSDSG
[			KSTPSNNGKKGSSTDISEDWEKDFDLDMTBEEVOMALSKVDASG
}			EVSGPGGSEGSEPNGPGCESSPQPAQLSPQEGPCSCLR
6504	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG
""	****	1237	SANMTKKKVSOKKORGRPSSOPCRNIVGCRISHGWKEGDEPITO
		İ	WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
		ļ	
			DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA
			PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
			REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
			DDDFHIYVYDLVKKS
6505	2131	1294	GKVCLVAHWVCLSILSPPPAGMKTPNAQEAEGQQTRAAAGRATG
j			SANMTKKKVSQKKQRGRPSSQPCRNIVGCRISHGWKEGDEPITQ
l		İ	WKGTVLDQVPINPSLYLVKYDGIDCVYGLELHRDERVLSLKILS
İ			DRVASSHISDANLANTIIGKAVEHMFEGEHGSKDEWRGMVLAQA
			PIMKAWFYITYEKDPVLYMYQLLDDYKEGDLRIMPESSESPPTE
		İ	REPGGVVDGLIGKHVEYTKEDGSKRIGMVIHQVEAKPSVYFIKF
			DDDFHIYVYDLVKKS
6506	1	1350	EVSPPTSCCLTVAVADPGVSEGFRGFGAGCEMPGRGRCPDCGST
ĺ		ļ	ELVEDSHYSQSQLVCSDCGCVVTEGVLTTTFSDEGNLREVTYSR
ŀ			STGENEQVSRSQQRGLRRVRDLCRVLQLPPTFEDTAVAYYQQAY
			RHSGIRAARLQKKEVLVGCCVLITCRQHNWPLTMGAICTLLYAD
ļ			LDVFSSTYMQIVKLLGLDVPSLCLAELVKTYCSSFKLFQASPSV
1			PAKYVEDKEKMLSRTMQLVELANETWLVTGRHPLPVITAATFLA
[			WQSLQPADRLSCSLARFCKLANVDLPYPASSRLQELLAVLLRMA
	1	Ì	EQLAWLRVLRLDKRSVVKHIGDLLQHRQSLVRSAFRDGTAEVET
1		1	REKEPPGWGQGQGEGEVGNNSLGLPQGKRPASPALLLPPCMLKS
		[	PKRICPVPPVSTVTGDENISDSEIEQYLRTPQEVRDFQRAQAAR
1			QAATSVPNPP
6507	1878	929	RSHASRLPELPSGCLVLQVQELVQMSGMEATVTIPIWONKPHGA
		1	ARSVVRRIGTNLPLKPCARASFETLPNISDLCLRDVPPVPTLAD
1		[	IAWIAADEEETYARVRSDTRPLRHTWKPSPLIVMQRNASVPNLR
			GSEERLLALKKPALPALSRTTELQDELSHLRSQIAKIVAADAAS
			ASLTPDFLSPGSSNVSSPLPCFGSSFHSTTSFVISDITEETEVE
ļ		1	VPELPSVPLLCSASPECCKPEHKAACSSSEEDDCVSLSKASSFA
ļ			DMMGILKDFHRMKQSQDLNRSLLKEEDPAVLISEVLRRKFALKE
			EDISRKGN
6508	862	342	WEARKRPORWPSERREVRVPPPHLORGRSGLEPGTFRKMAAARP
5508	002	342	_
1		İ	SLGRVLPGSSVLFLCDMQEKFRHNIAYFPQIVSVAARMLKNTTL
1		1	DLLDRGLQVHVVVDACSSRSQVDRLVALARMRQSGAFLSTSEGL
2500		ļ	ILQLVGDAVHPQFKEIQKLIKEPAPDSGLLGLFQGQNSLLH
6509	2	1053	FVWNPRGGRKRRQAAVTQAATRASGTPSPRDGTMTQGKLSVAN
1	1		KAPGTEGQQQVHGEKKEAPAVPSAPPSYBEATSGEGMKAGAFPP
!		!	APTAVPLHPSWAYVDPSSSSSYDNGFPTGDHELFTTFSWDDQKV
			RRVFVRKVYTILLIQLLVTLAVVALFTFCDPVKDYVQANPGWYW
			ASYAVFFATYLTLACCSGPRRHFPWNLILLTVFTLSMAYLTGML
·	-t		

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NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
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Ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
1		sequence	\=possible nucleotide insertion)
	sequence		l .5
			SSYYNTTSVLLCLGITALVCLSVTVFSFQTKFDFTSCQGVLFVL
			LMTLFFSGLILAILLPFQYVPWLHAVYAALGAGVFTLFLALDTQ
L			LLMGNRRHSLSPEEYIFGALNIYLDIIYIFTFFLQLFGTNRE
6510	37	1156	PCALDGCPQRGAVHPLLSSAMGLLAFLKTQFVLHLLVGFVFVVS
1			GLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLVMLLEWW
			SCTECTLFTDQATVERFGKEHAVIILNHNFEIDFLCGWTMCERF
i		1	GVLGSSKVLAKKELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVV
			EGLRRLSDYPEYMWFLLYCEGTRFTETKHRVSMEVAAAKGLPVL
		İ	KYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGIL
i			YGKKYEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIY
		1	NQKGMFPGEQFKPARRPWTLLNFLSWATILLSPLFSFVLGVFAS
			GSPLLILTFLGFVGAGNGHCR
6511	2541	1425	GEEQPLAAAPTECLEQVIGGAGDPGTWASFPSPLPGPAPLKGGK
			TMATNFSDIVKQGYVKMKSRKLGIYRRCWLVFRKSSSKGPQRLE
	1		KYPDEKSVCLRGCPKVTEISNVKCVTRLPKETKRQAVAIIFTDD
			SARTFTCDSELEAEEWYKTLSVECLGSRLNDISLGEPDLLAPGV
			QCEQTDRFNVFLLPCPNLDVYGECKLQITHENIYLWDIHNPRVK
ļ			LVSWPLCSLRRYGRDATRFTFRAGRMCDAGEGLYTFQTQEGEQI
•			YQRVHSATLAIAEQHKRVLLEMEKNVRLLNKGTEHYSYPCTPTT
ł			MLPRSAYWHHITGSONIAEASSYAGEGYGAAQASSETDLLNRFI
			LLKPKPSQGDSSEAKTPSQ
6512	159	807	FGKKSTWFPLSRSLRVASGRSCKLGHGGYTGSGPGFGEPRDSGA
		1	EVPSGSGRATGCERGGVRGARQGRAPGSSIWRKEPRMVCTRKTK
			TLVSTCVILSGMTNIICLLYVGWVTNYIASVYVRGOEPAPDKKL
			EEDKGDTLKIIERLDHLENVIKQHIQEAPAKPEEAEAEPFTDSS
			LFAHWGQELSPEGRRVALKQFQYYGYNAYLSDRLPLDRP
6513	2	756	FVSPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTA
0323	1	, , , ,	LFPDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQV
			AAPYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQ
			GVPLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPV
			LOODAHSSVTITPORSPTGAVEVQVPEDPVVALVGTDATLRCSF
1			SPEPGFSLAQLNLIWQLTDTKQLVHSFAEGQDQGSAYANRTALF
			PDLLAQGNASLRLQRVRVADEGSFTCFVSIRDFGSAAVSLQVAA
			PYSKPSMTLEPNKDLRPGDTVTITCSSYQGYPEAEVFWQDGQGV
l .			PLTGNVTTSQMANEQGLFDVHSILRVVLGANGTYSCLVRNPVLQ
1			ODAHSSVTITPORSPTGAVEVOVPEDPVVALVGTDATLRCSFSP
			EPGFSLAQLNLIWQLTDTRQLVHSFTEGR
6514	985	302	VGIPGPTISSAAEMEDLLDLDEELRYSLATSRAKMGRRAOOESA
0.31.4	300	302	QAENHLINGKNSSLTLTGETSSAKLPRCRQGGWAGDSVKASKFRR
	1		KASEBIEDFRLRPQSLNGSDYGGDIPIIPDLEEVQEEDFVLQVA
			APPSIOIKRVMTYRDLDNDLMKYSAIOTLDGEIDLKLLTKVLAP
1	1		. EHEVRERNPSWODDVGWDWDHLFTEVSSEVLTEWDPLOTEKEDP
		1	1
75	12.2	305	AGOARHT
6515	1345	305	GRVGSRRGAAVPGGCGAGSTQLEVSASASCGALGSADMNPIVV
			VHGGGAGPISKDRKERVHQGMVRAATVGYGILREGGSAVDAVEG
			AVVALEDDPEFNAGCGSVLNTNGEVEMDASIMDGKDLSAGAVSA
			VQCIANPI KLARLVMEKTPHCFLTDQGAAQFAAAMGVPEIPGEK
			LVTERNKKRLEKEKHEKGAQKTDCQKNLGTVGAVALDCKGNVAY
			ATSTGGIVNKMVGRVGDSPCLGAGGYADNDIGAVSTTGHGESIL
1		<u> </u>	KVNLARLTLFHIEQGKTVBEAADLSLGYMKSRVKGLGGLIVVSK
			TGDWVAKWTSTSMPWAAAKDGKLHFGIDPDDTTITDLP
6516	1	1402	FRRLRYLGQDATAAARDLRTRGLQGYCPSATARQQVLVSALQQL
1			KGRRSEHRNENQEMPYSTNKELILGIMVGTAGISLLLLWYHKVR
1			KPGIAMKLPEFLSLGNTFNSITLQDEIHDDQGTTVIFQERQLQI
			LEKLNELLTNMEELKEEIRFLKEAIPKLEEYIQDELGGKITVHK
1	1		ISPOHRARKRRLPTIQSSATSNSSEEAESEGGYITANTDTEEQS
			·

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ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
i	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ı	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			FPVPKAFNTRVEELNLDVLLQKVDHLRMSESGKSESFELLRDHK
			EKFRDEIEFMWRFARAYGDMYELSTNTQEKKHYANIGKTLSERA
			INRAPMNGHCHLWYAVLCGYVSEFEGLQNKINYGHLFKEHLDIA
ŀ	ļ		IKLLPEEPFLYYLKGRYCYTVSKLSWIEKKMAATLFGKIPSSTV
1	İ		QEALHNFLKAEELCPGYSNPNYMYLAKCYTDLEENQNALKFCNL
CE 3.5			ALLLPTVTKEDKEAQKEMQKIMTSLKR
6517	3	1414	GRVWGGSSSLNAMVYVRGHAEDYERWQRQGARGWDYAHCLPYFR
ĺ			KAQGHELGASRYRGADGPLRVSRGKTNHPLHCAFLEATQQAGYP
i			LTEDMNGFQQEGFGWMDMTIHEGKRWSAACAYLHPALSRTNLKA
]			EAETLVSRVLFEGTRAVGVEYVKNGQSHRAYASKEVILSGGAIN
ŀ			SPQLLMLSGIGNADDLKKLGIPVVCHLPGVGQNLQDHLEIYIQQ
	1		ACTRPITLHSAQKPLRKVCIGLEWLWKFTGEGATAHLETGGFIR
			SQPGVPHPDIQFHFLPSQVIDHGRVPTQQEAYQVHVGPMRGTSV
1			GWLKLRSANPQDHPVIQPNYLSTETDIEDFRLCVKLTREIFAQE ALAPFRGKELQPGSHIQSDKEIDAFVRAKADSAYHPSCTCKMGQ
			PSDPTAVVDPQTRVLGVENLRVVDASIMPSMVSGNLNAPTIMIA
			EKAADIIKGQPALWDKDVPVYKPRTLATQR
6518	242	1098	PAWNPGSBPRTRVRPRARSFPLPPPRAPRRRHRLLRAVPGPSR
1			RHRCRRRAPPPPSTMGDAGSBRSKAPSLPPRCPCGFWGSSKTMN
1			LCSKCFADFQKKQPDDDSAPSTSNSQSDLFSEETTSDNNNTSIT
			TPTLSPSQQPLPTELNVTSPSKEECGPCTDTAHVSLITPTKRSC
1			GTDSQSENEASPVKRPRLLENTERSEETSRSKQKSRRRCFOCOT
			KLELVQQELGSCRCGYVFCMLHRLPEQHDCTFDHMGRGREEAIM
			KMVKLDRKVGRSCQRIGEGCS
6519	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPFGKLQLSSRDPPGSLS
1	ĺ		AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS
			WSFAPLSAAPSPSSSRSSFSFSAGTAVPSSASASLSQPGPRKLL
			VPPTLLHAQPHHLLLPAAAAASANAKSRRPKEKREKERRRHGL
			GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK
			VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKKKK
			ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG KNLDTKNYDSKIPENSBFPFVSLKEPRVQNNLKRLDTLBFKQLI
			HIEHQPNGGASVIHCLO
6520	3	1113	ERKMAEPPSPVHCVAAAAPTATVSEKEPPGKLQLSSRDPPGSLS
			AKKVRTEEKKAPRRVNGEGGSGGNSRQLQPPAAPSPQSYGSPAS
			WSFAPLSAAPSPSSRSSFSFSAGTAVPSSASASLSQPGPRKLL
			VPPTLLHAQPHHLLLPAAAAAASANAKSRRPKEKREKERRRHGL
			GGAREAGGASREENGEVKPLPRDKIKDKIKERDKEKEREKKKHK
			VMNEIKKENGEVKILLKSGKEKPKTNIEDLQIKKVKKKKKKKKHK
[		ĺ	ENEKRKRPKMYSKSIQTICSGLLTDVEDQAAKGILNDNIKDYVG
]		i	KNLDTKNYDSKIPENSEFPFVSLKEPRVQNNLKRLDTLEFKQLI
·			HIEHQPNGGASVIHCLQ
6521	. 184	1798	KLFKMATDTSQGELVHPKALPLIVGAQLIHADKLGEKVEDSTMP
			IRRTVNSTRETPPKSKLAEGEEEKPEPDISSEESVSTVEEQENE
			TPPATSSEAEQPKGEPENBEKEENKSSEETKKDEKDQSKEKEKK
			VKKTIPSWATLSASQLARAQKQTPMASSPRPKMDAILTEAIKAC
			FQKSGASVVAIRKYIIHKYPSLELERRGYLLKQALKRELNRGVI
			KQVKGKGASGSFVVVQKSRKTPQKSRNRKNRSSAVDPEPQVKLE
			DVLPLAFTRLCEPKEASYSLIRKYVSQYYPKLRVDIRPQLLKNA
			LQRAVERGQLEQITGKGASGTFQLKKSGEKPLLGGSLMEYAILS
] ]			AIAAMNEPKTCSTTALKKYVLENHPGTNSNYQMHLLKKTLQKCE KNGWMEQISGKGFSGTFQLCFPYYPSPGVLFPKKEPDDSRDEDE
			DEDESSEEDSEDEEPPPKRRLQKKTPAKSPGKAASVKQRGSKPA
		1	PKVSAAQRGKARPLPKKAPPKAKTPAKKTRPSSTVIKKPSGGSS
			KKPATSARKE
6522	1042	391	NKWLRPSPRSHRTPESGRVLSLFRLPPPGMALSGSTPAPCWEED
	···	<del></del>	NO. 1 O. I MOOD TAY CHEED

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ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
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	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
]	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	Bequence	\=possible nucleotide insertion)
	sequence		ECLDYYGMLSLHRMFEVVGGQLTECELELLAFLLDEAPGAAGGL
l 1			SRARSGLKLLELERRGOCDESNLRLLGOLLRVLARHDLLPHLA
!			RKRRRPVSPERYSYGTSSSSKRTEGSCRRRQSSSSANSQQGSP
İ			PTKRQRRSRGRPSGGARRRRGPQPHPSSSQSPPDLPLKAK
6523		1097	ASCOTRRTAALDSGERIAGRRSPIALAMASNFNDIVKOGYVKI
6523	2	1097	RSRKLGIFRRCWLVFKKASSKGPRRLBKFPDEKAAYFRNFHKVT
[ [			ELHNIKNITTLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
			KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
1			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
			· · · · · · · · · · · · · · · · · · ·
			WFTFESGRMCDTGEGLFTFQTREGEMIYQKVHSATLAIAEQHER
[ :	1	1	LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
			IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF
			MDTSTCKVVHDLE
6524	2	1097	ASCQTRRRTAALDSGERIAGRRSPIALAMASNFNDIVKQGYVKI
			RSRKLGIFRRCWLVFKKASSKGPRRLEKFPDEKAAYFRNFHKVT
	<b>!</b>	!	ELHNIKNITRLPRETKKHAVAIIFHDETSKTFACESELEAEEWC
		}	KHLCMECLGTRLNDISLGEPDLLAAGVQREQNERFNVYLMPTPN
ì			LDIYGECTMQITHENIYLWDIHNAKVKLVMWPLSSLRRYGRDST
1		1	wftfesgrmcdtgeglftfqtregemiyQkvhsatlaiaeQher
			LMLEMEQKARLQTSLTEPMTLSKSISLPRSAYWHHITRQNSVGE
1			IYSLQGNHENRHSDLTGKSCKTSENRFLEENAPLVMYGITHHLF
			MDTSTCKVVHDLE
6525	1	1859	GESPFSERESIEFNPSSSGRSARTVSSNSFCSDDTGWPSSQSVS
1			PVKTPSDAGNSPIGFCPGSDEGFTRKKCTIGMVGEGSIQSSRYK
	1		KESKSGLVKPGSEADFSSSSSTGSISAPEVHMSTAGSKRSSSSR
	1		NRGPHGRSNGASSHKPGSSPSSPREKDLLSMLCRNQLSPVNIHP
1	Ì		SYAPSSPSSSNSGSYKGSDCSPIMRRSGRYMSCGENHGVRPPNP
į i	ì		EQYLTPLQQKEVTVRHLKTKLKESERRLHERESEIVELKSQLAR
			MREDWIEEECHRVEAQLALKEARKEIKQLKQVIETMRSSLADKD
			KGIQKYFVDINIQNKKLESLLQSMEMAHSGSLRDELCLDFPCDS
			PEKSLTLNPPLDTMADGLSLEEQVTGEGADRELLVGDSIANSTD
	1 '		LFDEIVTATTTESGDLELVHSTPGANVLELLPIVMGQEEGSVVV
1		1	ERAVQTDVVPYSPAISELIQSVLQKLQDPCPSSLASPDESEPDS
	1		MESFPESLSALVVDLTPRNPNSAILLSPVETPYANVDAEVHANR
1			LMRELDFAACVEERLDGVIPLARGGVVRQYWSSSFLVDLLAVAA
)			PVVPTVLWAFSTQRGGTDPVYNIGALLRGCCVVALHSLRRTAFR
			IKT
6526	2	2034	SGRAGEPEEWRGRQIIDSKETWIPFNSEDSQQLEEAYSSGKGCN
			GRVVPTDGGRYDVHLGERMRYAVYWDELASEVRRCTWFYKGDKD
			NKYVPYSESFSQVLEETYMLAVTLDEWKKKLESPNREIIILHNP
			KLMVHYQPVAGSDDWGSTPMEQGRPRTVKRGVENISVDIHCGEP
			LQIDHLVFVVHGIGPACDLRFRSIVQCVNDFRSVSLNLLQTHFK
	1		KAQENQQIGRVEFLPVNWHSPLHSTGVDVDLQRITLPSINRLRH
	1		
		}	FINDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK
1 .			FINDTILDVFFYNSPTYCQTIVDTVASEMNRIYTLFLQRNPDFK GGVSIAGHSLGSLILFDILTNQKDSLGDIDSBKGSLNIVMDQGD
			1
			GGVSIAGHSLGSLILFDILTNQKDSLGDIDSEKGSLNIVMDQGD
·			GGVSIAGHSLGSLILFDILTNOKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP
			GGVSIAGHSLGSLILFDILTNOKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN
			GGVSIAGHSLGSLILFDILTNOKDSLGDIDSEKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQEIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL
			GGVSIAGHSLGSLILFDILTNQKDSLGDIDSBKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQBIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY
			GGVSIAGHSLGSLILFDILTNOKDSLGDIDSBKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQBIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLBLREGLTRNSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV
			GGVSIAGHSLGSLILFDILTNOKDSLGDIDSBKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQBIGIP LGPRKKILNYFSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLBLREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV
6527		922	GGVSIAGHSLGSLILFDILTNOKDSLGDIDSBKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQBIGIP LGPRKKILNYPSTRKNSMGIKRPAPQPASGANIPKESEFGSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ
6527	1	922	GGVSIAGHSLGSLILFDILTNOKDSLGDIDSBKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQBIGIP LGPRKKILNYPSTRKNSMGIKRPAPQPASGANIPKESEFCSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ GWVPLLSRILPSDACKIYKQGINIRLDTTLIDFTDMKCQRGDLS
6527	1	922	GGVSIAGHSLGSLILFDILTNOKDSLGDIDSBKGSLNIVMDQGD TPTLEEDLKKLQLSEFFDIFEKEKVDKEALALCTDRDLQBIGIP LGPRKKILNYPSTRKNSMGIKRPAPQPASGANIPKESEFGSSSN TRNGDYLDVGIGQVSVKYPRLIYKPEIFFAFGSPIGMFLTVRGL KRIDPNYRFPTCKGFFNIYHPFDPVAYRIEPMVVPGVEFEPMLI PHHKGRKRMHLELREGLTRMSMDLKNNLLGSLRMAWKSFTRAPY PALQASETPEETEAEPESTSEKPSDVNTEETSVAVKEEVLPINV GMLNGGQRIDYVLQEKPIESFNEYLFALQSHLCYWESEDTVLLV LKEIYQTQGIFLDQPLQ

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ĺ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
			LVLESRKRREHLSEEDILRNKAIMESLSKGGNIMEQNFEPIRRQ
j			SLTPPPQNTITWEEYISAENGKAPHLGRELVCKESKKTFKATIA
1			MSQEFPLGIELLLNVLEVVAPFKHFNKLREFVQMKLPPGFPVKL
}			DIPVFPTITATVTFQEFRYDEFDGSIFTIPDDYKEDPSRFPDL
6528	1	1073	LTGPAAAEPRCAADAGMKRALGRRKGVWLRLRKILFCVLGLYIA
			IPFLIKLCPGIQAKLIFLNFVRVPYFIDLKKPQDQGLNHTCNYY
1			LQPEEDVTIGVWHTVPAVWWKNAQGKDQMWYEDALASSHPIILY
1			LHGNAGTRGGDHRVELYKVLSSLGYHVVTFDYRGWGDSVGTPSE
l			RGMTYDALHVFDWIKARSGDNPVYIWGHSLGTGVATNLVRRLCE
			RETPPDALILESPFTNIREEAKSHPFSVIYRYFPGFDWFFLDPI
l		i	TSSGIKFANDENVKHISCPLLILHAEDDPVVPFQLGRKLYSIAA
1			PARSFRDFKVQFVPFHSDLGYRHKYIYKSPELPRILREFLGKSE
1			РЕНОН
6529	363	2215	THIRYNKIGVVKTMSCGNEFVETLKKIGYPKADNLNGEDFDWLF
			EGVEDESFLKWFCGNVNEQNVLSERELEAFSILQKSGKPILEGA
			ALDEALKTCKTSDLKTPRLDDKELEKLEDEVQTLLKLKNLKIQR
	1	-	RNKCOLMASVTSHKSLRLNAKEEEATKKLKQSQGILNAMITKIS
			NELQALTDEVTQLMMFFRHSNLGQGTNPLVFLSQFSLEKYLSQE
			EOSTAALTLYTKKOFFOGIHEVVESSNESOFFNFLKIOTPSICD
			NOEILEERRLEMARLOLAYICAOHOLIHLKASNSSMKSSIKWAE
			ESLHSLTSKAVDKENLDAKISSLTSEIMKLEKEVTQIKDRSLPA
			VVRENAOLLNMPVVKGDFDLQIAKQDYYTARQELVLNQLIKQKA
			SFELLOLSYEIELRKHRDIYRQLENLVQELSQSNMMLYKQLEML
			TDPSVSQQINPRNTIDTKDYSTHRLYQVLEGENKKKELFLTHGN
			LEEVAEKLKONISLVODOLAVSAQEHSFFLSKRNKDVDMLCDTL
Ī			YOGGNOLLLSDQELTEOPHKVESQLNKLNHLLTDILADVKTKRK
			TLANNKLHOMEREFYVYFLKDEDYLKDIVENLETOSKIKAVSLE
1			D
6530	128	2986	GAAHHGAIVQVHPLLPGSSTIMIHDLCLVFPAPAKAVVYVSDIQ
6530	120	2,500	ELYIRVVDKVEIGKTVKAYVRVLDLHKKPFLAKYFPFMDLKLRA
	.		ASPIITLVALDEALDNYTITFLIRGVAIGOTSLTASVTNKAGOR
			INSAPQQIEVFPPFRLMPRKVTLLIGATMQVTSEGGPQPQSNIL
			FSISNESVALVSAAGLVQGLAIGNGTVSGLVQAVDAETGKVVII
ļ			SQDLVQVEVLLLRAVRIRAPIMRMRTGTQMPIYVTGITNHQNPF
	[		SFGNAVPGLTFHWSVTKRDVLDLRGRHHEASIRLPSQYNFAMNV
l .			LGRVKGRTGLRAVVKAVDPTSGQLYGLARELSDEIQVQVFEKLQ
			LLNPEIEAEQILMSPNSYIKLQTNRDGAASLSYRVLDGPEKVPV
ļ .	1		VHVDEKGFLASGSMIGTSTIEVIAQEPFGANQTIIVAVKVSPVS
	i		YLRVSMSPVLHTQNKEALVAVPLGMTVTFTVHFHDNSGDVFHAH
			SSVLNFATNRDDFVQIGKGPTNNTCVVRTVSVGLTLLRVWDAKH
	1		PGLSDFMPLPVLQAISPELSGAMVVGDVLCLATVLTSLEGLSGT
1	1		WSSSANSILHIDPKTGVAVARAVGSVTVYYEVAGHLRTYKEVVV
			SVPQRIMARHLHPIQTSFQBATASKVIVAVGDRSSNLRGECTPT
			QREVIQALHPETLISCQSQFKPAVFDFPSQDVFTVEPQFDTALG
			QYFCSITMHRLTDKQRKHLSMKKTALVVSASLSSSHFSTEQVGA
1			EVPFSPGLFADQAEILLSNHYTSSEIRVFGAPEVLENLEVKSGS
i	1		PAVLAFAKEKSFGWPSFITYTVGVLDPAAGSQGPLSTTLTFSSP
1			VTNQAIAIPVTVAFVVDRRGPGPYGASLFQHFLDSYQVMFFTLF
			ALLAGTAVMIIAYHTVCTPRDLAVPAALTPRASPGHSPHYFAAS
1	1		SPTSPNALPPARKASPPSGLWSPAYASH
6531	845	1425	PSASIPPSASPDPVPDIRTCHFCLVEDPSVGCISGSEKCTISSS
			SLCMVITIYYDVKVRFIVRGCGQYISYRCQEKRNTYFAEYWYQA
1			QCCQYDYCNSWSSPQLQSSLPEPHDRPLALPLSDSQIQWFYQAL
			NLSLPLPNFHAGTEPDGLDPMVTLSLNLGLSFAELRRMYLFLNS
			SGLLVLPQAGLLTPHPS
6532	2 -	954	AAGPPSEVVNQDSLFPEPEPGPAPQVLLGPQGPGLIKGVAPPTL
	1		. I I I I I I I I I I I I I I I I I I I

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ļ	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
l .	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid'	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			ITDSTGTHLVLTVTNKNAHSPGLSRGSPQQPSSQPGSPAPAPSA
	i		QMDLEHPLQPLFGTPTSLLKKEPPGYEEAMSQQPKQQENGSSSQ
		ļ	QMDDLFDILIQSGEISADFKEPPSLPGKEKPSPKTVCWSPLAAQ
İ			PSPSAELPQAAPPPPGSPSLPGRLEDFLESSTGLPLLTSGHDGP
			EPLSLIDDLHSQMLSSTAILDHPPSPMDTSELHFVPEPSSTMGL
1			DLADGHLDSMDWLELSSGGPVLSLAPLSTTAPSLFSTDFLDGHD
1		1	LQLHWDSCL
6533	1798	373	STISWLARVEPPRRSSGVGAARLRFPGGSRPLRARACVLALAVL
			ALLERNNADSMSAHSMLCERIAIAKELIKRAESLSRSRKGGIEG
			GAKLCSKLKAELKFLOKVEAGKVAIKESHLOSTNLTHLRAIVES
			AENLEEVVSVLHVFGYTDTLGEKQTLVVDVVANGGHTWVKAIGR
1			KAEALHNIWLGRGQYGDKSIIEQAEDFLQASHQQPVQYSNPHII
			FAFYNSVSSPMAEKLKEMGISVRGDIVAVNALLDHPEELQPSES
			ESDDEGPELLOVTRVDRENILASVAFPTEIKVDVCKRVNLDITT
1		[	LITYVSALSYGGCHFIFKEKVLTEQAEQERKEQVLPQLEAFMKD
			KELFACESAVKDFQSILDTLGGPGERERATVLIKRINVVPDQPS
			ERALRLVASSKINSRSLTIFGTGDTLKAITMTANSGFVRAANNO
1			GVKFSVFIHOPRALTESKEALATPLPKDYTTDSEH
6534	47	596	KATRFISAAFVVLNKQGVSPAKLPHTSWSWSLQTLSFLFSGDLA
6554	1	3,50	EKSLOCFPCSAMLLELIPLLGIHFVLRTARAQSVTQPDIHITVS
1	1		EGASLELRCNYSYGATPYLFWMERTVEEAFILLVCLKPWRVASS
		1	LEKKEKEDESFOLLLGSRYNVLKAHCLLPLIRWLTSGDSLLSAQ
1			PHCPOGL
6535	250	964	LIKTFFRDVAIORDLLPKEKNLETLLTLAFLEIDKAFSSHARLS
6535	2,50	) 334	ADATLLTSGTTATVALLRDGIELVVASVGDSRAILCRKGKPMKL
			TIDHTPERKDEKERIKKCGGFVAWNSLGQPHVNGRLAMTRSIGD
1			LDLKTSGVIAEPETKRIKLHHADDSFLVLTTDGINFMVNSQEIW
1			DFVNOCHDPNEAAHAVTEQAIQYGTEDNSTAVVVPFGAWGKYKN
Ĭ			SEINFSFSRSFASSGRWA
6536	242	1174	SLVKEMTNOYGILFKQEQAHDDAIWSVAWGTNKKENSETVVTGS
6536	242	11/3	LDDLVKVWKWRDERLDLQWSLEGHQLGVVSVDISHTLPIAASSS
			LDAHIRLWDLENGKQIKSIDAGPVDAWTLAFSPDSQYLATGTHV
ŀ			GKVNIFGVESGKKEYSLDTRGKFILSIAYSPDGKYLASGAIDGI
			INIFDIATGKLLHTLEGHAMPIRSLTFSPDSQLLVTASDDGYIK
1	1		IYDVOHANLAGTLSGHASWVLNVAFCPDDTHFVSSSSDKSVKVW
			DVGTRTCVHTFFDHQDQVWGVKYNGNGSKIVSVGDDQEIHIYDC
1		1	PI
6537	1638	921	NRFNPPPTQGPDPSLVYRPDVDPEVAKDKASFRNYTSGPLLDRV
6537	1038	321	FTTYKLMHTHOTVDFVRSKHAQFGGFSYKKMTVMEAVDLLDGLV
	1		DESDPDVDFPNSFHAFQTAEGIRKAHPDKDWFHLVGLLHDLGKV
i			LALFGEPOWAVVGDTFPVGCRPQASVVFCDSTFQDNPDLQDPRY
1	1		STELGMYQPHCGLDRVLMSWGHDGEARGGQWGGGGRWGTVGGGG
			•
L	<del> </del>		AEAVPAGDTLSPQSTCTR
6538	3345	2412	PYLYDFLDALITCOTAPEEAFIKLDGLAGMLTEQLRRLTKQVQE
ł	1		ARHNRDDEAIKKAVNEYDETMEKYIPVLMAQAKIYWNLENYPMV
1			EKIFRKSVEFCNDHDVWKLNVAHVLFMQENKYKEAIGFYEPIVK
1	1		KHYDNILNVSAIVLANLCVSYIMTSQNEKAEELMRKIEKEEEQL
1			SYDDPNRKMYHLCIVNLVIGTLYCAKGNYEFGISRVIKSLEPYN
1	1		KKLGTDTWYYAKRCFLSLLENMSKHMIVIHDSVIQECVQFLGHC
1			BLYGTNIPAVIEQPLEEERMHVGKNTVTDESRQLKALIYEIIGW
	<u> </u>	<u> </u>	NK
6539	218	339	FLGAASPHPHFSSLAPHPDQPEFTPVQDELEAMELWGPGV
6540	3	391	LERLWLLLLRRPEDAMAECPTLGEAVTDHPDRLWAWEKFVYLDE
ļ			KQHAWLPLTIEIKDRLQLRVLLRREDVVLGRPMTPTQIGPSLLP
			IMWQLYPDGRYRSSDSSFWRLVYHIKIDGVEDMLLELLPDD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Cluberia Daid D Phanel 3
	location		Glutamic Acid, F=Phenylalanine, G=Glycine,
		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion.
	sequence		\=possible nucleotide insertion)
6541	1165	536	RTLVQRRILMLLRKPARGRDLRGRGRGTPRGGRKGLLPTPDEFP
			RFEGGRKPDSWDGNREPGPGHEHFRDTPRPDHPPHDGHSPASRE
			RSSSLQGMDMASLPPRKRPWHDGPGTSEHREMEAPGGPSEDRGG
1	1		KGRGGPGPAQRVPKSGRSSSLDGEHHDGYHRDEPFGGPPGSGTP
	ļ <u> </u>		SRGGRSGSNWGRGSNMNSGPPRRGASRGGGRGR
6542	3	3775	SWPRGRGETGGHPGALRTRTMQKSVRYNEGHALYLAFLARKEGT
1	1	ł	KRGFLSKKTAEASRWHEKWFALYQNVLFYFEGEQSCRPAGMYLL
			EGCSCERTPAPPRAGAGQGGVRDALDKQYYFTVLFGHEGQKPLE
			LRCEEEQDGKEWMEAIHQASYADILIEREVLMQKYIHLVQIVET
			EKIAANQLRHQLEDQDTEIERLKSEIIALNKTKERMRPYQSNQE
1			DEDPDIKKIKKVQSFMRGWLCRRKWKTIVQDYICSPHAESMRKR
			NQIVFTMVEAESEYVHQLYILVNGFLRPLRMAASSKKPPISHDD
1			VSSIFLNSETIMFLHEIFHQGLKARIANWPTLILADLFDILLPM
j	1		LNIYQEFVRNHQYSLQVLANCKQNRDFDKLLKQYEANPACEGRM
			LETEL TVDMPOLDBYLTEL HELL ALEDDER TERMPACEGEM
	1		LETFLTYPMFQIPRYIITLHELLAHTPHEHVERKSLEFAKSKLE
İ			ELSRVMHDEVSDTENIRKNLAIERMIVEGCDILLDTSQTFIRQG
			SLIQVPSVERGKLSKVRLGSLSLKKEGERQCFLFTKHFLICTRS
[			SGGKLHLLKTGGVLSLIDCTLIEEPDASDDDSKGSGQVFGHLDF
	İ		KIVVEPPDRAAFTVVLLAPSRQEKAAWMSDISQCVDNIRCNGLM
			TIVFEENSKVTVPHMIKSDARLHKDDTDICFSKTLNSCKVPQIR
			YASVERLLERLTDLRFLSIDFLNTFLHTYRIFTTAAVVLGKLSD
1	1		IYKRPFTSIPVRSLELFFATSQNNRGEHLVDGKSPRLCRKFSSP
1			PPLAVSRTSSPVRARKLSLTSPLNSKIGALDLTTSSSPTTTTQS
			PAASPPPHTGQIPLDLSRGLSSPEQSPGTVBENVDNPRVDLCNK
ł	1		LKRSIQKAVLESAPADRAGVESSPAADTTELSPCRSPSTPRHLR
	]		YRQPGGQTADNAHCSVSPASAFAIATAAAGHGSPPGFNNTERTC
1			DKEFI IRRTATNRVLNVLRHWVSKHAQDFELNNELKMNVLNLLE
1	ì		
	i .		EVLRDPDLLPQERKAAANILMALSQDDQDDIHLKLEDIIQMTDC
1			MKAECFESLSAMELAEQITLLDHVIFRSIPYBEFLGQGWMKLDK
	<u> </u>		NERTPYIMKTSQHFNDMSNLVASQIMNYADVSSRANAIEKWVAV
	l i		ADICRCLHNYNGVLEITSALNRSAIYRLKKTWAKVSKQTKALMD
1			KLQKTVSSEGRFKNLRETLKNCNPPAVPYLGMYLTDLAFIEEGT
			PNFTEEGLVNFSKMRMISHIIREIRQFQQTSYRIDHQPKVAQYL
	<u> </u>		LDKDLIIDEDTLYELSLKIEPRLPA
6543	1857	950	FVSGCGRAGIGLSWAMAAEARVSRWYFGGLASCGAACCTHPLDL
	{ i		LKVHLQTQQEVKLRMTGMALRVVRTDGILALYSGLSASLCRQMT
			YSLTRFAIYETVRDRVAKGSQGPLPFHEKVLLGSVSGLAGGFVG
	[		TPADLVNVRMQNDVKLPQGQRRNYAHALDGLYRVAREEGLRRLF
			SGATMASSRGALVTVGQLSCYDQAKQLVLSTGYLSDNIFTHFVA
			SFIAGGCATFLCQPLDVLKTRLMNSKGEYQGVFHCAVETAKLGP
			LAFYKGLVPAGIRLIPHTVLTFVFLEQLRKNFGIKVPS
6544	630	70	
~311	630	79	PSPCFIRSRLDGQPWMAGLEAWLSQNFSLHQPQSRVRVRRASIS
			EPSDTDPEPRTLNPSPAGWFVQQHPELELMSSFRERFGRNWLQY
			RSHLEPSGNPLPATPTTSAPSAPPASSQGPDTAPRPSPPQBEAR
l		(	GPQESPQKMSEEVRAEPQEEEE3KEGKEEKEEGEMAPLPEAHLG
			EGKQKECP
6545	176	560	PPHSHAALLPAAMTPLLTLILVVLMGLPLAQALDCHVCAYNGDN
			CFNPMRCPAMVAYCMTTRTYYTPTRMKVSKSCVPRCFETVYDGY
1		l	SKHASTTSCCQYDLCNGTGLATPATLALAPILLATLWGLL
6546	1657	364	HLLNGLDEVAAFFVADLGAIVRKHFCFLKCLPRVRPFYAVKCNS
			SPGVLKVLAQLGLGFSCANKAEMELVQHIGIPASKIICANPCKQ
1		ľ	
1			IAQIKYAAKHGIQLLSFDNBMELAKVVKSHPSAKMVLCIATDDS
1			HSLSCLSLKFGVSLKSCRHLLENAKKHHVEVVGVSFHIGSGCPD
1			PQAYAQSIADARLVFEMGTELGHKMHVLDLGGGFPGTEGAKVRF
1 .			EEIASVINSALDLYFPEGCGVDIFAELGRYYVTSAPTVAVSIIA
L	l		KKEVLLDQPGREEENGSTSKTIVYHLDEGVYGIFNSVLFDNICP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ļ	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	
			P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence		\=possible nucleotide insertion)
			TPILQKKPSTEQPLYSSSLWGPAVDGCDCVAEGLWLPQLHVGDW
			LVFDNMGAYTVGMGSPFWGTQACHITYAMSRVAWEALRROLMAA
]	1		EQEDDVEGVCKPLSCGWEITDTLCVGPVFTPASIM
6547	1	541	LHSKYLAPALCSQPGMMRCCRRCCCRQPPHALRPLLLLPLVLL
			PPLAAAAAGPNRCDTIYQGFAECLIRLGDSMGRGGELETICRSW
			NDFHACASQVLSGCPEEAAAVWESLQQEARQAPRPNNLHTLCGA
	1		PVHVRERGTGSETNQETLRATAPALPMAPAPPLLAAALALAYLL
			RPLA
6548			1.772.727
6548	2	219	FVSRLSVRDVRFPTFLGGHGADAMHTDPDYSAAYVPIETDAEDG
			IKGCGITFTLGKGTEVGELKILSRFQNA
6549	73	1490	ETGRVCEDARPACGSRSRRRRKEAAPGIPTPSPSSSSPTSSRPA
			ARAFSKAPARLSRPRAREEPPDPGRRYIQEEIIQARKHKLIKMC
			SSVAAKLWFLTDRRIREDYPQKEILRALKAKCCEEELDFRAVVM
	1		DEVVLTIEQGNLGLRINGELITAYPQVVVVRVPTPWVQSDSDIT
			VLRHLEKMGCRLMNRPQAILNCVNKFWTFQELAGHGVPLPDTFS
			YGGHENFAKMIDEAEVLEFPMVVKNTRGHRGKAVFLARDKHHLA
i			DLSHLIRHEAPYLFQKYVKESHGRDVRVIVVGGRVVGTMLRCST
			DGRMQSNCSLGGVGMMCSLSEQGKQLAIQVSNILGMDVCGIDLL
1			MKDDGSFCVCEANANVGFIAFDKACNLDVAGIIADYAASLLPSG
1			RLTRRMSLLSVVSTASETSEPELGPPASTAVDNMSASSSSVDSD
			PESTERELLTKLPGGLFNMNQLLANEIKLLVD
6550	2293	922	
0330	2233	322	FRVSRDGAPDCGIEQMGLAMEHGGSYARAGGSSRGCWYYLRYFF
			LFVSLIQFLIILGLVLFMVYGNVHVSTESNLQATERRAEGLYSQ
	1		LLGLTASQSNLTKELNFTTRAKDAIMQMWLNARRDLDRINASFR
			QCQGDRVIYTNNQRYMAAIILSEKQCRDQFKDMNKSCDALLFML
1			NQKVKTLEVEIAKEKTICTKDKESVLLNKRVAEEQLVECVKTRE
(			LQHQERQLAKEQLQKVQALCLPLDKDKFEMDLRNLWRDSIIPRS
1	i .		LDNLGYNLYHPLGSELASIRRACDHMPSLMSSKVEELARSLRAD
			IERVARENSDLQRQKLEAQQGLRASQEAKQKVEKEAQAREAKLQ
			AECSRQTQLALEEKAVLRKERDNLAKELEEKKREAEQLRMELAI
			RNSALDTCIKTKSQPMMPVSRPMGPVPNPQPIDPASLEEFKRKI
1			LESQRPPAGIPVAPSSG
6551	157	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
1			ADTVDLNWCVISDMEVIELNKCTSGQSFEVILKPPSFDGVPEFN
			ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER
1			EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLO
1			
6552	107	740	EKDKHAEEVRKNKELKERASR
0332	157	748	IQPPDPRNMTLAAYKEKMKELPLVSLFCSCFLADPLNKSSYKYE
1			ADTVDLNWCVISDMEVIBLNKCTSGQSFEVILKPPSFDGVPEFN
1			ASLPRRRDPSLEEIQKKLEAAEERRKYQEAELLKHLAEKREHER
			EVIQKAIEENNNFIKMAKEKLAQKMESNKENREAHLAAMLERLQ
			EKDKHAEEVRKNKELKEBASR
6553	2	1807	FVWSKMAAHLSYGRVNLNVLREAVRRELREFLDKCAGSKAIVWD
			EYLTGPFGLIAQYSLLKEHEVEKMFTLKGNRLPAADVKNIIFFV
1			RPRLELMDIIAENVLSEDRRGPTRDFHILFVPRRSLLCEQRLKD
			LGVLGSFIHREEYSLDLIPFDGDLLSMESEGAFKECYLEGDQTS
			LYHAAKGLMTLQALYGTIPQIFGKGECARQVANMMIRMKREFTG
			SQNSIFPVFDNLLLLDRNVDLLTPLATQLTYEGLIDEIYGIONS
			YVKLPPEKFAPKKQGDGGKDLPTEAKKLOLNSAEELYAEIRDKN
			FNAVGSVLSKKAKIISAAFEERHNAKTVGEIKQFVSQLPHMQAA
J	]		RGSLANHTSIAELIKDVTTSEDFFDKLTVEQEFMSGIDTDKVNN
			YIEDCIAQKHSLIKVLRLVCLQSVCNSGLKQKVLDYYKREILQT
			YGYEHILTLHNLEKAGLLKPQTGGRNNYPTIRKTLRLWMDDVNE
			QNPTDISYVYSGYAPLSVRLAQLLSRPGWRSIEEVLRILPGPHF
			EERQPLPTGLQKKRQPGENRVTLIFFLGGVTFAEIAALRFLSQL
			EDGGTEYVIATTKLMNGTSWIEALMEKPF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
6554	119	1244	FEMGSQVSVESGALHVVIVGGGFGGIAAASQLQALNVPFMLVDM
0334	1 -13		KDSFHHNVAALRASVETGFAKKTFISYSVTFKDNFRQGLVVGID
	1	1	LKNOMVLLOGGEALPFSHLILATGSTGPFPGKFNEVSSQOAAIQ
			AYEDMVROVORSRFIVVVGGGSAGVEMAABIKTEYPBKEVTLIH
			SOVALADKELLPSVROEVKEILLRKGVOLLLSERVSNLEELPLN
		į.	EYREYIKVOTDKGTEVATNLVILCTGIKINSSAYRKAFESRLAS
		1	
	į.		SGALRVNEHLQVEGHSNVYAIGDCADVRTPKMAYLAGLHANIAV
			ANIVNSVKQRPLQAYKPGALTFLLSMGRNDGVGQISGFYVGRLM
			VRLTKSRDLFVSTSWKTMRQSPP
6555	1552	498	IHMALLRKINQVLLFLLIVTLCVILYKKVHKGTVPKNDADDESE
			TPEELEEEIPVVICAAAGRMGATMAAINSIYSNTDANILFYVVG
			LRNTLTRIRKWIEHSKLREINFKIVEFNPMGLKGKIRPDSSRPE
			LLQPLNFVRFYLPLLIHQHEKVIYLDDDVIVQGDIQELYDTTLA
			LGHAAAFSDDCDLPSAQDINRLVGLQNTYMGYLDYRKKAIKDLG
ļ.		İ	ISPSTCSFNPGVIVANMTEWKHORITKQLEKWMQKNVEENLYSS
			SLGGGVATSPMLIVFHGKYSTINPLWHIRHLGWNPDARYSEHFL
			QEAKLLHWNGRHKPWDFPSVHNDLWESWFVPDPAGIFKLNHHS
6556	241	1449	ASLCKGCFFVTHVLVIILPSLQSPPTFGFLLDIDGVLVRGHRVI
6556	241	1447	PAALKAFRRLVNSQGQLRVPVVFVTNAGNILQHSKAQELSALLG
}			CEVDADQVILSHSPMKLFSEYHEKRMLVSGQGPVMENAQGLGFR
	İ		
1			NVVTVDELRMAFPLLDMVDLERRLKTTPLPRNDFPRIEGVLLLG
			EPVRWETSLQLIMDVLLSNGSPGAGLATPPYPHLPVLASNMDLL
			WMAEAKMPRFGHGTFLLCLETIYQKVTGKELRYEGLMGKPSILT
I		1	YQYAEDLIRRQAERRGWAAPIRKLYAVGDNPMSDVYGANLFHQY
ļ			LQKATHDGAPELGAGGTRQQQPSASQSCISILVCTGVYNPRNPQ
			STEPVLGGGEPPFHGHRDLCFSPGLMEASHVVNDVNEAVQLVFR
1			KEGWALE
6557	2598	1534	RMCGRTSCHLPRDVLTRACAYQDRRGQQRLPEWRDPDKYCPSYN
			KSPQSNSPVLLSRLHFEKDADSSERIIAPMRWGLVPSWFKESDP
i			SKLQFNTTNCRSDTVMEKRSFKVPLGKGRRCVVLADGFYEWQRC
			OGTNOROPYFIYFPQIKTEKSGSIGAADSPENWEKVWDNWRLLT
			MAGIFDCWEPPEGGDVLYSYTIITVDSCKGLSDIHHRMPAILDG
	}	1	EEAVSKWLDFGEVSTQEALKLIHPTENITFHAVSSVVNNSRNNT
		1	PECLAPVDLVVKKELRASGSSQRMLQWLATKSPKKEDSKTPQKE
		1	ESDVPQWSSQFLQKSPLPTKRGTAGLLEQWLKREKEEEPVAKRP
		1	YSO
	<del> </del>	1111	FHGRRRGGRKMELGSCLEGGREAAEEBGEPEVKKRRLLCVEFAS
6558	21	1138	
			VASCDAAVAQCFLAENDWEMERALNSYFEPPVEESALERRPETI
1			SEPKTYVDLTNEETTDSTTSKISPSEDTQQENGSMFSLITWNID
			GLDLNNLSERARGVCSYLALYSPDVIFLQEVIPPYYSYLKKRSS
		J	NYEIITGHEEGYPTAIMLKKSRVKLKSQEIIPFPSTKMMRNLLC
			VHVNVSGNELCLMTSHLESTRGHAAERMNQLKMVLKKMQEAPES
			ATVIFAGDTNLRDREVTRCGGLPNNIVDVWEFLGKPKHCQYTWD
Ī		1	TQMNSNLGITAACKLRFDRIFFRAAAEEGHIIPRSLDLLGLEKL
			DCGRFPSDHWGLLCNLDIIL
6559	3	364	GPELSGLPTRPKKLKANOTPIAMDCCASRSCSVPTGPATTICSS
-555			DKSCRCGVCLPSTCPHTVWLLEPTCCDNCPPPCHIPQPCVPTCF
1			LLNSCOPTPGLETLNLTTFTQPCCEPCLPRGC
6560	3	1435	TATSGGIWLRRKWRCHWPRPLPQSCVGTEGGLQVRDTSSRIAKG
0500	٦	7.47.7	GVDHTKMSLHGASGGHERSRDRRRSSDRSRDSSHERTESQLTPC
1			
1			IRNVTSPTRQHHVEREKDHSSSRPSSPRPQKASPNGSISSAGNS
[			SRNSSQSSSDGSCKTAGEMVFVYENAKEGARNIRTSERVTLIVD
1			NTRFVVDPSIFTAQPNTMLGRMFGSGREHNFTRPNEKGEYEVAB
[			GIGSTVFRAILDYYKTGIIRCPDGISIPELREACDYLCISFEYS
			TIKCRDLSALMHELSNDGARRQFEFYLEEMILPLMVASAQSGER
			ECHIVVLTDDDVVDWDEEYPPQMGEEYSQIIYSTKLYRFFKYIE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
{			NRDVAKSVLKERGLKKIRLGIEGYPTYKEKVKKRPGGRPEVIYN
İ			YVQRPFIRMSWEKEEGKSRHVDFQCVKSKSITNLAAAAADIPQD
			QLVVMHPTPQVDELDILPIHPPSGNSDLDPDAQNPML
6561	3	1086	PGRRFRRKESSSRWFPADCLLGLRGPASSLLSPEPSPSWPSHS
-			PCPMAALTDLSFMYRWFKNCNLVGNLSEKYVFITGCDSGFGNLL
	(		AKQLVDRGMQVLAACFTEEGSQKLQRDTSYRLQTTLLDVTKSES
			IKAAAQWVRDKVGEQGLWALVNNAGVGLPSGPNEWLTKDDFVKV INVNLVGLIEVTLHMLPMVKRARGRVVNMSSSGGRVAVIGGGYC
			VSKFGVEAFSDSIRRELYYFGVKVCIIEPGNYRTAILGKENLES
			RMRKLWERLPQETRDSYGEDYFRIYTDKLKNIMQVAEPRVRDVI
	Į		NSMEHAIVSRSPRIRYNPGLDAKLLYIPLAKLPTPVTDFILSRY
			LPRPADSV
6562	1	1562	MSTLYDIRAHKAQLLRFFASSDSNKALEQRRTLHTPKLEHLDRV
	_		LYEWFLGKRSEGVPVSGPMLIEKAKDFYEQMQLTEPCVFSGGWL
			WRFKARHGIKKLDASSEKQSADHQAAEQFCAFFRSLAAEHGLSA
			EQVYNADETGLFWRCLPNPTPEGGAVPGPKQGKDRLTVLMCANA
			TGSHRLKPLAIGKCSGPRAFKGIQHLPVAYKAQGNAWVDKEIFS
		}	DWFHHIFVPSVREHFRTIGLPEDSKAVLLLDSSRAHPQEAELVS
			SNVFTIFLPASVASLVQPMEQGIRRDFMRNFINPPVPLQGPHAR
		1	YNMNDAIFSVACAWNAVPSHVFRRAWRKLWPSVAFAEGSSSEEE
			LEAECFPVKPHNKSFAHILELVKEGSSCPGQLRQRQAASWGVAG
			REAEGGRPPAATSPAEVVWSSEKTPKADQDGRGDPGEGEEVAWE
			QAAVAFDAVLRFAERQPCFSAQEVGQLRALRAVFRSQQQVRRRR
			GALGAVVKVEALQEGPGGCGATAQSPLPCSSTAGDN
6563	1319	2694	LARPAQPVLLREPEGAGPPVPAGHLVHHLQGGHLRERAHPDLEA
	1	i	HEHPLPCDQMFWRQMGGHLRMVEANSRGVVWGIGYDHTAWVYTG
			GYGGGCFQGLASSTSNIYTQSDVKCVHIYENQRWNPVTGYTSRG LPTDRYMWSDASGLQECTKAGTKPPSLQWAWVSDWFVDFSVPGG
			TDQEGWQYASDFPASYHGSKTMKDFVRRRCWARKCKLVTSGPWL
	}		EVPPIALRDVSIIPESPGAEGSGHSIALWAVSDKGDVLCRLGVS
			ELNPAGSSWLHVGTDQPFASISIGACYQVWAVARDGSAFYRGSV
			YPSQPAGDCWYHIPSPPRQRLKQVSAGQTSVYALDENGNLWYRQ
		1	GITPSYPQGSSWEHVSNNVCRVSVGPLDQVWVIANKVQGSHSLS
			RGTVCHRTGVQPHEPKGHGWDYGIGGGWDHISVRANATRAPRSS
		ļ	SQEQEPSAPPEAHGPVCC
6564	1	975	APGSCALWSYCGRGWSRAMRGCQLLGLRSSWPGDLLSARLLSOE
	]		KRAAETHFGPETVSEEEKGGKVYQVFESVAKKYDVMNDMMSLGI
			HRVWKDLLLWKMHPLPGTQLLDVAGGTGDIAFRFLMYVQSQHQR
	1		KQKRQLRAQQNLSWEEIAKEYQNEEDSLGGSRVVVCDINKEMLK
	1		VGKQKALAQGYRAGLAWVLGDAEELPFDDDKFDIYTIAFGIRNV
			THIDQALQEAHRVLKPGGRFLCLEFSQVNNPLISRLYDLYSFQV
	1		IPVLGEVIAGDWKSYQYLVESIRRFPSQEEFKDMIEDAGFHKVT
	1		YESLTSGIVAIHSGFKL
6565	1464	999	RSAVANGLTKRRMGLKLNGRYISLILAVQIAYLVQAVRAAGKCD
		Ì	AVFKGFSDCLLKLGDSMANYPQGLDDKTNIKTVCTYWEDFHSCT
	1		VTALTDCQEGAKDMWDKLRKESKNLNIQGSLFELCGSGNGAAGS
CECC			LLPAFPVLLVSLSAALATWLSF
6566	3	1385	KYESAQPGGTQPEPGLGARMAIHKALVMCLGLPLFLFPGAWAQG
			HVPPGCSQGLNPLYYNLCDRSGAWGIVLEAVAGAGIVTTFVLTI
	1		ILVASLPFVQDTKKRSLLGTQVFFLLGTLGLFCLVFACVEKPDF
			STCASRRFLFGVLFAICFSCLAAHVFALNFLARKNHGPRGWVIF
	1		TVALLLTLVEVIINTEWLIITLVRGSGEGGPQGNSSAGWAVASP
	1		CAIANMDFVMALIYVMLLLLGAFLGAWPALCGRYKRWRKHGVFV
			LLTTATSVAIWVVWIVMYTYGNKQHNSPTWDDPTLAIALAANAW AFVLFYVIPEVSOVTKSSPBOSYOGDMYPTRGVGYETILKEOKG
			QSMFVENKAFSMDEPVAAKRPVSPYSGYNGQLLTSVYQPTEMAL

ID	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Location	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
to first amino acid residue of amino acid residue of amino acid sequence  Peptoline, Osditamine, Rarginine, SSECTINE, T-Threonine, VaValine, Mattyptophan, Yatytoohen, Yatytokohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatytoohen, Yatyto	NO:			Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequ		location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
### ### ### ### ### ### ### ### ### ##		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence (Codon, *possible nucleotide deletion, *possible nucleotide deletion), *possible nucleotide deletion, *possible nucleotide insertion)  6567 125 863 1785 863 1785 863 1785 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 863 1885 8	ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence    Codon, /=possible nuclectide insertion    NHKVPSEGATDIILERATANSC/WGSANSTLRAEDMYSAGSNQA ATPROGNASO/VERPYWND   ATPROGNASO/VERPYWND     6567   125	{	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Sequence   N-possible nucleotide insertion		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Sequence   N-possible nucleotide insertion		amino acid	sequence	Codon, /=possible nucleotide deletion,
### ATPPKOGNSOVERNEYVND    STERLIKENSCHIETHSTWYVENDSSCTNVPLIQACILODER		sequence		\=possible nucleotide insertion)
FRESHLEAGEPHINESSYNVELIGACINOPER	-			MHKVPSEGAYDIILPRATANSQVMGSANSTLRAEDMYSAOSHOA
YSKRLLESGFPPNIRDSAGRTGLHLAARARUVDICOLLIKFGAD LLAPTOGONTALLIGGHUTOPLVSNALKIDICOHGGATPLVIL AKRRGVUKUVIRLLESLEOGEVAGFNRGTHSKLETMQTAESESA MESHSLLINPILQOGEGVLSSFRTTTWQEPVEDLGFWRVLLLIFVI ALISLIGIAYIVSGVUPPVENQEELWH  6568 3 1183 HASDRLUVEPNIVSHESGASANLQOPSRTTELFHPTLASISSEM LEGAGLIYRIVHGVUPPVENQEELWH LEGAGLIYRIVHGVILSGWCKASALTQOPSRTTELFHPTLASISSEM LEGAGLIYRIVHGVILSGWCKASALTQOPSITLASIGSEM LEGAGLIYRIVHGVILSGWCKASALTQOPVILNUQCETLEDL KIHLQTTDYGNFLANHTNPLTVSKIDTEMERKELGGEBEYFRINB LEPLSTFLITMTCSYMIDNILLIMBGLQKKSVELIGKCHELG RPTEMBAUNIAETPSDLENAILLETPILAPFPQDCMSENALDEIN IELLRIKKLYKSYLEAPFYRFCKHIGDVTAEWGCVFLIGKCHELG RPTEMBAUNIAETPSDLENAILLETPILAPFPQDCMSENALDEIN ITHINSFGTELSKEDRBTLYPTTGKLIYPEGLELLAQAEDFDOMK NVADHYGVYKJEPFAVGGSGGKTLEDVYFTERGLIPOTDMK NVADHYGVYKJEPFAVGGSGGKTLEDVYFTERGVARPOTLEFADRASF ITTINSFGTELSKEDRBTLYPTTGKLIYPEGLELLAQAEDFDOMK NVADHYGVYKJEPFAVGGSGGKTLEDVYFTERGVARPOTLEPTDMK NVADHYGVYKJEPFAVGGSGGKTLEDVYFTERGVARPOTLEPTDMK NVADHYGVYKJEPFAVGGSGGKTLEDVYFTERGVARPOTLEPTDMK NVADHYGVYKJEPFAVGGSGGKTLEDVYFTERGVARPOTLEPTDMK NVADHYGVYKJEPFAVGGSGGKATLEDVYFTERGVARPOTLEPTDMK NVADHYGVYKJEPFAVGGSGGKATLEDVYFTERGVARPOTLEPTDMK NVADHYGVYKJEVARVARVERGERFTLICHAPTGGSHEKKOMPLAVARPOTLEPTDMK NVADHYGVYKJEVARVERGERFTLICHAPTGGSHEKKOMPLSVYPPIR RMSWLPPLTKSASSAAGSPGGLTSLOQOKQULLEGURITLOQIK GUTTOKDOLVSE BELLARNILLEBSLEAKRGTVLDKYKELTQOK KSTPKKMQRQHELSESGSASALQARLKVAARBAERESINTAED FLEGKMETDDPLSSYMEKRTI-GHCRARKEEKUQAJAMHSGPHA PARKMGSKALPAPPLHIPSLQLITNTSFLQANUTFPATVDHLQG LYGLSAVOTHMMHNITLSFUNHETTRSTTEMAAQGIVDARP PPRALPFTTHLEPPKCGAIAHVLPALHKROPRFDPANLAVAATO EDDPKMGDLSKLSPHKSTERGEGKALGVKTKKE PPRALPFTTHLEPPKCGAIAHVLPALHKROPRFDPANLAVAATO EDDPKMGDLSKLSPHKSTERGEGKRANGVKKKGREMESTAA SSAAKCSGETVICOGT  6572 49 1646 TPERAQPGALIGAGAGCCCGGRWBPRSHERGYFSSAKMGSKRIN LSGSEHGKVCOMPRACKALTOMPNENDAN LSGSEHGKVCOMPNOKATSCLLLEKRINDEVKRIKENGELEMA GLAKHESILKOMPNOKATSCLLLEKRINDEVKRIKENGELIGE LGWGGGESGKFRAQUANNARGYFLLKKKRINDEVKRIKILEG LEQWGGGLYQEGGAKTVAGWRKKGREMEERGKRIK EPAMAQOREDGBALTVKSKLEEABEKRILKELQUKOERINKI PPRAMPORATERGERFRTCHALARAFBEDDTELTGNIKGNIKA KAQYYLLLEKGGEBKKKLOMPNIKG				
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ALISLIJAYYYSGULPYENOPELIVH  ASSRILLUYENOVERGASANLOGOSPRITELPHPTLASISSPM  LEGAELYFNVDHGYLEGLVRGCKASLLTQQDYINLVQCETLEDL  KIHLQTIDYGGYLANHTMPLTVSKIDTEMRRALCGESFYFRNHS  LEGAELYFNVDHGYLEGLVRGCKASLLTQQDYINLVQCETLEDL  KIHLQTIDYGGYLANHTMPLTVSKIDTEMRRALCGESFYFRNHS  LEGLRYKLYFNTGSYMIDNILLMINGALQKKSVKEILGKCHPLG  RPTEMBANNIAETTSDLRNAILLETPLASPFQDOMBENALDELIN  IELLRYKLYKSYLBAPYKECKINHDVTASVVCPILBFEADRRAF  LITLINSFGTBLSKEDBRITLYFTFGKLYPBGLRLLAQAEDFDQMK  NVADHYGVYKLFLFBANGSGKKILEDYFRGVANLAPROCE  HYGYYYAYVKLKEDERRYDYETRKLYPBGLRLLAQAEDFDQMK  NVADHYGVYKLFLFBANGSGKKILEDYFRGVANFYGDEFDQMK  NVADHYGVYKLFBLANGSGKKILEDYFRGVANFYGDEFDQMK  NVADHYGVYKLFBLANGSGKKILEDYFRUNGAFYGGLBFUDDPR  RMSWLPPLTKSASSSAAGSPGGLTSLQQQKQRLIESLRNSHSSI  AEIQKDVEYRIPPTINNLITININILLLPEQFPQEKPYDYSYPPIR  HHLMDKQGYVYTSPLNNNFHHSDLGKLIGJSLLDEFWKNPPVLA  PTSTAPPYLYSNPSGMSPYASQGFPFLPPYPDGASHTSONG  FGYKMPDVPDAFPELSELSVSGLIDDNEGEEVLLEGFLTLPQLK  GITDKDDLVKSIELLARKNLLLEFSELSAFGLJSLLTPTDASIFTSONG  FGYKMPDVPDAFPELSELSVSGLIDDNEGEEVLLEGFLTLPQLK  KSTPEKKMQRGHELSESCSASALQARLKVAAHBAEBESDNITAED  FLEGKMEIDDLSSFMEKRTICHCRRAKEEKLQALAMHSQFHA  PLEGKMEIDDLSSFMEKRTICHCRRAKEEKLQALAMHSQFHA  PLEGKMEIDDLSSFMEKRTICHCRRAKEEKLQALAMHSQFHA  PLEGKMEIDDLSSFMEKRTICHCRRAKEEKLQALAMHSQFHA  PARSKNISSKALPAPIFLHPSLQGLINNSFLQAVNTFPATVDHLQG  LYGLSAVOTMMMHNHNTLGYPNVHEITRSTITEMAAAGGLVDARF  PFPALPFITHHPHFKQGALAMVLDAHLMGETPFDANLAVAATO  EDPFKMGDLSKLSSGLGSFISGLSKLTPDRFPSRGLVDKTKKK  FICKFGGMFFKSYNLLIHETHTDERPTYTOLICHKAFRRQDHL  RDHRYTHSKERPFKCQBCCKGFCQSRTLAVHKTLHMQTSSFTAA  SSAAKCSGETVICGGT  6571  169  6571  169  656  APDWRKKKLQKLIDTLTKNCKHLFRGFDXDNDGCVNVLEWIHGL  SCHLKGSLEEMMYCCGFGWBFREHERGYFSSAKMGSKRRN  LSCSBHQKLVDRNYCKKLHVQALKWNSOLTNNWONSOLNNN  CROFFELLIGKGEEMMACVGGFBWBFBERGYFSSAKMGSKRRN  LSCSBHQKLVDRNYCKKLHVALKINNSOLTNNWONSOLNNN  CROFFELLIGKGEEMMACVGGFBWBFBERGYFSSAKMGSKRRN  LSCSBHQKLVDRNYCKKLHVALKINNSOLTNNWONSOLNNN  CROFFELLIGKGEEMMACVGGFBWBFBERGKLIGLBKQEERLAM  ELAKLKESLKDBERNARCYGERERGLCLOALTEKKLIGLBKOERLAML  LGCEKSKORDARKVGGERERGLCLOALTGKLEEMLICHDERNKLLEE  CLEXCHARDALKFREEMRIT.  EFPANMQOGREDHARKVUGBERKLICHALTEKENN				
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HYGYPYAYVKLEQEINNIWHAECISQRHRYKINSYIPIL  6569  205  1532  RRRGPQRIGHGRFTPLLCRWRTAGPSHWEKQARAFQGLRPVDPR RMSWLFPLTKSASSSAAGSPGGITSLQQKQRLIESLENSHSSI AEIQKDVEYRLPFTINNITININILLPQFPGEKPVISVYPPIR HHIMDKQGVVYTSELVNNFTHHSLGITGSLIDBFFWNPPVLA PTSTAPPYLYSKPSGMSPYASQGFPFLPPYPPGEANRSITSLSV ADTVSSSTISHTTAKPAAPSFGVLSNIPLPIPTVDASIPTSQGG FGYKMPDVPDAFPELSELSSVSGUIDDNEQEEVLLEGFLTLPQUK KSTFEKKMQRQHELSEGSGSASLAGKUAVAAHEAEESDMIAED FLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLQQALAMHSQFHA PL  6570  330  1304  ARIPRITFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVPSAP PASRKMSSKALPAPIPLHPSLQLINYSFLQAVNTFPATVOHLQG LYGLSAVQTMHNNHNTHLGYPNVELSTITEMAAQGLVDARF PFPALPFTTHLFHPKQGAIAHVLPALHKDRPRFDFANLAVAATQ EDDPKMGDLSKLSPGLGSPISGLSKLTPDRKSRGRLPSKTKKE FICKFCGRHFTKSYNLLHERKTIDEPRYTCDICHKAFRRQDEL RDHRYHISKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT  6571  169  6571  169  656  APPMINRKLQKLTDTLTKNCKHLPRGFDKDNDGCVNVLEWHGL SLFLRGSLEEKMKYCFEVFDLNGGFISKEMFHMLKNSLLKQP SEBDPDEG IKBLVEITLKKMDHDHDKKLSFADYBLAVREFTLLL EARGPCLPDPKSQMSFERQVKKDPSNDM  6572  49  1646  TPERAQPGALLGAAGCCVCGGRWPRSHERGYFSSAKMGSKRRN LSCSERHQKLVDBNYCKKLHVQALKNVNSQIRNQMVQNENDNSV QRKOFLRLLQNRGFELDMEBAIQKARENNSQIRNGMKYNRA KAQYYLDLEKQLBEGEKKKKQRATEQLLKEKLMATHNERAA QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEELGLKKLKAATMINKERAA QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEELGLKKLKAATMINKERAA QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEEMAAEDKRNKA KAQYYLDLEKQLBEGEKKKKQRATEQLLKEKLMATHOKEDRED LEQVOGGLVGEGGAIVSSKLKERSKLRKKKKRKOOPEEQMA LKELVLQAAKEEEBNFRKTMLAKFAEDDRIELMNAQKQRMKQLE HRRAVSKLIEBERGOFLYKSLKLEBGLEWKLRKGKREMGERDE LEQVOGGLVGEGGAIVSKIKLKERKLRKJCKINKOOPEEQMA LKELVLQAAKEEEBNFRKTMLAKFAEDDRIELMNAQKQRMKQLE HRRAVSKLIEBRROOFLADKGREEEWGLOORGGFINATIEEE RLKLLKHATNLLGYLYKKEPTLOURGEFRKVYQQRSEI CEEK  6573  767  275  GGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LIFLDFFRRRLSQRFTABELEQRIILKFRNEGEEGEBEREIKRRL	1			
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HILMDKQGVYYTSPLWNFTMHSDLGKIIQSLLDEPKKNPPVLA PTSTAPPYLYSNPSGMSPYASQGFPFLPPYPPQBANKSITSLSV ADTYSSTTSHTTAKPAAPSFGVLSNLPLPIPTVDASIPTSQNG FGYKMPDVPDAFPELSELSVSQLTDKMBQEEVLLEQFLTLPQLK QIITDKDDLVKSIEELARKNLLLEPSLEAKRQTVLDKYELLTQM KSTFEKKMQRQHELSESCSASALQARLKVAAHBAEEESDNIAED FLEGKMEIDDFLSSFMEKRTICHCRRAKEEKLQQAIAMHSQFHA PL  6570 330 1304 ARLFRLTFLREGFLYVLLSHWVFVGAPRPPASDSWKKGLVPSAP PASRKMSSKALPAPIPLHPSLQLITNYSFLQAVTTFPATVDHLQG LYGLSAVQTHMMHNTLGYPDVWEITRSTITEMAAQGLVDARF PFPALPFTTHLFFP KQGAIAHVLPALHKDRPRFPFANLAVAATQ EDPPKMGDLSKLSPGLGSPISGLSKLTPDRKPSRGRLPSKTKKE FICKPCGRHFTKSYNLLIHEATTDERPYTCDICHCAFRQOBL RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT APPDMNRKLQKLTDTLTKNCKHLFRGFDKDNDGCVNVLEWIHGL SLFLRGSLEEKMKYCFEVFDLNGDGFISKEEMFHMLKNSLLKQP SEBDPDEGIKDLVEITLKKNDHEHDGKKSFADYELAVREETLLL EARGPCLPPDKSQMEFFAGVFKDPNEFNDM ORKOFLELLONGOFEAGVKKDHPAGRAFKAVQNENDMSV V ROSSERRYLVUBRNYCKKHLVQALKNSQIRNQMQNENDMSV V ROSSERRYLVUBRNYCKKHLVQALKNSQIRNQMQNENDMSV V ROSSERRYLVUBRNYCKKHLVQALKERILKEELGKKKKAAYMNKERAA GLAKLKHESLKDBKMRQQVRENSIELRELBEKKKLKAAYMNKERAA GLAKLKHESLKDBKMRQQVRENSIELRELBEKKKLKAAYMNKERAA GLAKLKHESLKDBKMRQQVRENSIELRELBEKKLKAAYMNKERAA GLAKLKHESLKDBKMRQQVRENSIELRELBEKKLKAAYMNKERAA GLAKDAIKYEOMKRDAEIAKTMMEHKRIIKEENAAEDKRNKA KAQYYLDLERQLEEGEKKKQBAYEQLLKEKLMIDEIVRKIYEBD QLEKQOKLEKMNAMRRYIEFPQKEQALWRKKKREEMEERNRII EFANMQQQREEDRMAKVQENEEKKQLQLQNALTQKLEEMIRQRED LEQVRGELYQEEGAEIYKSKLEEBABKKLRKQKEMMQDFEEGMA LKELVLQAAKEEENFRKIMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEBRRQQFLADKKRELEEWQLQURACTGKLEEMLRQRED LEQVRGELYQEEGAEITYRSKLEEBEBWRLOLQBRAKGRINGEER RLKLLKEHATNLLGYLPKGVFKEDDIDLLGEEFRKVYQQREEI CEEK GGGGGESQSFRAQDGTRTPATDCLMYLQGFRKMTQGGYDMVQK LFLDFFFRRILSQRPTAEELEGQNNILKPRNEQEEQEEKREIKRRL				
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PASRKMGSKALPAP IPLHPSLQLTNYSFLQAVNTFPATVDHLQG LYGLSAVQTMHMNHWTLGYPNVHEITRSTITEMAAAQGLVDARF PFPALPFTTHLFHPKQGALAHVLPPALHKDRPRFDFANLAVAATQ EDPPKMGDLSKLSPGLSSFLSGLSKLTPDRKPSRGRLPSKTKKE FICKFCGRHFTKSYNLLIHERTHTDERPYTCDICHKAFRRQDHL RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT  6571 169 656 APDMNRKLQKLTDTLTKNCKHLFRGFDKDNDGCVNVLEWIHGL SLFLRGSLEEKMKYCFEVFDLMGDGFISKEEMFHMLKNSLLKQP SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYBLAVREETLLL EAFGPCLPDPKSQMEFFAQVFKDPNDM  6572 49 1646 TPERAQPGALLGAAGCCVCGGRWWPRSHERGYFSSAKMGSKRRN LSCSERHQKLVDBNYCKKLHVQALKNVNSQIRNQMVQNENDNRV QRKQFLRLLQNEQFELDMEEAIQKAEENKRLKELQLKQEEKLAM ELAKLKHESLKDEKMRQQVRENSIELBELBKKLKKAYMNKERAA QIAEKDAIKYEQMKRDADVRENSIELBELBKKLKKAYMNKERAA QIAEKDAIKYEQMKRDADVRENKKRIIKEENAAEDKRNKA KAQYYLDLEKQLBEQEKKKQBAYEQLLKEKLMIDEIVRKIYBED QLEKQQKLEKMNAMRRYIEEFQKEQALWRKKKREEMEEENRKII EFANMQQQREEDRMAKVQENBEKRLQLQNALTQKLEEMLRQRED LEQVRQELYGEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA LKELVLQAAKEEEFNFRKTMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRQQFLADKQRELEEWQLQQRRQGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK  6573 767 275 GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL	6570	330	1304	1
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PFPALPFTTHLFHPKQGAIAHVLPALHKDRPRFDFANLAVAATQ EDPPKMGDLSKLSPGIGSPISGLSKLTPDRKPSKGRLPSKTKKE FICKFCGRHFTKSYNLLIHERTHTDERPYTCDICHKAFRRQDHL RDHRYIHSKEKPFKCQECGKGFCQSRTLAVHKTLHMQTSSPTAA SSAAKCSGETVICGGT  169 656 APDMNRKKLQKLTDTLTKNCKHLFRGFDKDNDGCVNVLEWIHGL SLFLRGSLEERMKYCFEVFDLNBGDFISKEEMFHMLKNSLLKQP SEEDPDEGIKDLVEITLKKMDHDHDGKLSFADYELAVREETLLL EAPGPCLPDPKQMBFEAQVFKDPNEFMDM  6572 49 1646 TPERAQPGALLGAAGCCVCGGRWPRSHERGYFSSAKMGSKRRN LSCSERHQKLVDBNYCKKLHVQALKNVNSQIRNQMVQNENDINRV QRKQFLRLLQNEQFELDMEEAIQKAEENKRLKELQLKQEEKLAM ELAKLKHESLKDEKMRQQVRENSIELRELEKKLKAAYMNKERAA QIAEKDAIXYEQMKRDAEIAKTMMEEHKRIIKENAAEDKRNKA KAQYYLDLEKQLEBQEKKKQBAYEQLLKEKLMIDEIVRKIYBED QLEKQQKLEKMNAMRRYIEEFÇKEQALWRKKKREEMEEENRKII EFANMQQQREEDRMAKVQENBEKRLQLQNALTQKLEEMLRQRED LEQVRQELYQEEQABIYKSKLKEEAEKKLRKQKEMKQDFEEQMA LKELVLQAAKEEEBNFRKTMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRQOFLADKQRELEEWQLQQRRGGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK  6573 767 275 GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL	ŀ			
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EAFGPCLPDPKSQMEFEAQVFKDPNEFNDM  6572 49 1646 TPERAQPGALIGAAGCCVCGGRWWPRSHERGYFSSAKMGSKRRN LSCSERHQKLVDBNYCKKLHVQALKNVNSQIRNQMVQNENDNRV QRKQFLRILQNEQFELDMEEAIQKAEENKRLKELQLKQEEKLAM ELAKLKHESLKDBKMRQQVRENSIELRELEKKLKAAYMNKERAA QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEENAAEDKRNKA KAQYYLDLEKQLEBQEKKKQBAYEQLLKEKIMIDEIVRKIYBED QLEKQQKLEKMNAMRRYIEEFQKEQALWRKKKREEMEEENRKII EFANMQQQREEDRMAKVQENEEKRLQLQNALTQKLEEMLRQRED LEQVRQELYQEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA LKELVIQAAKEEENFRKTMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRQQFLAKGVRELEEWQLQQRRQGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK  6573 767 275 GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL			1	7
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QRKQFLRLLQNEQFELDMEEAIQKAEENRRLKELQLEQEEKLAM ELAKLKHESLKDEKMRQQVRENSIELRELEKKLKAAYMNKERAA QIAEKDAIKYEGMKRDAEIAKTMMEEHKRIIKEENAAEDKRNKA KAQYYLDLEKQLEBQEKKKQBAYEQLLKEKLMIDEIVRKIYBED QLEKQQKLEKMNAMRRYIEEFQKEQALWRKKKREEMEEENRKII EFANMQQREEDRMAKVQENEEKRLQLQMALTQKLEEMLRQRED LEQVRQELYQEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA LKELVLQAAKEEEENFRKTMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRQOFLADKQRELEEWQLQQRRQGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK  6573 767 275 GGGGGESQ\$FRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL	03/2	12.7	1040	
ELAKLKHESLKDEKMRQQVRENSIELRELEKKLKAAYMNKERAA QIAEKDAIKYEQMKRDAEIAKTMMEEHKRIIKEENAAEDKRNKA KAQYYLDLEKQLEBQEKKKQBAYEQLLKEKLMIDEIVRKIYBED QLEKQQKLEKMNAMRRYIEBFQKEQALMEKKKREMEEENRKII EFANMQQQREEDMAKVQENBEKRLQLQNALTQKLEEMLRQRED LEQVRQELYQEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA LKELVLQAAKEEEBNFRKTMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEBRRQQFLADKQRELEEWQLQQRRQGFINAIIBEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK 6573 767 275 GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL				
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QLEKQQKLEKMNAMRRYIEEFQKEQALWRKKKREEMEEENRKII EFANMQQQREEDRMAKVQENBEKRLQLQNALTQKLEEMLRQRED LEQVRQELYQEEQAEIYKSRLKEEAEKKLRKQKEMKQDFEEQMA LKELVIQAAKEEEBNFRKTMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRQQFLADKQRELEEWQLQQRRQGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK 6573 767 275 GGGGGESQ\$FRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL	1			
EFANMQQQREEDRMAKVQENBEKRLQLQNALTQKLEEMLRQRED LEQVRQELYQEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA LKELVLQAAKEEENFRKIMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRQOFLADKQRELEEWQLQQRRQGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK  6573 767 275 GGGGGESQ\$FRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL	1			
LEQVRQELYQEEQAEIYKSKLKEEAEKKLRKQKEMKQDFEEQMA LKELVLQAAKEEENFRKTMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRQQFLADKQRELEEWQLQQRRQGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK 6573 767 275 GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL				1 - 1-1-1
LKELVLQAAKEEENFRKTMLAKFAEDDRIELMNAQKQRMKQLE HRRAVEKLIEERRQQFLADKQRELEEWQLQQRRQGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK 6573 767 275 GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL				
HRRAVEKLIEERROOFLADKORELEEWQLOORROGFINAIIEEE RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK 6573 767 275 GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL				
RLKLLKEHATNLLGYLPKGVFKKEDDIDLLGEEFRKVYQQRSEI CEEK 6573 767 275 GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL	1			1
CEEK  6573 767 275 GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL		1		_ =
6573 767 275 GGGGGESQSFRAQDGTRTPATDCLMYLQGPRKLMTQGGYDMVQK LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL	1			
LFLDFFRRRLSQRPTAEELEQRNILKPRNEQEEQEEKREIKRRL		ļ <u>.</u>	ļ	
	6573	767	275	1 = 1
TRKLSQRPTVEELRERKILIRFSDYVEVADAQDYDRRADKPWTR				
		<u> </u>	L	TRKLSQRPTVEELRERKILIRFSDYVEVADAQDYDRRADKPWTR

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	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
j	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
<del> </del>			LTAADKVSRGECWRVGGRTVCWVSLGSPLGSV
6574	204	1159	LESSVPVSVGVFWACGVSWTGAAGLODGALSDTMARNAEKAMTA
03/1			LARFROAQLEEGKVKERRPFLASECTELPKAEKWRRQIIGEISK
1	1		KVAQIQNAGLGEFRIRDLNDEINKLLREKGHWEVRIKELGGPDY
	Ì		GKVGPKMLDHEGKEVPGNRGYKYFGAAKDLPGVRELFEKEPLPP
			PRKTRAELMKAIDFEYYGYLDEDDGVIVPLEQEYEKKLRAELVE
			KWKAEREARLARGEKEEEEEEEEINIYAVTEEESDEEGSQEKG
Į.			GDDSQQKFIAHVPVPSQQEIEEALVRRKKMELLQKYASETLQAQ
1	1		SEEARRLLGY
6575	117	820	SPALASQSGGITEKKMLEPQENGVIDLPDYEHVEDRTFPPFPPP
03/3	1	525	ASPERODGEGTEPDEESGNGAPVPVPPKRTVKRNIPKLDAQRLI
			SERGLPALRHVFDKAKFKGKGHEAEDLKMLIRHMEHWAHRLFPK
		1	LOFEDFIDRVEYLGSKKEVQTCLKRIRLDLPILHEDFVSNNDEV
			AENNEHDVTSTELDPFLTNLSESEMFASELSISLTEEQQQRIER
			NKQLALERRQAKLP
6576	1	1060	PEPOALVGOKRGALRILVARLVLTVSAPAEVRRRVLRPVLSWMD
1 03/0	-	1000	RETRALADSHFRGLGVDVPGVGQAPGRVAFVSEPGAFSYADFVR
1			GFLLPNLPCVFSSAFTQGWGSRRRWVTPAGRPDFDHLLRTYGDV
į.			VVPVANCGVQEYNSNPKEHMTLRDYITYWKEYIQAGYSSPRGCL
l			YLKDWHLCRDFPVEDVFTLPVYFSSDWLNEFWDALDVDDYRFVY
			AGPAGSWSPFHADIFRSFSWSVNVCGRKKWLLFPPGQBEALRDR
ļ			HGNLPYDVTSPALCDTHLHPRNQLAGPPLEITQEAGEMVFVPSG
1			WHHOVHNLVMCCFSCPLSGAFLQEDGSTTSPLSQPELGWNGVAH
		1	G
6577	2271	987	SDRMASDDFDIVIEAMLEAPYKKEEDEQQRKEVKKDYPSNTTSS
1 03,,,		30,	TSNSGNETSGSSTIGETSNRSRDRDRYRRRNSRSRSPGRQCRHR
			SRSWDRRHGSESRSRDHRREDRVHYRSPPLATGYRYGHSKSPHF
l		1	REKSPVREPVDNLSPBERDARTVFCMQLAARIRPRDLEDFFSAV
ł			GKVRDVRIISDRNSRRSKGIAYVEFCEIQSVPLAIGLTGQRLLG
1			VPIIVQASQAEKNRLAAMANNLQKGNGGPMRLYVGSLHFNITED
İ			MLRGIFEPFGKIDNIVLMKDSDTGRSKGYGFITFSDSECARRAL
			EQLNGFELAGRPMRVGHVTERLDGGTDITFPDGDQELDLGSAGG
1			RFOLMAKLAEGAGIOLPSTAAAAAAAAAAAAAAQAAALQLNGAVPLGA
		!	LNPAALTALSPALNLASQCLQLSSLFTPQTM
6578	377	1489	PSSSATMNRAPLKRATILHMALTGASDPSAEAEANGEKPFLLRA
		[	LQIALVVSLYWVTSISMVFLNKYLLDSPSLRLDTPIFVTFYQCL
1			VTTLLCKGLSALAACCPGAVDFPSLRLDLRVARSVLPLSVVFIG
			MITFNNLCLKYVGVAFYNVGRSLTTVFNVLLSYLLLKQTTSFYA
1		1	LLTCGIIIGGFWLGVDQEGAEGTLSWLGTVFGVLASLCVSLNAI
			YTTKVLPAVDGSIWRLTFYNNVNACILFLPLLLLLGELQALRDF
		1	AQLGSAHFWGMMTLGGLFGFAIGYVTGLQIKFTSPLTHNVSGTA
			KACAQTVLAVLYYEETKSFLWWTSNMMVLGGSSAYTWVRGWEMK
			KTPEEPSPKDSEKSAMGV
6579	2	711	RPPRVWYPELRELSAAAPRWSHRTAPGIMVFYFTSSSVNSSAYT
		1	IYMGKDKYENEDLIKHGWPEDIWFHVDKLSSAHVYLRLHKGENI
			EDIPKEVLMDCAHLVKANSIQGCKMNNVNVVYTPWSNLKKTADM
			DVGQIGFHRQKDVKIVTVBKKVNEILNRLEKTKVERFPDLAAEK
	İ	1	ECRDREERNEKKAQIQEMKKREKEEMKKKREMDELRSYSSLMKV
			ENMSSNQDGNDSDEFM
6580	62	1571	LVALKNWKPKGTNIPAPQSPVFGEAVSGVYMMTKVLGMAPVLGP
	1	1	RPPOEQVGPLMVKVEEKEEKGKYLPSLEMFRQRFRQFGYHDTPG
			PREALSQLRVLCCEWLRPEIHTKEQILELLVLEQFLTILPQELQ
1		1	AWVOEHCPESAERAVTLLEDLERELDEPGHQVSTPPNEQKPVWE
			KISSSGTAKESPSSMQPQPLETSHKYESWGPLYIQESGEEQEFA
			QDPRKVRDCRLSTQHEESADEQKGSEAEGLKGDIISVIIANKPE
			ASLERQCVNLENEKGTKPPLQEAGSKKGRESVPTKPTPGERRYI
L	<del></del>	<del></del>	

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ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
""	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid		Codon, /=possible nucleotide deletion,
		sequence	\=possible nucleotide insertion)
L	sequence		CAECGKAFSNSSNLTKHRRTHTGEKPYVCTKCGKAFSHSSNLTL
1		İ	
ŀ		ļ	HYRTHLVDRPYDCKCGKAFGQSSDLLKHQRMHTEEAPYQCKDCG
l		Ì	KAFSGKGSLIRHYRIHTGEKPYQCNECGKSFSQHAGLSSHQRLH
i			TGEKPYKCKECGKAFNHSSNFNKHHRIHTGEKPYWCHHCGKTFC
			SKSNLSKHQRVHTGEGEAP
6581	228	476	RVFLKDLSSTPMASNNTASIAQARKLVEQLKMEANIDRIKVSKA
			AADLMAYCEAHAKEDPLLTPVPASENPFREKKFFCAIL
6582	1428	718	CFTTKTHCSPVSVPYLSPLVLRKELESLLENEGDQVIHTSSFIN
			QHPIIFWTLVWYFRRLDLPSNLPGLILTSEHCNEGVQLPLSSLS
			QDSKLVYIQLLWDNINLHQEPREPLYVSWRNFNSEKKSSLLSEE
			QQETSTLVETIRQSIQHNNVLKPINLLSQQMKPGMKRQRSLYRE
		1	ILFLSLVSLGRENIDIEAFDNEYGIAYNSLSSEILERLQKIDAP
1			PSASVEWCRKCFGAPLI
6583	487	41	RIFSMTSGRLRWRCTWRPATALWSASLRLGTSSMHPSPRSISLP
			LSMMLSPLPSNTRGLSPTALFRSPDSEHATSCPRLHLWRCRAPL
			RSPSPLGRLQVLPRSPLHVHTHNSGKEVLGLQVQRSRSGTGPAC
ł			SQAGSGAVQGGNWCIF
6584	189	1750	PLPMAALGPSSONVTEYVVRVPKNTTKKYNIMAFNAADKVNFAT
""			WNQARLERDLSNKKIYQEEEMPESGAGSEFNRKLREBARRKKYG
			IVLKEFRPEDOPWLLRVNGKSGRKFKGIKKGGVTENTSYYIFTO
1			CPDGAFEAFPVHNWYNFTPLARHRTLTAEKAEEEWERRNKVLNH
İ			FSIMOORRLKDODODEDEEEKEKRGRRKASELRIHDLEDDLEMS
			SDASDASGEEGGRVPKAKKKAPLAKGGRKKKKKKGSDDEAFEDS
ì			DDGDFEGQEVDYMSDGSSSSQEEPESKAKAPQQEEGPKGVDEQS
			DSSEESEERKPPEEDKEEEEEKKAPTPQEKKRRKDSSEESDSSE
1			ESDIDSEASSAFFMAKKKTPPKRERKPSGGSSRGNSRPGTPSAE
			GGSTSSTLRAAASKLEQGKRVSEMPAAKRLRLDTGPQSLSGKST
			POPPSGKTTPNSGDVQVTEDAVRRYLTRKPMTTKDLLKKFQTKK
			TGLSSEQTVNVLAQILKRLNPERKMINDKMHFSLKE
	<del> </del>	1678	GPIRNSRIDDFVGGDPRAEASCSVLHSKPHAMADSRDPASDQMQ
6585	. 3	10/0	HWKEQRAAQKADVLTTGAGNPVGDKLNVITVGPRGPLLVQDVVF
	ļ		TDEMAHFDRERIPERVVHAKGAGAFGYFEVTHDITKYSKAKVFE
			1
			HIGKKTPIAVRFSTVAGESGSADTVRDPRGFAVKFYTEDGNWDL
			VGNNTPIFFIRDPILFPSFIHSQKRNPQTHLKDPDMVWDFWSLR
			PESLHQVSFLFSDRGIPDGHRHMNGYGSHTFKLVNANGEAVYCK
			FHYKTDQGIKNLSVEDAARLSQEDPDYGIRDLFNAIATGKYPSW
	1		TFYIQVMTFNQAETFPFNPFDLTKVWPHKDYPLIPVGKLVLNRN
			PVNYFAEVEQIAFDPSNMPPGIEASPDKMLQGRLFAYPDTHRHR
	1		LGPNYLHIPVNCPYRARVANYQRDGPMCMQDNQGGAPNYYPNSF
			GAPEQQPSALEHSIQYSGEVRRFNTANDDNVTQVRAFYVNVLNE
			EQRKRLCENIAGHLKDAQIFIQKKAVKNFTEVHPDYGSHIQALL
			DKYNAEKPKNAIHTFVQSGSHLAAREKANL
6586	32	804	PLPEQPAESTSTMPVSGTPAPNKKRKSSKLIMBLTGGGQBSSGL
			NLGKKISVPRDVMLEELSLLTNRGSKMFKLRQMRVEKFIYENHP
			DVFSDSSMDHFQKFLPTVGGQLGTAGQGFSYSKSNGRGGSQAGG
			SGSAGQYGSDQQHHLGSGSGAGGTGGPAGQAGRGGAAGTAGVGE
		1	TGSGDQAGGEGKHITVFKTYISPWERAMGVDPQQKMELGIDLLA
	.l		YGAKAELPKYKSFNRTAMPYGGYEKASKRMTFQMPKV
6587	75	1117	RRVPSLGKMPECWDGEHDIETPYGLLHVVIRGSPKGNRPAILTY
1	1		HDVGLNHKLCFNTFFNFEDMQEITKHFVVCHVDAPGQQVGASQF
		1	PQGYQFPSMEQLAAMLPSVVQHFGFKYVIGIGVGAGAYVLAKFA
	1		LIFPDLVEGLVLVNIDPNGKGWIDWAATKLSGLTSTLPDTVLSH
		]	LFSQEELVNNTELVQSYRQQIGNVVNQANLQLFWNMYNSRRDLD
1			INRPGTVPNAKTLRCPVMLVVGDNAPAEDGVVECNSKLDPTTTT
			FLKMADSGGLPQVTQPGKLTEAFKYFLQGMGYMPSASMTRLARS
1		1	RTASLTSASSVDGSRPQACTHSESSEGLGQVNHTMEVSC
	J	<del></del>	<u> </u>

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1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		I	
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
6588	137	501	LGLQAQLLELRINNYQLSDELRKNGVELTSLRQKVAYLDKEFSK
			AQKALSKSKKAQEVEVLLSENEMLQAKLHSQEEDFRLQNSTLMA
]			EFSKLCSQMEQLEQENQQLKEGAAGAGVAQAGP
6500		1405	
6589	2	1405	RPWGSAMATFSRQEFFQQLLQGCLLPTAQQGLDQIWLLLAICLA
	1		CRLLWRLGLPSYLKHASTVAGGFFSLYHFFQLHMVWVVLLSLLC
	Į.		YLVLFLCRHSSHRGVFLSVTILIYLLMGEMHMVDTVTWHKMRGA
	j	1	QMIVAMKAVSLGFDLDRGEVGTVPSPVEFMGYLYFVGTIVFGPW
1			ISFHSYLQAVQGRPLSCRWLQKVARSLALALLCLVLSTCVGPYL
			FPYFIPLNGDRLLRNKKRKARGTMVRWLRAYESAVSFHFSNYFV
ì			l .
			GFLSEATATLAGAGFTEEKDHLEWDLTVSKPLNVELPRSMVEVV
į.			TSWNLPMSYWLNNYVFKNALRLGTFSAVLVTYAASALLHGFSFH
1	1		LAAVLLSLAFITYVEHVLRKRLARILSACVLSKRCPPDCSHQHR
1			LGLGVRALNLLFGALAIFHLAYLGSLFDVDVDDTTBEQGYGMAY
1			TVHKWSELSWASHWVTFGCWIFYRLIG
6590	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR
0390	21//	050	
		}	GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY
ļ			GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY
į.		}	VDFFEDPSSERKEKKERIPVFCIDVERNDRRAVGHEPEHWSVYR
i			RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREE
i			FQEYLQKLLQHPELSNSQLLADFLSPNGGETQFLDKILPDVNLG
			KIIKSVPGKLMKEKGQHLEPFIMNFINSCESPKPKPSRPELTIL
	1		
	i	1	SPTSENNKKLFNDLFKNNANRAENTERKQNQNYFMEVMTVEGVY
		i	DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL
		l	EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM
<b>!</b>		1	MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI
			VIQELFPELNKVQKEVTSVTSWM
6591	2177	656	VRAYEHVLSLLENVFTPMFCHRDEYFRQLLRGAESPTRNSKLNR
0331	21//	930	
			GSLSLDDFRNTQKRGESFGISRIGSKIKGVFKSTTMEGAMLPNY
	1	t	GVAEGEDDFIEEGIVVMEDDSPVEAVSTPNTPRNLAAWKISIPY
			VDFFEDPSSBRKEKKERIPVFCIDVERNDRRAVGHEPBHWSVYR
	1		RYLEFYVLESKLTEFHGAFPDAQLPSKRIIGPKNYEFLKSKREE
	1		FQBYLQKLLQHPELSNSQLLADFLSPNGGBTQFLDKILPDVNLG
			KIIKSVPGKLMKEKGOHLEPFIMNFINSCESPKPKPSRPELTIL
		[	SPTSENNKKLFNDLFKNNANRAENTERKONONYFMEVMTVEGVY
ł		1	
			DYLMYVGRVVFQVPDWLHHLLMGTRILFKNTLEMYTDYYLQCKL
		[	EQLFQEHRLVSLITLLRDAIFCENTEPRSLQDKQKGAKQTFEEM
]	}	1	MNYIPDLLVKCIGEETKYESIRLLFDGLQQPVLNKQLTYVLLDI
		1	VIQBLFPELNKVQKEVTSVTSWM
6592	3	1861	APEFLGSTISSGSMIDANLKLLQBAEQRLKATVAEKFAIATKEG
	1	-3	DLPQVERFFKIFPLLGLHEEGLRKFSEYLCKQVASKAEENLLMV
Ì		1	LGTDMSDRRAAVIFADTLTLLFEGIARIVETHOPIVETYYGPGR
		[	
}		1	LYTLIKYLQVECDRQVEKVVDKFIKQRDYHQQFRHVQNNLMRNS
		1	TTEKIEPRELDPILTEVTLMNARSELYLRFLKKRISSDFEVGDS
		1	MASEEVKQEHQKCLDKLLNNCLLSCTMQELIGLYVTMEEYFMRE
		1	TVNKAVALDTYEKGQLTSSMVDDVFYIVKKCIGRALSSSSIDCL
į		1	CAMINLATTELESDFRDVLCNKLRMGFPATTFQDIQRGVTSAVN
ŀ			IMHSSLOOGKFDTKGIESTDEAKMSFLVTLNNVEVCSENISTLK
		1	
			KTLESDCTKLFSQGIGGEQAQAKFDSCLSDLAAVSNKFRDLLQE
İ			GLTELNSTAIKPQVQPWINSFFSVSHNIEEEEFNDYEANDPWVQ
!			QFILNLEQQMAEFKASLSPVIYDSLTGLMTSLVAVELEKVVLKS
			TFNRLGGLQFDKELRSLIAYLTTVTTWTIRDKFARLSOMATILN
	1		-
1			LERVTEILDYWGPNSGPLTWRLTPAEVRQVLALRIDFRSEDIKR
			LRL
6593	3	1837	EAFSAGSRRRGLALQRGVLGGLGGYCPCCCRRRGRLLVLLLLVR
1			RGGEGGGGRGRGDKRRRRQARRQRRRPEPAEARGGKMADVLSVL
		•	ROYNIOKKEIVVKGDEVIFGEFSWPKNVKTNYVVWGTGKEGOPR
L	·		

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	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
	<del> </del>		EYYTLDSILFLLNNVHLSHPVYVRRAATENIPVVRRPDRKDLLG
	•		YLNGEASTSASIDRSAPLEIGLQRSTQVKRAADEVLAEAKKPRI
			EDEECVRLDKERLAARLEGHKEGIVQTEQIRSLSEAMSVEKIAA
			IKAKIMAKKRSTIKTDLDDDITALKQRSFVDAEVDVTRDIVSRE
			RVWRTRTTILOSTGKNFSKNIFAILOSVKAREEGRAPEORPAPN
			AAPVDPTLRTKOPIPAAYNRYDQERFKGKEETEGFKIDTMGTYH
			GMTLKSVTEGASARKTOTPAAQPVPRPVSQARPPPNQKKGSRTP
			IIIIPAATTSLITMLNAKDLLQDLKFVPSDEKKKQGCQRENETL
			IQRRKDQMQPGGTAISVTVPYRVVDQPLKLMPQDWDRVVAVFVQ
			GPAWOFKGWPWLLPDGSPVDIFAKIKAFHLKYDEVRLDPNVOKW
		1	DVTVLELSYHKRHLDRPVFLRVWETLDRYMVKHKSHLRF
6594	1	1096	EFPGRRFRGSOASPLCATCGPALLRAPTRAAMTRSLFKGNFWSA
0277	1		DILSTIGYDNIIQHLNNGRKNCKEFEDFLKERAAIBERYGKDLL
			NLSRKKPCGQSEINTLKRALEVFKQQVDNVAQCHIQLAQSLREE
	1		ARKMEEFREKOKLORKKTELIMDAIHKOKSLOFKKTMDAKKNYE
			OKCRDKDEAEQAVSRSANLVNPKQQEKLFVKLATSKTAVEDSDK
			AYMLHIGTLDKVREBWQSEHIKACEAFEAQECERINFFRNALWL
			HVNOLSOOCVTSDEMYEOVRKSLEMCSIQRDIEYFVNQRKTGQI
			PPAPIMYENFYSSOKNAVPAGKATGPNLARRGPLPIPKSSPDDP
			NYSLVDDYSLLYQ
6595	57	781	PLGTMSDSDLGEDEGLLSLAGKRKRRGNLPKESVKILRDWLYLH
0330			RYNAYPSEQEKLSLSGQTNLSVLQICNWFINARRRLLPDMLRKD
			GKDPNQFTISRRGGKASDVALPRGSSPSVLAVSVPAPTNVLSLS
			VCSMPLHSGQGEKPAAPFPRGELESPKPLVTPGSTLTLLTRAEA
			GSPTGGLFNTPPPTPPEQDKEDFSSFQLLVEVALQRAAEMELQK
			QQDPSLPLLHTPIPLVSENPQ
6596	2	1026	PRLPVRRYHGRRRLOGRSRGHMAEGDAGSDORONEEIBAMAAIY
			GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP
			PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD
			VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD
			FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
			KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA
			AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN
	ļ		ILVEKNYTNSPEESSKALGKNKKVRKDKKRNEH
6597	2	1026	PRLPVRRYHGRRRLQGRSRGHMAEGDAGSDQRQNEEIEAMAAIY
	Ì		GEEWCVIDDCAKIFCIRISDDIDDPKWTLCLQVMLPNEYPGTAP
			PIYQLNAPWLKGQERADLSNSLEEIYIQNIGESILYLWVEKIRD
			VLIQKSQMTEPGPDVKKKTEEEDVECEDDLILACQPESSVKALD
			FDISETRTEVEVEELPPIDHGIPITDRRSTFQAHLAPVVCPKQV
			KMVLSKLYENKKIASATHNIYAYRIYCEDKQTFLQDCEDDGETA
			AGGRLLHLMEILNVKNVMVVVSRWYGGILLGPDRFKHINNCARN
			ILVEKNYTNSPBESSKALGKNKKVRKDKKRNEH
6598	1099	419	PRVRWATTMAMSFEWPWQYRFPPFFTLQPNVDTRQKQLAAWCSL
			VLSPCRLHKQSSMTVMEAQESPLFNNVKLQRKLPVESIQIVLEE
			LRKKGNLEWLDKSKSSFLIMWRRPEEWGKLIYQWVSRSGQNNSV
			FTLYELTNGEDTEDEEFHGLDEATLLRALQALQQEHKAEIITVS
			DGPRRQVLLAGTCLPLLLTSHLSRAFKRRQTQCPPKTGSVTPPD
			SKGLQS
6599	164	1593	KMAALTTLFKYIDENODRYIKKLAKWVAIQSVSAWPEKRGEIRR
			MMEVAAADVKQLGGSVELVDIGKQKLPDGSEIPLPPILLGRLGS
			DPOKKTVCIYGHLDVOPAALEDGWDSEPFTLVERDGKLHGRGST
			DDKGPVAGWINALEAYQKTGQEIPVNVRFCLEGMEESGSEGLDE
			LIFARKDTFFKDVDYVCISDNYWLGKKKPCITYGLRGICYFFIE
			VECSNKDLHSGVYGGSVHEAMTDLILLMGSLVDKRGNILIPGIN
			EAVAAVTEEEHKLYDDIDFDIEEFAKDVGAQILLHSHKKDILMH
			RWRYPSLSLHGIEGAFSGSGAKTVIPRKVVGKFSIRLVPNMTPE
	1	L	

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
2.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	bequeenee		VVGEOVTSYLTKKFAELRSPNEFKVYMGHGGKPWVSDFSHPHYL
			AGRRAMKTVFGVEPDLTREGGSIPVTLTFQEATGKNVMLLPVGS
			ADDGAHSQNEKLNRYNYIEGTKMLAAYLYEVSQLKD
6600	2	934	PGRLFRVAAMESAGLEOLLRELLLPDTERIRRATEQLQIVLRAP
0000	•	, , , ,	AALSALCDLLASAADPQIRQFAAVLTRRRLNTRWRRLAAEQRES
			LKSLILTALORETEHCVSLSLAQLSATIFRKEGLEAWPOLLQLL
			OHSTHSPHSPEREMGLLLLSVVVTSRPEAFQPHHRELLRLLNET
	i		LGEVGSPGLLFYSLRTLTTMAPYLSTEDVPLARMLVPKLIMAMQ
			TLIPIDEAKACEALEALDELLESEVPVITPYLSEVLTFCLEVAR
			NVALGNAIRIRILCCLTFLVKVKSKALLKNRLLATLAAHPFPHC
			GC
6601	529	1420	PRABARAPPPAVLRRDRRAATAPGAGEMTLHGPLAQRYFLNHIE
0301	,22,	1	KITTWQDPRKAMNQPLNHMNLHPAVSSTPVPQRSMAVSQPNLVM
			NHOHOOOMAPSTLSOONHPTONPPAGLMSMPNALTTOOOQOOKL
		1	RLORIOMERERIRMRQEELMRQEAALCROLPMEAETLAPVQAAV
		}	NPPTMTPDMRSITNNSSDPFLNGGPYHSREQSTDSGLGLGCYSV
1			PTTPEDFLSNVDEMDTGENAGQTPMNINPQQTRFPDFLDCLPGT
			NVDLGTLESEDLIPLFNDVESALNKSEPFLTWL
6602	127	617	LLDFPALPKFVLAQSPKAGKPSTMTSMTQSLREVIKAMTKARNF
0002	127		ERVLGKITLVSAAPGKVICEMKVEEEHTNAIGTLHGGLTATLVD
			NISTMALLCTERGAPGVSVDMNITYMSPAKLGEDIVITAHVLKQ
			GKTLAFTSVDLTNKATGKLIAQGRHTKHLGN
6603	79	660	PVGPSSLAARTGLGHLPFLHRLASSRGLDMDLLQFLAFLFVLLL
	1		SGMGATGTLRTSLDPSLEIYKKMFEVKRREQLLALKNLAQLNDI
		1	HOOYKILDVMLKGLFKVLEDSRTVLTAADVLPDGPFPQDEKLKD
1			AFSHVVENTAFFGDVVLRFPRIVHYYFDHNSNWNLLIRWGISFC
		İ	NOTGVFNQGPHSPILSLM
6604	3	688	TSTAQROGGERMSFRGGGRGGFNRGGGGGGFNRGGSSNHFRGGG
""			GGGGGNFRGGGRGGFGRGGGRGGFNKGQDQGPPERVVLLGEFL
1		i	HPCEDDIVCKCTTDENKVPYFNAPVYLENKEQIGKVDEIFGQLR
		İ	DFYFSVKLSENMKASSFKKLQKFYIDPYKLLPLQRFLPRPPGEK
1			GPPRGGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
1			GGFRGRGH
6605	<del>  7</del>	848	SGSRRGAMRAAGVGLVDCHCHLSAPDFDRDLDDVLEKAKKANVV
			ALVAVAEHSGEFEKIMQLSERYNGFVLPCLGVHPVQGLPPEDQR
		ì	SVTLKDLDVALPIIENYKDRLLAIGEVGLDFSPRFAGTGEQKEE
}			QRQVLIRQIQLAKRLNLPVNVHSRSAGRPTINLLQEQGAEKVLL
		1	HAFDGRPSVAMEGVRAGYFFSIPPSIIRSGQQKLVKQLPLTSIC
			LETDSPALGPEKQVRNEPWNISISAEYIAQVKGISVEEVIEVTT
		1	QNALKLFPKLRHLLQK
6606	2	1682	FVEIRPRAEVANLSAHSASPIQDAVLKRLSLLEDIVYRQLNGLS
	1	1	KSLGLIEGYGGRGKGGLPATLSPAEEEKAKGPHBKYGYNSYLSE
			KISLDRSIPDYRPTKCKELKYSKDLPQISIIFIFVNEALSVILR
		1	SVHSAVNHTPTHLLKEIILVDDNSDEEELKVPLEEYVHKRYPGL
1		1	VKVVRNQKREGLIRARIEGWKVATGQVTGFFDAHVEFTAGWAEP
		1	VLSRIQENRKRVILPSIDNIKQDNFEVQRYENSAHGYSWELWCM
		1	YISPPKDWWDAGDPSLPIRTPAMIGCSFVVNRKFFGEIGLLDPG
		1	MDVYGGENIELGIKVWLCGGSMEVLPCSRVAHIERKKKPYNSNI
į		1	GFYTKRNALRVAEVWMDDYKSHVYIAWNLPLENPGIDIGDVSER
		1	RALRKSLKCKNFQWYLDHVYPEMRRYNNTVAYGELRNNKAKDVC
1			LDQGPLENHTAILYPCHGWGPQLARYTKEGFLHLGALGTTTLLP
}	1		DTRCLVDNSKSRLPQLLDCDKVKSSLYKRWNFIQNGAIMNKGTG
			RCLEVENRGLAGIDLILRSCTGQRWTIKNSIK
6607	137	986	VPACAGLKKEARSLLASPPRLLNTKLQASCRALFSPPIQSRQTT
""	13,	700	GISFQGRGGAGPGVPTRTQVFAAMGAVMGTFSSLQTKQRRPSKD
			KIEDELEMTMVCHRPEGLEQLEAQTNFTKRELQVLYRGFKNECP
L	<del></del>		

No: notleotide location corresponding to first amino acid amino acid amino acid sequence   Location corresponding to first amino acid amino acid amino acid sequence   Location corresponding to first amino acid amino acid sequence   Location corresponding to first amino acid amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid sequence   Location corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid sequence   Location corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corresponding to first amino acid corres	- 650	Predicted	Predicted end	Amino acid segment containing signal peptide
No:   nucleotide	SEQ		•======	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
location corresponding to first smino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequen	_	, ,	1	
corresponding to first amino acid residue of residue of amino acid residue of amino acid amino acid sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence sequence se	NO:		1	
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residue of amino acid sequence				
amino acid sequence   Codon, /-possible nucleotide deletion,				
Apposible nucleotide insertion		1		
SGVVNEDTEKOJ VAOFFPHODAS TVAHYLENAR DITUTGSSVKEE DPYTALSILLEGTVHEKLRKTENLYDINGS THOERMONI UVXA IYDMIGKYTYPVLKEDTPROHVDVFFQKMCKNKDGIVTLDEFLE SCQEDDNINSSLOLFORWM  RPCFSSFTGLOFREYSPMILLCHAVLPPFKOPSPSPPMSVATRS TOTLOLPPOKPFOGRASIPLAGEBELGKGGEODCALBELCKPIV, CKLCHVINSAQOQAJHYOKKHIGKKLRHYAANSCPPPARMSN VVEPAATPVVPVPPQMGSFKPGGRVILATENDYCLCDAFSSP AVAQAHYOKKHIAKALABAQSINSFSESSELGGRARKEGINER KMMPRIKMITVONNSGFYPNDRSKORI PROBLAMCVITSGGFYC SMCNVGAGEEMEFRQHLESKQHKSKVSSGYRNEMENLGYV FRIERCREFVAGGRILAGGIESERVPAEPGRISATILLSWSAVT PAAREGNFOLSPABERGPLASPVRAAPRAPAPCPAARMSEINTKIS PATNQAAGGEKGKAGNVKKAEEEEIDIDLTAFBTEKAALAIO GKPRRFQKKKKADPSS  6610 319 881 GKKSLCNLHIFTRFPLTYPDMYMGMCTAKKCGIRPGPPAILIL DDKELLKRKSIMBELFEKNYLASGGSLAGTMEGTPTDPPEDINKIL DDKELLKRKSIMBELFEKNYLASGGSLAGTMEGTPTDPEDDINKIL DDKELLKRKSIMBELFEKNYLASGGSLAGTMEGTPTDPEDDINKIL DDKELLKRKSIMBELFEKNYLASHESSEGRVSFFVDDECQUAREREKAA HISKASLPTGGGSTSHEKGKSVTAYSGHAAIQDKLPQVAKREEEAA LUGVULSENVVINMKEPSSPPAPTSSTFGLQDGALRAPHKEST LPRSGSSGGOPSGKKEGVKYKYDGHAAIQDKLPQVAKREEEAA THISKASLPTGGGSTSHEKGKSVTLATRAFDPTYKK EQLBRIRKKAAMYKLSSEGPHEAASKMESTIKPRVEPVCSGL QAQILLEGVARPPHEULLGSLUKVAYQGCVSAARKG STEAQRVDDSPSTSGGSSDGDGRESVQQEBERQVOFKKKEGGIN SKATAKLSTSAKTIGKLEGILTUDPPPINCSAGPKKOHIN YENKS TILGPGSVYEGGVFFDLITFSBUPFFPROKAGPKKOHIN YENKS TILGPGSVYEGGVFFDLITTSSDYPFFPROKAGPKKOHIN YENKS TILGPGSVYEGGVFFDLITTSSDYPFFPROKAGPKKOHIN YENKS TILGPGSVYEGGVFFLOLITTSSDYPFFPROKAGPKKOHIN YENKS TILGPGSVYEGGVFFLOLITTSSDYPFFPROKAGPKKOHIN YENKS TILGPGSVYEGVFFROLITISSHOFPAMGLISKGHA FILVYSITSRGSLELKE ITLGPTPNCSAGPKKOHI YENKS TILGPGSVYEGVFFROLITISSHOFPAMGLISKGHA FILVYSITSRGSLELKE ITLGPTCEIKGDVEST PHUNGNKCDE SPSBFVOSSERALLARTWCAMPSPOWALARLIGMEDUR KRRTVSLQIIGKKSKQOKKEKIKKCVIM SCAVICLDILIKMPSFALTIKCAAHNIN KELFCELLINLE VVYMSPSPFRGBFVKQPAKCAMBRAPVIHTVLHGGTVT GVTIMOIRPRFPVGFILKGETVPVPPFSTAKELBRAVLSKIGAN MLISVLKNIPHSCLERMEGAPVIHTULHGGTVT GVTIMOIRPRFPVGFILKGETVPVPPFSTAKELBRAVLSKIGAN MLISVLKNIPHSCLERMEGAPVIHTVLHGGTVT GVTIMOIRPRFPVGFILKGETVPVPPFSTAKELKRAVLSKIGAN MLISVLKNIPHOSLORGORPGACATARAGRAPLIKHTVEGTTY GQALIFBCGGRAFAGGRORPGACATARAGTSCIKKEG	ı	,	bequence	
DEVITALSILLRGTVHEKLENTENLYDINKOGIVNÖGEMMDIVKA IYDMMGKYTYPVLKEDTPRQHVDVPFQKMDKNKGGIVTLDEFLE SCQEDDNIMSLQLEQAVM  RECFSSFTGLCPRLSYPMILLQHAAVLEPPKQPSPSPPMSVATKS TOTLQLEPQDFYPGQESALPLAGEFELSKGEGQDCALEELCKPLY CKLCNVTLASAQQAQAHYQGKHIGKKLENYYAANSCEPPAMMSN VVEPAATPVVPVPPQMGSFKYGGKVILATRENDYCKLCDASFSSP AVQAHYQGKNIARKELABAQSNSFSESSELGQRRARKEGNEF KMMPNRRNMTVQNNSGFYNPRSRQRIPRDLAMCVITSGGFYC SCHCNVGAGGEMEPPGQHLESKQMEKKVSPYRMEMENLGYV  FELECREPRVAGGRLAGGLESGRYPAPEGRLSAUTLLSWSAVT PAAEPONFQLSPAEPBRAPPAPEPABAMSELNYKTS PATNQAAGGSEKGKAGRUKKAEEBEEDIDLTAPBTEKAALAIQ GKFRFFCKRKUDPSS  6610  319  881  6RSSLCNLHFITFFFLTYPDMYMGMMCTAKKCGIRFQPPAIILI VISSELKGKIRQRIMPVNNFSKFSDCTRAADQLKNNPRHKSYLEQ VSLRQLEKLFSPLAGVLAGGGLESTENDGFTTDPEDEINKL DDKELARKSIMDELFSPLAGVLAGGGLESTENDGFTTDPEDEINKL DDKELARKSIMDELFSPLAGVLAGGGLETTDEPEDINKL DDKELARKSIMDELFSPLAGVLAGGLAETHOLGFTTDPEDEINKL LGVVLISGNUWKKNDPFVYDIEVEFPQDDQLOS COMDTESADEF  FOCSGAGSSRVMLPPALRHLAMGSTESSEGRRVSFGVDEEERVRV LGGVKLSENVVNRMKBPSSPPPAPTSSTFGLQDGNLAPHKESTL LPPSGSSAGGOPSGMKRGVKYRDGHAAIQDKLPFQVAREREAA LTHSKASLPTGEGSISHEQKSVRLARELESERBELRRDTPYK EQLBRIRRNAEMYKLSSEQFHEAASKMESTIKARVEPVCVGGL AQAILHCYRRPBEHLLCSJUKVAYGRCVSAAHKG  5612  1724  992  VSTHASALSRTQOPPGRPRAASGAGAGTAGGGSGGAGSTM STHAGVUDSPSTSGGSSGGORGEKVKROENTKARTHERPRVEPVCGGL AQAILHCYRRPBEHLLCSJUKVAYGRCVSAAHKG SKTAAKLSTSAKTICKELAETILDPPDNCSAGPKGDNIYEMS STHAGVBOFSFTSGSSGGORGESKOKKREGKU SKATAAKLSTSAKTICKELAETILDPPDNCSAGPKGDNIYEMS STHAGVBOFSGNDTVANVRGAGGVGKSSUVLFFVKGFTRESYT PTVEDTYRQVISCOKSICTLQITDTTGSHOPPAMGRLSISKGRA FILVYSITSRQSLEELKPIYEQICEIKGDVSKSSLVLFFVKGFFRESYT PTVEDTYRQVISCOKSICTLQITDTTGSHOPPAMGRLSISKGRA FILVYSITSRQSLEELKPIYEQICEIKGDVSGGSPDVGVVASF GRILLMENLYNFRCKEPDLAARGRAFPPHWALARRIGMEDCR SPSREVGSBRARLARTWKCAFMETSAKHNINKELFQELINLE KRRTVSLQIIGKKSKQQKREKLKKCVIM  SSAREAMFULVERCKOPPLAARGRAPPYHRYSTAKLBAULSILGAA MLISVLKNLPESISSNORQPRGAATARALHAARRIKEELIDKLE GGALIPESYTHYGGCILHVPSCLARGRAPVIHTVLIGGTVT GVTIMQIRPRREPVGPILKGETVPVPPKSTAKLBAUNSILGAN MLISVLKNLPESISSNORGOMEATIKAGANGAKKSKUKKSUTAMOQCIE  GGALIPESYTHYGRGLPVYVPPKSTAKLBAUSHLGAN MLISVLKNLPESISSNORGOM		Bequence		
IYOMMGKYTYPULKEDTPRQHUVFFQKMDKNKDGIVTLDEFLE   SCQEDDNIMRSLQLFOWN   GROTSSPTGICERLSYMILLQHAVLPPPKQPSPSPPMSVATRS   TGTLQLPPQKPFQGRASLPLAGEBLGKCRUX   CKLCNVTINAQQQQAUFYQKHIGKKLRKINAGNASCPPPARMSN   VVEPAATPVVPVPPQMGSFKPGGRVILATENDYCKLCASFSSS   AVQAHVQGKNIHAKKLBLARAGNSFSESSELGQRARKGENDEF   KMMPNRRNMYTVQNNSGPYFNPSRQRIPRGHAMCVTFSQGYC   SMCNVGAGEMEFRQHLESKQHKSKVESQFYNLMEMBLGIV     6609		<b>,</b>		
SCQEDDNIMBSLQLFQNTM				
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VVTMPSPSPKGLPVKQYAVQSQLPVYEWPDVGSGEYDVGVVASF GRLLNEALILKFPYGILNVHPSCLPRWRGPAPVIHTVLHGDTVT GVTIMQIRPKRFDVGPILKQETVPVPPKSTAKELEAVLSRLGAN MLISVLKNLPESLSNGRQQPMEGATYAPKISAGTSCIKWEEQTS EQIFRLYRAIGNIIPLQTLWMANTIKLLDLVEVNSSVLADPKLT GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVVMLKKSLTATDFY NGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTVAMQQCIE	5614	3	1134	
GRLLNEALILKFPYGILNVHPSCLPRWRGPAPVIHTVLHGDTVT GVTIMQIRPKRFDVGPILKQETVPVPPKSTAKELEAVLSRLGAN MLISVLKNLPESLSNGRQQPMEGATYAPKISAGTSCIKWEEQTS EQIFRLYRAIGNIIPLQTLWMANTIKLLDLVEVNSSVLADPKLT GQALIPGSVIYHKQSQILLVYCKDGWIGVRSVMLKKSLTATDFY NGYLHPWYQKNSQAQPSQCRFQTLRLPTKKKQKKTVAMQQCIE				
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6615 832 35 GRVGAGASAMSELPGDVRAFLREHPSLRLQTDARKVRCILTGHE	((35	033	75	GRVGAGASAMSELPGDVRAFLREHPSLRLQTDARKVRCILTGHE
	6612	832	35	LPCRLPELQVYTRGKKYQRLVRASPAFDYAEFEPHIVPSTKNPH
				QLFCKLTLRHINKCPEHVLRHTQGRRYQRALCKYBECQKQGVEY
				VPACLVHRRRRRBDQMDGDGPRPREAFWEPTSSDEGGAASDDSM
				TDLYPPELFTRKDLGSTEDGDGTDDFLTDKEDEKAKPPREKATD
				EGRRETTVYRGLVQKRGKKQLGSLKKKPKSHHRKPKSFSSCKQS
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	6616	347	1886	LLPPCQGARPLSSPPHASEDNLFLFWNCILCAFPHPSPQPLQYP VWPLLLVITQIPAPRHLRNRPFSFSRGGLDSFSGSLSTPSICRS
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	No. 32 - 5 - 3	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ì	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
,	sequence	sequence	\=possible nucleotide insertion)
	Bequesice		PAWVKMAPWPPKGLVPAVLWGLSLFLNLPGPIWLQPSPPPQSSP
1			PPOPHPCHTCRGLVDSFNKGLERTIRDNFGGGNTAWEEENLSKY
			KDSETRLVEVLEGVCSKSDFECHRLLBLSEBLVESWWFHKQQEA
			PDLFOWLCSDSLKLCCPAGTFGPSCLPCPGGTERPCGGYGQCEG
			EGTRGGSGHCDCQAGYGGEACGQCGLGYFEAERNASHLVCSACF
			GPCARCSGPEESNCLQCKKGWALHHLKCVDIDECGTEGANCGAD
			OFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKC
			LDVDECETEVCPGENKQCENTEGGYRCICAEGYKQMEGICVKEQ
ĺ			IPESAGFFSEMTEDELVVLQQMFFGIIICALATLAAKGDLVFTA
			IFIGAVAAMTGYWLSERSDRVLEGFIKGR
	710	673	VWMAWQVSLLELEDRLQCPICLEVFKBSLMLQCGHSYCKGCLVS
6617	118	""	LSYHLDTKVRCPMCWQAVDGSSSLPNVSLAWVIEALRLPGDPEP
			KVCVHHRNPLSLFCEKDQELICGLCGLLGSHQHHPVTPISTVCS
			RMKEELAALFSELKQEQKKVDELIAKLVKNRTRIDGSAPSLCPC
			LGPATFTFL
6618	548	136	DGKVARRAPNSPAFQNDIYPLVSAPRATTAESPWSKVLQNTQCR
9979	] 540	1	NVPKMTSERSRIPCLSAAAAEGTGKKQQEGRAMATLDRKVPSPE
			AFLGKPWSSWIDAAKLHCSDNVDLEEAGKEGGKSREVMRLNKEA
			WKYGT
	246	842	PASSEVLTAAVMFLLLNCIVAVSQNMGIGKNGDLPRPPLRNEFR
6619	240	042	YFORMTTTSSVEGKQNLVIMGRKTWFSIPEKNRPLKDRINLVLS
			RELKEPPOGAHFLARSLDDALKLTERPELANKVDMIWIVGGSSV
İ			YKEAMNHLGHLKLFVTRIMODFESDTFFSEIDLEKYKLLPEYPG
1			ILSDVOEGKHIKYKFEVCEKDD
6620	3	1879	NSRVDDFVARARMAAENEASQESALGAYSPVDYMSITSFPRLPE
6620	3	1075	DEPAPAAPLRGRKDEDAFLGDPDTDPDSFLKSARLQRLPSSSSE
1			MGSODGSPLRETRKDPFSAAAAECSCRQDGLTVIVTACLTFATG
			VTVALVMQIYFGDPQIFQQGAVVTDAARCTSLGIEVLSKQGSSV
			DAAVAAALCLGIVAPHSSGLGGGGVMLVHDIRRNESHLIDFRES
1			APGALREETLQRSWETKPGLLVGVPGMVKGLHEAHQLYGRLPWS
]	1		OVLAFAAAVAQDGFNVTHDLARALAEQLPPNMSERFRETFLPSG
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}			RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ
			RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVL9PPPPHTGPALI
			RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD
			RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT
			RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS
			RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT
			RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA
		662	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGFALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG
6621	1	662	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVL9PPPPHTGFALI SALNILEGFNLTSLVSREQALHWVAETLKIALIASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAFAPLLFVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLKNSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VOGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP
6621	1	662	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGFALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAFAPLLFVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT
6621	1	662	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVL9PPPPHTGPALI SALNILEGFNLTSLVSREQALHWVAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAFAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVPEAHLGSHILQSLDGYVFALNQEG
6621	1	662	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHLQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK
			RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLBPPPPHTGPALI SALNILEGFNLTSLVSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AALTSQLDKASIIRLITSYLKNRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHLQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL
6621	1	662	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVL9PPPHTGPALI SALNILEGFNLTSLVSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLITISYLKNRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVPEAHLGSHLQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARMEANMPKRKEPGRSLRIKVISMGN
			RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVL9PPPHTGPALI SALNILEGFNLTSLVSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AALTSQLDKASIIRLITSYLKNRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHLQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARAMEANMPKREPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN
6622	2	319	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVL9PPPHTGPALI SALNILEGFNLTSLVSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLFVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKWRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRSSPSALAIEVFEAHLGSHLQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARAMEANMPKREPGRSLRIKVISMGN AEVCKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF
			RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVL9PPPHTGFALI SALNILEGFNLTSLVSREQALHWVAETLKIALIASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSSSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARAMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA
6622	2	319	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGFALI SALNILEGFNLTSLVSREQALHWVAETLKIALIASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAGEDGASSASSSSSSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARAMEANMPKREPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF
6622	2	319	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGPALI SALNILEGFNLTSLVSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AQVLIMGPDDFIVAMVSSLNOPFGSGLITPSGILLNSOMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGTTSYQQRLQALRKEKSRDAARSRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYWHFGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARAMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVKFF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKWFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDF
6622	2	319	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVLSPPPPHTGFALI SALNILEGFNLTSLVSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSOMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGTTSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHLQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARAMEANMPKRKEPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYMLFYRSLREYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL
6622	2	319	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVL9PPPHTGPALI SALNILEGFNLTSLVSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLPVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLITISYLKMRDFANQGDPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHILQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARAMEANMPKREPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVKRFF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLREYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM
6622	2	319	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVL9PPPHTGPALI SALNILEGFNLTSLVSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLFVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLITISYLKMRDFANQOPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHLQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL GRASGAQBETEAGGPERARAMEANMPKREPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIITAYNSA LVSKVQFTVDCNUDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLEELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD
6622	2	319	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVL9PPPHTGPALI SALNILEGFNLTSLVSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLFVYELDGAPT AQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLTISYLKMRDFANQGDPFWNLRMEGPPPNT SVKVIGAQRRRSFSALAIEVFEAHLGSHLQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSSSETPEPVVCFPPASDQFLL GRASGAQEETEAGGPERARAMEANMPKREPGRSLRIKVISMGN AEVCKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIIIAYNSA LVSKVQFTVDCNVDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYMLFYRSLREYSFEYVRQETGFDDIPDVKDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKKKQLNLNNEWTPDKL RQKLQTNAHNRLELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKHSAALSFLKENLKVLSVKFDD MRELPPWMYGLRNLBELYLVGSLSHDISRNVTLESLRDLKSLKI
6622	2	319	RPPLPGSLLHRPDLAEVLDVLGTSGPAAFYAGGNLTLEMVAEAQ HAGGVITEEDFSNYSALVEKPVCGVYRGHLVL9PPPHTGPALI SALNILEGFNLTSLVSREQALHWAETLKIALALASRLGDPVYD STITESMDDMLSKVEAAYLRGHINDSQAAPAPLLFVYELDGAPT AAQVLIMGPDDFIVAMVSSLNQPFGSGLITPSGILLNSQMLDFS WPNRTANHSAPSLENSVQPGKRPLSFLLPTVVRPAEGLCGTYLA LGANGAARGLSGLTQVRFTPWLAFFSREPSCGLDCRCLSYLWLV SIPHAANMG VQGITSYQQRLQALRKEKSRDAARSRRGKENFEFYELAKLLPLP AAITSQLDKASIIRLITISYLKMRDFANQOPPWNLRMEGPPPNT SVKVIGAQRRRSPSALAIEVFEAHLGSHLQSLDGYVFALNQEG KFLYISETVSIYLGLSQVELTGSSVFDYVHPGDHVEMAEQLGMK LPPGRGLLSQGTAEDGASSASSSSQSETPEPVVCFPPASDQFLL GRASGAQBETEAGGPERARAMEANMPKREPGRSLRIKVISMGN AEVGKSCIIKRYCEKRFVSKYLATIGIDYGVTKVHVRDREIKVN IFDMAGHPFFYEVRKPF KALFEKVKKFRLHVEEGDILYAMYVRQTVLKVIKFLIITAYNSA LVSKVQFTVDCNUDIQDMTGYKNFSCNHTMAHLFSKLSFCYLCF VSIYGLTCLYTLYWLFYRSLRBYSFEYVRQETGFDDIPDVKNDF AFMLHMIDQYDPLYSKRFAVFLSEVSENKLKQLNLNNEWTPDKL RQKLQTNAHNRLEELPLIMLSGLPDTVFEITELQSLKLEIIKNVM IPATIAQLDNLQELSLHQCSVKIHSAALSFLKENLKVLSVKFDD

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
İ	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence	•	\=possible nucleotide insertion)
	bequeine	<del> </del>	HLRKLTVLKLWHNSITYIPEHIKKLTSLERLSFSHNKIEVLPSH
			LFLCNKIRYLDLSYNDIRFIPPEIGVLQSLQYFSITCNKVESLP
			DELYFCKKLKTLKIGKNSLSVLSPKIGNLLFLSYLDGKGNHFEI
1			LPPELGDCRALKRAGLVVEDALFETLPSDVREQMKTE
		1206	GSRRGGGSRIPAVSTHVAPGRSVLRPFASGALRLRSLVKALGGC
6624	218	1786	
1			RGRPSGLAHLSQETSHWRAKRSGRACLGDFPGEILRSFIMKCTA
1	1		REWLRVTTVLFMARAIPAMVVPNATLLEKLLEKYMDEDGEWWIA
1			KQRGKRAITDNDMQSILDLHNKLRSQVYPTASNMEYMTWDVELE
			RSAESWAESCLWEHGPASLLPSIGQNLGAHWGRYRPPTFHVQSW
I			YDEVKDFSYPYEHECNPYCPFRCSGPVCTHYTQVVWATSNRIGC
			AINLCHNMNIWGQIWPKAVYLVCNYSPKGNWWGHAPYKHGRPCS
1			ACPPSFGGGCRENLCYKEGSDRYYPPRBEETNEIERQQSQVHDT
1			HVRTRSDDSSRNEVISAQQMSQIVSCEVRLRDQCKGTTCNRYEC
			PAGCLDSKAKVIGSVHYEMQSSICRAAIHYGIIDNDGGWVDITR
	-		OGRKHYFIKSNRNGIQTIGKYQSANSFTVSKVTVQAVTCETTVE
ļ			OLCPFHKPASHCPRVYCPRKLYASKSTLCSCNWNSSLF
6625	1124	543	PGPRGGGGSLLSTKALGRSRGLGMHPGPSSGGTEGGVPTALRPP
0023	1124	343	GPLVPSTSDDNLLKNIELFDKLALRFHGRLLFLKDVLGDEICCW
1		}	SFYGQGRKIAEVCCTSIVYATBKKQTKVBFPEARIFEETLNILI
1		1	YETPRGPDPALLEATGGAAGAGGAGRGEDEENREHRVRRIHVRR
	j		
			HITHDERPHGQQIVFKD
6626	3	1498	SAVEFVYTDRFHLILGISVEFLCSLRSDATMESITACLHALQAL
1			LDVPWPRSKIGSDQDSGIELLNVLHRVILTRESPSIQLASLEVV
1			RQIICAAQEHVKEKRRSAEVDDGAAEKETLPEFGEGKDTGGLVP
1			GKSLVFATLELCVCILVRQLPELNPKLTGSPGVKATKPQILLED
1	1	1	GSRLVSAALVILSELPAVCSPEGSISILPTILYLTIGVLRETAV
1			KLPGGQLSSTVAASLQALKGILSSPMARAEKSRTAWTDLLRSAL
ì			TTILDCWDPVDETHQELDEVSLLTAITVFILSTSPEVTTIPCLQ
			KRCIDKFKATLEIKDPVVQIKTYQLLHSIFQYPNPAVSYPYIYS
1			LASCIMEKLQEIDKRKPENTAELEIFQEGIKVLETLVTVAEEHH
			RAQLVACLLPILISFLLDENSLGSATSIMRNLHDFALQNLMQIG
Į.			POYSSVFKSLVASSPALKARLEAAIKGNQESVKVKIPTSKYTKS
			PGKNSSIQLKTSFL
6607	<del> </del>	697	GIPHLSSRDMTGTPGAVATRDGEAPERSPPCSPSYDLTGKVMLL
6627	1	1 697	GDTGVGKTCFLIQFKDGAFLSGTFIATVGIDFRNKVVTVDGVRV
			KLOIWDTAGOERFRSVTHAYYRDAQALLLLYDITNKSSFDNIRA
			1
			WLTEIHEYAQRDVVIMLLGNKADMSSERVIRSEDGETLAREYGV
			PFLETSAKTGMNVELAFLAIAKELKYRAGHQADEPSFQIRDYVE
			SQKKRSSCCSFM
6628	1	1861	QCAEFGGGSGGGGGGGGGGGGGGGEENKENERPSAGSKAN
			KEFGDSLSLEILQIIKESQQQHGLRHGDFQRYRGYCSRRQRRLR
1			KTLNFKMGNRHKFTGKKVTEELLTDNRYLLLVLMDAERAWSYAM
			QLKQEANTEPRKRFHLLSRLRKAVKHAEELERLCESNRVDAKTK
			LEAQAYTAYLSGMLRFEHQEWKAAIEAFNKCKTIYEKLASAFTE
1	1		EQAVLYNQRVEEISPNIRYCAYNIGDQSAINELMQMRLRSGGTE
1			GLLAEKLEALITOTRAKQAATMSEVEWRGRTVPVKIDKVRIFLL
(	1		GLADNEAAIVQAESEETKERLFESMLSECRDAIQVVREELKPDQ
i			KORDYILEGEPGKVSNLQYLHSYLTYIKLSTAIKRNENMAKGLQ
			RALLQQQPEDDSKRSPRPQDLIRLYDIILQNLVELLQLPGLEED
	1		KAFQKEIGLKTLVFKAYRCFFIAQSYVLVKKWSEALVLYDRVLK
	Ī		YANEVNSDAGAFKNSLKDLPDVQELITQVRSEKCSLQAAAILDA
1			NDAHQTETSSSQVKDNKPLVERFETFCLDPSLVTKQANLVHFPP
	1	1	GFQPIPCKPLFFDLALNHVAFPPLEDKLEQKTKSGLTGYIKGIF
			GFRS
6629	5653	4549	GATPLGSVGGRTGKMDAATLTYDTLRFAEFEDFPETSEPVWILG
			RKYSIFTEKDEILSDVASRLWFTYRKNFPAIGGTGPTSDTGWGC

SLAVHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDRHCNG PAGAEVTNRPSPWRPLVLLIPLRLGLTDINEAYVETLKHCFMM QSLGVIGGKPNSAHYFIGYVGEELIYLDPHTTQPAVEPTDGCF PDESFHCQHPPCRMSIAELDPSIAVVRGGHLSTQAFGAECCLG TRKTFGFLRFFFSMLG  6630 2 423 LVQCGGTRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLK LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENR NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQRATKPNRQFS SBSMKPKF  6631 2 423 LVQCGGTRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLK LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENR NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFS SBSMKPKF  6632 1273 588 WNSRGRTQRGAAPLAPAAAMKAVVQRVTRASVTVGGEQISAIG GICVLLGISLEDTQKELBHMVRKILNLRVFEDESGKHWSKSVM KQYEILCVSQFTLQCVLKGNKPDFHLAMPTEQAEGFYNSFLEQ RKTYRPELIKDGKFGAYMQVHIQNDGPVTIELESPAPGTATSD KQLSKLEKQQQRKEKTRAKGPSESSKERNTPRKEDRSASSGAE DVSSEREP  6633 1145 617 ATGRHEGVPTLEGIIQQLVNGIITPATIPSLGPWGVLHSNPMD		i Predicted		
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location corresponding to first amino acid amino acid residue of amino acid sequence    P=Proline, Q=Glutamine, N=Asparagine,   P=Proline, Q=Glutamine, N=Arginine,   S=Serine, T=Threonine, V=Valine,   M=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop   Amino acid sequence			1	
Corresponding to first amino acid amino acid amino acid amino acid residue of amino acid amino acid amino acid amino acid amino acid amino acid aequence   S=Serine, T=Threonine, V=Valine, V=Valine, amino acid aequence   Codon, /=possible nucleotide deletion, \	NO:			
to first amino acid residue of amino acid residue of amino acid sequence  ##TYPYtophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,				
amino acid residue of amino acid sequence "Threonine, Vevaline, wellow amino acid sequence "Threonine, Vevaline, xeluknown, *-Stop Codon, /-possible nucleotide deletion, \-possible nucleotide insertion)  MRCGGMIFAQALVCRHLGRDWRWTGKROPDSYFSVLNAFID KDSYYSIHOIAQMGVGCKSIGOWYGPNTVAQVLKKLAVFDIW SLAVHIAMDNTVVMEEIRRLCRTSVPCAGATAFPADSDRHCNG PAGAEVTNRPSPWRPLVLLIPLRIGLIDINBAYVETLKHCFMM QSLGVIGGKPNSAHYFIGYVGGELIYLDPHTTQPAVEPTDGCC PDESFHCQHPPCRMSIAELDPSIAVVRGGHLSTQAFGAECCLG TRKTFGFLRFFFSMLG  6630 2 423 LVQCGGIRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPPDLK LGDQYVKDBFRRRKTVGSDEAQRFLQEWEVYATALLQQANENR NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFS SESMKRKF  6631 2 423 LVQCGGIRRRSAWGAMPGRHVSRVRALYKRVLQLHRVLPPDLK LGDQYVKDEFRRRKTVGSDEAQRFLQEWEVYATALLQQANENR NSTGKACFGTFLPEEKLNDFRDEQIGQLQELMQEATKPNRQFS SESMKRKF  6632 L1273 588 WNSRGRTGGGAAPLAPAAMKAVVQRVTRASVTVGGEQISAIG GICVLLGISLEDTQKELBHMVRKILNLRVFEDESGKHWSKSVM KQVEILCVSGFTLQCVLKGNKPDFHLAMPHQAAGFYNSFLEQ RKTYRPELKDGKFGAYMOVHIQNGPVTTELESPAPGTATSD KQLSKLEKQQQRKEKTRAKGPSESSKERNTFRKEDRSASSGAE DVSSEREP  6633 1145 617 ATGHEGSVFTLEGIIQQLVNGIITPATTPSLGFWGVLHSNPHD AWGANGLDAIITOLLNGFRNGPSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS				
residue of amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide deletion, /=possible nucleotide insertion)  MLRGGQMIFAQALVCRHLGRDMRWTORKROPDSYFSVLNAFID KDSYYSIHQIAQMGVGGRSIGQWYGPNTVAQVLKKLAVFDTW KDSYYSIHQIAQMGVGGRSIGQWYGPNTVAQVLKKLAVFDTW KDSYYSIHQIAQMGVGGRSIGQWYGPNTVAQVLKKLAVFDTW GAGAEVTNRPSPWRPLVLLIPLRLGITDINEAYVETLKHCFMM QSLGVIGGKDNSAHYFIGYVGGELIYLDPHTTOPAVEPTDGCF PDESFHQQHPPCRMSIAELDPSIAVVRGGHLSTQAFGACCLG TRKTFGFLRFFSMLGM LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENR NSTGKACFGFFLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF LGDQYVKDEFRRHKTVGSDEAQRFLQEWEVYATALLQQANENR NSTGKACFGFFLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF WINSTGKACFGFFLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF WINSTGKACFGFFLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF WINSTGKACFGFFLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF WINSTGKACFGFFLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF WINSTGKACFGFFLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF WINSTGKACFGFFLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF WINSTGKACFGFFLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF WINSTGKACFGFTLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF WINSTGKACFGFTLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF WINSTGKACFGFTLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF WINSTGKACFGFTLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF WINSTGKACFGFTLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKPKF WINSTGKACFGFTLPEEKLNDFRDEQIGQLQELMQRATKENRQFS SESMKSSSSSSSSSSSSP SERNAFS NGAE DVSSEREP ATTERPACATE SESMENT SESSESSSSSSSSSSSSP SENRAFS NGAE DVSSEREP ATTERPACATE SESSESSSSSSSSSSSSSP SENRAFS NGAE DVSSEREP ATTERPACATE SESSESSSSSSSSSSSSSP SENRAFS NGAE DVSSEREP ATTERPACATE SESSESSSSSSSSSSSSSSP SENRAFS NGAE DVSSEREP ATTERPACATE SESSESSSSSSSSSSSSSSP SENRAFS NGAE DVSSEREP ATTERPACATE SESSESSSSSSSSSSSSSSSP SENRAFS NGAE DVSSEREP ATTERPACATE SESSESSSSSSSSSSSSSSSSSSSSSSSSSSP NGAE NGAE WAS A STANDARD SESSES SESSSSSSSSSSSSSSSSSSSSSSS NGAE NGAE WAS A STANDARD SESSESSSSSSSSSSSSSSSSSSSP NGAE NGAE WAS A STANDARD SESSES NGAE NGAE WAS A STANDARD SESSESS NGAE NGAE WAS A STANDARD SESSES NGAE NGAE WAS A STANDARD SESSE				
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GSGLECPVCKDDYALGERVRQLPCNHLFHDGCIVPWLEQHDSC VCRKSLTGQNTATNPPGLTGVSFSSSSSSSSSSSSSSNENATSN 6634  1 1134 CGGIPRKGSGPRRLPMARLRDCLPRLMLTLRSLLFWSLVYCY GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTH YVRIKDSGLRFHYVAAGERGKPLMLLHGFPEFWYSWRYQLRE KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLG SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEY LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHST IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLK HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEAS WLQQDQPDIVNKLIWTFLKEETRKKD				AWGANGLDAIITOLLNOFENTGPPPADKEKIQALPTVPVTEEHV
VCRKSLTGQNTATNPPGLTGVSFSSSSSSSSSSSSSSSSSSSNENATSN  6634  1 1134  CGGIPRKGSGPRRRLPMARLRDCLPRLMLTLRSLLFWSLVYCY GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTH YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRYQLRE KSEYRVVALDLRGGGTLAPHRQNYKLDCLITDLKDLLDSLG SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEY LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHST IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLK HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEAS WLQQDQPDIVNKLIWTFLKEETRKKD				
6634 1 1134 CGGIPRKGSGPRRLPMARLRDCLPRLMLTLRSLLFWSLVYCY GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTH YVRIKDSGLRFHYVAAGERGKPIMLLLHGFPEFWYSWRYQLRE KSEYRVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLG SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEY LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHST IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLK HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEAS WLQQDQPDIVNKLIWTFLKEETRKKD		İ		1
GLCASIHLLKLLWSLGKGPAQTFRRPAREHPPACLSDPSLGTH YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRYQLRE KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLG SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEY LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHST IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLK HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEAS WLQQDQPDIVNKLIWTFLKEETRKKD	6634	<del></del>	1134	
YVRIKDSGLRFHYVAAGERGKPLMLLLHGFPEFWYSWRYQLRE KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLG SKCVLIGHDWGGMIAWLIAICYPEMMWKLIVINFPHPNVFTEY LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHST IGRKGCQLTTBDLEAYIYVFSQPGALSGPINHYRNIFSCLPLK HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEAS WLQQDQPDIVNKLIWTFLKEETRKKD	0034	_		
KSEYRVVALDLRGYGETDAPIHRQNYKLDCLITDIKDILDSLG SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEY LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHST IGRKGCQLTTBDLEAYIYVFSQPGALSGPINHYRNIFSCLPLK HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEAS WLQQDQPDIVNKLIWTFLKEETRKKD				<u> </u>
SKCVLIGHDWGGMIAWLIAICYPEMVMKLIVINFPHPNVFTEY LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHST IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLK HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEAS WLQQDQPDIVNKLIWTFLKEETRKKD				_
LRHPAQLLKSSYYYFFQIPWFPEFMFSINDFKVLKHLFTSHST IGRKGCQLTTBDLEAYIYVFSQPGALSGPINHYRNIFSCLPLK HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEAS WLQQDQPDIVNKLIWTFLKEETRKKD				1 · ·
IGRKGCQLTTEDLEAYIYVFSQPGALSGPINHYRNIFSCLPLK HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEAS WLQQDQPDIVNKLIWTFLKEETRKKD				
HMVTTPTLLLWGENDAFMEVEMAEVTRFYVKNYFRLTILSEAS WLQQDQPDIVNKLIWTFLKEETRKKD				
WLQQDQPDIVNKLIWTFLKEETRKKD				<u>-</u>
0000   Time   Time   Time Offerior   Transport   Time Offerior   Transport   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior   Time Offerior	6635 •	1420	470	
GDCCAEDDDI.DI.SYRI.I.DGEAAI.DAVVEI.UCI.RGCKTMRNGTA	0033	1440	1 3/0	GRGGAEPRPLPLSYRLLDGEAALPAVVFLHGLFGSKTNFNSIAK
				ILAOOTGRRVLTVDARNHGDSPHSPDMSYEIMSODLODLLPOLG
				LVPCVVVGHSMGGKTAMLLALQRPELVERLIAVDISPVESTGVS
		1		HFATYVAAMRAINIADELPRSRARKLADEQLSSVIQDMAVRQHL
		{		LTNLVEVDGRFVWRVNLDALTQHLDKILAFPQRQESYLGPTLFL
				LGGNSQFVHPSHHPEIMRLFPRAQMQTVPNAGHWIHADRPQDFI
AAIRGFLV				
l	6626	1514	1901	SFCMFSHKODSHFQAVPVQEKKKRLRRAPWRAFAQPQRLKHPAE
	0030	1514	1001	OPIVROCLORPPLCGVLGPVQQQLPPSLGPVLSPHSDPGWCRVD
DGGDGVF		ļ		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	~~~~~	1	1501	CSSSPCFHDGTCVLDKAGSYKCACLAGYTGQRCENLLEAGKSKI
	1500	4	1501	KASEDSLSVLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGT
		1		· ·
1 1		1		VVSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISD
1 1 ,				LVRRRVLPMQVQSRETPLHQLYSAAFSKQKLQSAPTKKPALPFG
		1		DLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGKWSGRAPS
				CIPICGKIENITAPKTQGLRWPWQAAIYRRTSGVHDGSLHKGAW
		1		FLVCSGALVNERTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYR
				DDDRDEKTIQSLQISAIILHPNYDPILLDADIAILKLLDKARIS
				TRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNDTL
				RSGVVSVVDSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDIC
			1	TAETGGIAAVSFPGRASPEPRWHLMGLVSWSYDKTCSHRLSTAF

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		sequence	Codon, /=possible nucleotide deletion,
	amino acid	Bedgence	\=possible nucleotide insertion)
	sequence		TKVLPFKDWIERNMK
			GGIPQAGGKMAAPWWRAALCECRRWRGFSTSAVLGRRTPPLGPM
6638	1391	224	GGIPQAGGKMAAPWWRAALCECKRWRGFSTSAVLGRRTPPLGPM
	ł.		PNSDIDLSNLERLEKYRSFDRYRRRAEQEAQAPHWWRTYREYFG
		1	EKTDPKEKIDIGLPPPKVSRTQQLLERKQAIQELRANVEEERAA
	l .	1	RLRTASVPLDAVRAEWERTCGPYHKQRLAEYYGLYRDLFHGATF
	1		VPRVPLHVAYAVGEDDLMPVYCGNEVTPTEAAQAPEVTYEAEEG
			SLWTLLLTSLDGHLLEPDAEYLHWLLTNIPGNRVAEGQVTCPYL
	1	1	PPFPARGSGIHRLAFLLFKQDQPIDFSEDARPSPCYQLAQRTFR
		Í	TFDFYKKHQETMTPAGLSFFQCRWDDSVTYIFHQLLDMREPVFE
	1	1	FVRPPPYHPKQKRFPHRQPLRYLDRYRDSHEPTYGIY
		1	IGCFIMDGGDDGNLIIKKRFVSEAELDERRKRRQEBWEKVRKPE
6639	2046	1268	TGC: THIOGODGNOT TAKE VSEMEDDEKKKKKÖZEBREKVKKE
}			DPEECPEEVYDPRSLYBRLQEQKDRKQQEYEEQFKFKNMVRGLD
			EDETNFLDEVSRQQELIEKQRREBELKELKEYRNNLKKVGISQE
[NKKEVEKKLTVKPIETKNKFSQAKLLAGAVKHKSSESGNSVKRL
1	1		KPDPEPDDKNQEPSSCKSLGNTSLSGPSIHCPSAAVCIGILPGL
ł		Ì	GAYSGSSDSESSSDSEGTINATGKIVSSIFRTNTFLEAP
6640	117	1043	VLEPPDVSMAESEDRSLRIVLVGKTGSGKSATANTILGEEIFDS
0040			RIAAQAVTKNCQKASREWQGRDLLVVDTPGLFDTKESLDTTCKE
ļ	1		ISRCIISSCPGPHAIVLVLLLGRYTEEEQKTVALIKAVFGKSAM
Ì	1		KHMVILFTRKEELEGQSFHDFIADADVGLKSIVKECGNRCCAFS
	ļ		NSKKTSKAEKESQVQELVELIEKMVQCNEGAYFSDDIYKDTEER
1		1	LKQREEVLRKIYTDQLNEEIKLVBEDKHKSEEKKEKEIKLLKLK
	1	Ì	YDEKIKNIREEAERNIFKDVFNRIWKMLSEIWHRFLSKCKFYSS
	<u> </u>	<u> </u>	SAAVGRRSEVRGCAPRPRLRRSARRMDPVPGTDSAPLAGLAWSS
6641	1.	894	SAAVGRRSEVRGCAPRPRIBRISARRINDPVPGTDSAFLAGDAMSS
ļ	1	İ	ASAPPPRGFSAISCTVEGAPASFGKSFAQKSGYFLCLSSLGSLE
	1		NPQENVVADIQIVVDKSPLPLGFSPVCDPMDSKASVSKKKRMCV
ļ	1	1	KLLPLGATDTAVFDVRLSGKTKTVPGYLRIGDMGGFAIWCKKAK
			APRPVPKPRGLSRDMQGLSLDAASQPSKGGLLERTASRLGSRAS
i i		1	TLRRNDSIYEASSLYGISAMDGVPFTLHPRFEGKSCSPLAFSAF
(Ĭ	GDLTIKSLADIEEEYNYGFVVEKTAAARLPPSVS
6642	22	1296	PLEERMMTKMDPNDQAQRDIIFELRRIAFDAESDPSNAPGSGTE
0042		1	KRKAMYTKDYKMLGFTNHINPAMDFTQTPPGMLALDNMLYLAKV
1			HQDTYIRIVLENSSREDKHECPFGRSAIELTKMLCEILQVGELP
	1	,	NEGRNDYHPMFFTHDRAFEELFGICIQLLNKTWKEMRATAEDFN
1			KVMQVVREQITRALPSKPNSLDQFKSKLRSLSYSEILRLRQSER
1			MSQDDFQSPPIVELREKIQPEILELIKQQRLNRLCEGSSFRKIG
1		1	MSQDDFQSFFIVEBREKIQFEIDEBIRQQKIAKBEESSSFKKIC NRRRQERFWYCRLALNHKVLHYGDLDDNPQGBVTFESLQEKIPV
1			ADIKAIVTGKDCPHMKEKSALKQNKEVLELAFSILYDPDETLNF
1		1	ADIRALVIGRUCPHMAEASADAQINAEVDEDAFSIDIDPDETIME
			IAPNKYEYCIWIDGLSALLGKDMSSELTKSDLDTLLSMEMKLRL
1			LDLENIQIPEAPPPIPKEPSSYDFVYHYG
6643	3049	2265	SLHAPAEGRTRGRLAEKPKMLTRKIKLWDINAHITCRLCSGYLI
1			DATTVTECLHTFCRSCLVKYLEENNTCPTCRIVIHQSHPLQYIG
1	1		HDRTMQDIVYKLVPGLQBAEMRKQREFYHKLGMEVPGDIKGETC
1	ł		SAKOHLDSHRNGETKADDSSNKEAAEEKPEEDNDYHRSDEQVSI
1	1		CLECNSSKLRGLKRKWIRCSAQATVLHLKKFIAKKLNLSSFNEL
1			DILCNEELLGKDHTLKFVVVTRWRFKKAPLLLHYRPKMDLL
		300	FRPLATEPRGSSPVQLVSSTMSVRTLPLLFLNLGGEMLYILDQR
6644	1489	290	LRAQNIPGDKARKVLNDIISTMFNRKFMEELFKPQELYSKKALR
1			TRAUNT PURCENCY MONCHOYT OF THE WAY ERACTURED BY A BRITISHING
1		1	TVYERLAHASIMKLNQASMDKLYDLMTMAFKYQVLLCPRPKDVL
1		1	LVTFNHLDTIKGFIRDSPTILQQVDETLRQLTEIYGGLSAGEFQ
1			LIRQTLLIFFQDLHIRVSMFLKDKVQNNNGRFVLPVSGPVPWGT
1		J	EVPGLIRMFNNKGEEVKRIEFKHGGNYVPAPKEGSFEFYGDRVL
			KLGTNMYSVNQPVETHVSGSSKNLASWTQESIAPNPLAKEELNF
1			LARLMGGMEIKKPSGPEPGFRLNLFTTDEEEEQAALTRPEELSY
}			EVINIQATQDQQRSEELARIMGEFEITEQPRLSTSKGDDLLAMM
1			DEL
	1	1	

		I was all and and	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
ı	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6645	6530	4646	FVEGLAGYVYKAASEGKVLTLAALLLNRSESDIRYLLGYVSQQG
			GQRSTPLIIAARNGHAKVVRLLLEHYRVQTQQTGTVRFDGYVID
l			GATALWCAAGAGHFEVVKLLVSHGANVNHTTVTNSTPLRAACFD
			GRLDIVKYLVENNANISIANKYDNTCLMIAAYKGHTDVVRYLLE
l		}	QRADPNAKAHCGATALHFAAEAGHIDIVKELIKWRAAIVVNGHG
			MTPLKVAAESCKADVVELLLSHADCDRRSRIEALELLGASFAND
Ì	i		RENYDIIKTYHYLYLAMLERFQDGDNILEKEVLPPIHAYGNRTE
			CRNPQELESIRQDRDALHMEGLIVRERILGADNIDVSHPIIYRG
			AVYADNMEFEQCIKLWLHALHLRQKGNRNTHKDLLRFAQVFSQM
		j	IHLNETVKAPDIECVLRCSVLEIEQSMNRVKNISDADVHNAMDN
			YECNLYTFLYLVCISTKTQCSBEDQCKINKQIYNLIHLDPRTRE
			GFTLLHLAVNSNTPVDDFHTNDVCSFPNALVTKLLLDCGAEVNA
			VDNEGNSALHIIVQYNRPISDFLTLHSIIISLVEAGAHTDMTNK
ļ			QNKTPLDKSTTGVSEILLKTQMKMSLKCLAARAVRANDINYQDQ
		1	IPRTLEEFVGFH
6646	176	890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
5545	1,0	1	EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL
1	1		EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
ĺ			TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD
1			FKVLPQEAEEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
1			GSEEAEEKODSEKPLLEL
		890	PSSRMNHLPEDMENALTGSQSSHASLRNIHSINPTQLMARIESY
6647	176	890	EGREKKGISDVRRTFCLFVTFDLLFVTLLWIIELNVNGGIENTL
			EKEVMQYDYYSSYFDIFLLAVFRFKVLILAYAVCRLRHWWAIAL
			TTAVTSAFLLAKVILSKLFSQGAFGYVLPIISFILAWIETWFLD
	,		FKVLPQEAKEENRLLIVQDASERAALIPGGLSDGQFYSPPESEA
			GSEEAEEKQDSEKPLLEL
		897	RNCWNCFTKYFNSPPEDIDHKDSYLITRSIMAEPDYIEDDNPEL
6648	413	897	IRPOKLINPVKTSRNHQDLHRELLMNQKRGLAPQNKPBLQKVME
			KRKRDQVIKQKEEEAQKKKSDLEIELLKRQQKLEQLELEKQKLQ
			EEQENAPEFVKVKGNLRRTGQEVAQAQES
			WIPRAAGIRHEVKWDVKEIMSQHNIYVDALLKEFEQFNRRLNEV
6649	1357	832	SKRVRIPLPVSNILWEHCIRLANRTIVEGYANVKKCSNEGRALM
1			QLDFQQFLMKLEKLTDIRPIPDKEFVETYIKAYYLTENDMERWI
			CLDFQQFLMKLEKLIDIRFIFDKEFVETITRATILIENDMBRAT KEHREYSTKQLTNLVNVCLGSHINKKARQKLLAAIDDIDRPKR
			LVPLVFSLLVQSCKQVYRSIAMKFVPCLLLVTLSCLGTLGQAPR
6650	32	765	QKQGSTGEEFHFQTGGRDSCTMRPSSLGQGAGEVWLRVDCRNTD
1			QKQGSTGEEFHFQTGGKDSCTMKPSSLGQGAGEVWDKVDCKN1D QTYWCEYRGQPSMCQAFAADPKSYWNQALQELRRLHHACQGAPV
1			QTYWCEYRGQPSMCQAFAADPKSIWNQALQEDRRLHHACQGAPV LRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTPSLRPKAT
1			LRPSVCREAGPQAHMQQVTSSLKGSPEPNQQPEAGTPSLKPKAT VKLTEATQLGKDSMEELGKAKPTTRPTAKPTQPGPRPGGNEEAK
1	1		
			KKAWEHCWKPFQALCAFLISFFRG
6651	3425	1353	AKELLKVGDFSLCAGPYQNTADTMENLSKEPLASFVSESFDISA
	1	1	CGIATEHVKIDNSGEGLTAEAGSETLSRDGEVGVNSDMHYELSG
	1		DSDLDLLGDCRNPRLDLEDSYTLRGSYTRKKDVPTDGYESSLNF
	1		HNNNQEDWGCSSWVPGMETSLPPGHWTAAVKKEEKCVPPYVQIR
			DLHGILRTYANFSITKELKDTMRTSHGLRRHPSFSANCGLPSSW
			TSTWQVADDLTQNTLDLEYLRFAHKLKQTIKNGDSQHSASSANV
-		1	FPKESPTQISIGAFPSTKISEAPFLHPAPRSRSPLLVTVVESDP
			RPQGQPRRGYTASSLDSSSSWRERCSHNRDLRNSQRNHTVSFHL
-			NKLKYNSTVKESRNDISLILNEYAEFNKVMKNSNQFIFQDKELN
			DVSGEATAQEMYLPFPGRSASYEDIIIDVCTNLHVKLRSVVKEA
			CKSTFLFYLVETEDKSFFVRTKNLLRKGGHTEIEPQHFCQAFHR
			ENDTLIIIIRNEDISSHLHQIPSLLKLKHFPSVIFAGVDSPGDV
1			LDHTYQELFRAGGFVISDDKILEAVTLVQLKEIIKILEKLNGNG
			RWKWLLHYRENKKLKEDERVDSTAHKKNIMLKSFQSANIIELLH
			YHQCDSRSSTKAEILKCLLNLQIQHIDARFAVLLTDKPTIPREV

Deginning Docation Cortesponding Cocation Cortesponding Cocation Coffee Cocation Coffee Coffee Cocation Coffee C	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
No. nucleotide corresponding to first amino acid residue of amino acid residue of amino acid sequence sequence sequence sequence sequence sequence code, /-possible nucleotide deletion, /-pos		1	l .	
cotation coffee	1		1	_ · · · · · · · · · · · · · · · · · · ·
to first amino acid residue of amino acid residue of amino acid sequence 6552 2 1343 FENERICA T-Threonine, V-Valine, S-Serine, T-Threonine, V-Valine, W-Trytophan, Y-Tyrosine, S-Undknown, **Stop Codon, /=possible mucleotide deletion, \[\] \[\	NO:			
to first amino acid residue of amino acid residue of amino acid sequence Sestine, T-Threonine, V-Valine, W-Tryptophan, Y-Tyrosine, X-Unknown, *=Stop codon, *=possible nucleotide deletion, -=possible nucleotide insertion) PENGILVITOVINFISHIEMIANPESSYY 1343 FIGSTISCSCHERRIRGSSFAPELSLAMSPREPSSLPLPLPL PPLEIPTRIRGHAMISSRASSWYGMEVPRILAMSHSFISPC EVINKLELBAIQLORDONNSQOSGIABMEELPVEHNIKISH, TODSFKISMBOMSKNERTHYPIOLMKKNNNNNNFHRUNDT KLVAKAVPLEMPTVGRHRESSPETTVAVQTASKQVDDVVVSE WSEITEFCTADYSKYHITQLLERABYJAGRMEYSPLFSCSTERN KLVAKAVPLEMPTVGRHRESSFRETTVAVQTASKQVDDVVVSE WSEITEFCTADYSKYHITQLLERABYJAGRMEYSPLFSCSTERN TORPOSDSTRONGTHEABELINGULKKNNNNNNFHRUNDT KLVAKAVPLEMPTVGRHRESSPETTVAVQTASKQVDDVVVSE WSEITEFCTADYSKYHITQLLERABYJAGRMEYSPLFSCSTERN TORPOSDSTRONGTHEABELARVINGULKKNNNNNNFHRUNDT KLVAKAVPLEMPTVGRHRESSPETTVAVQTASKQVDDVVSE WSEITEFCADYSKYHITQLLERABYJAGRMEYSPLFSCSTERN TORPOSDSTRONGTHEABELARVINGULKKNNNNNNFHRUNDT KLVAKAVPLEMPTVGRHRESSPETTVAVQTASKQVDDVVSE WSEITEFCADYSKYHITQLERABYJAGRMEYSPLSCHINGULTYAHIY LIVIAPUSSPOEPSCKQRLPGIASKDHKFLINGTHAYITQHY LIVIAPUSSPOEPSCKQRLPGIASKDHKFLINGULTYATHYY LIVIAPUSSPOEPSCKQRLPGIASKDHKFLINGULTYATHYY LIVIAPUSSPOEPSCKQRLPGIASKDHKFLINGULTYATHYY LIVIAPUSSPOEPSCKQRLPGIASKDHKFLINGULTYATHYY LIVIAPUSSPOEPSCKQRLPGIASKDHKSTCYTURENGULTYAHIY LOQUALDRIBUTSPHROGSDPTTOLITURENGULTYAHIY RVAAAASKGADDAMSSKKGPUQVALVQKOGHSEKALASI LLQOHITDRIDVAVVYSVAGAFKKKSFLITDHMRYTUNGSKLAHKEING SKYCKGGLEPFKAPITATSVQCATHYSHQULDHFKKTTLLPHG LQVATSPDPOSKLKOLJAGFKKEGLQALITYVLNPSKLMKEENING SKYCKGGLEPFKAPITATSVQCATHYSHQULDHFKKTTLLPHG LQVATSPDPOSKLKOLJAGFKKEGLQALITYVLNPSKLMKEENING SKYCKGGLEPFKAPITATSVQCATHYSHQULDHFK		1		1
amino acid residue of amino acid sequence whypophan, Y-Tyrosine, K-Unknown, **stop Codon, /=possible nucleotide deletion,			i .	
### ### ##############################	1	l .	1	
amino acid sequence Codon, /=possible mucleotide deletion,	1			
Apposable nucleotide insertion	1	1	1	
FENNGLLYTDWNP TENIER LIAAPPRSS W 1343 1PGSTISCSCISER SERRAGESPARD LIGALASPREPPS LIPLPL PPD.FL.P.PT PAREAU INSERIA SERVICIMEN PROPERTY OF THE	1	amino acid	sequence	
1343 IPGSTISCSCISSRIERGCSFAPELSJCAASPRERPPSELDEJA PPPLPJPTPREAPERATISKRASEWCKMEVPELDIKANSFTSPC EBVIKHLSLERIGLCDRCONKSODSIJAMPELPVEHNIKISK TCDSFKISHEMDSKSKORITHYTYTUDIKKEKKNSKKFKHKUVT KLVAKAVPLPTTVRGHHFLSPTETYTAVOTTASKOVDGDYVVSE WSSIISFCTADYSKYHLTGLLEKARVIAGMKLKFSVFKORGDYV KUNKAVPLPTTVRGHHFLSPTETYTAVOTTASKOVDGDYVVSE WSSIISFCTADYSKYHLTGLLEKARVIAGMKLKFSVFKORGDYVVSE WSSIISFCTADYSKYHLTGLLEKARVIAGMKLKFSVFKORGDYVVSE WSSIISFCTADYSKYHLTGLLEKARVIAGMKLKFSVFKORGDYVVSE WSSIISFCTADYSKYHLTGLLEKARVIAGMKLKFSVFKORGDYVVSE WSSIISFCTADYSKYHLTGLLEKARVIAGMKLKFSVFKORGDYVVSE WSSIISFCTADYSKYHLTGLLEKARVIAGMKLKFSVFKORGDYVVSE WSSIISFCTADYSKYHLTGLEKARVIAGMKLKFSVFKORGDYVVIV ILVIAPVGSGDEPFCKRIPLGNISKONKKITCTEEEDGGLVYHHA ODVILEVIYTDEVUDLSJSTVARITGSIQLMSJSTANAKKDESCKY CNIEVCR CNIEVCR ODVILEVIYTDEVUDLSJSTVARITGSIQLMSJSTANAKKDESCKY CNIEVCR FFLEPRLRFFFASRARFVPARTRSPLHPCCFCFGGGGSCKCK NULLDPERPLIGGSVARGSDEPTTGCJURSEVFTHGEKKLASI LLQDHIRDLDVVVVSVAGARFKKSFILDPMLRYLYSQKSCHS NULLDPERPLIGGSVARGSDEPTTGCJURSEVFTHGGKKVA VVLMDTQGAFBSCSTVKDCATFLGLWSSVFTYNLSONICGS OGGARALIKRLQVKEHGHESIONVRHIHISGFSDVTCCLLPHRG LQVATSPDPORKLADJAGFKGYDGALTPVVLNSPSYPEYSYGL QGGARALIKRLQVKEHGHESIONVRHIHISGFSDVTCCLLPHRG LQVATSPDPORKLADJAGRETICQLALTPVVLNSPSYPEYSYGL QGGARALIKRLQVKEHGHESIONVRHIHISGFSDVTCCLLPHRG SKYTCKGLLEVFKAYIKIYQGBDLPHRSKMQATABAYNLAAAA SKADIYYNNMESVCQGEKPYLSPTITICQUKSVSTCFTRTAA VLFTGIVALVIJAGAKGTCVAGARVSTRATUDAVGR KNOMGKDFSFTYQGLEESIKKINDRVCKNYSSTANAKVSTFTRTAA VLFTGIVALVIJAGAKGTCVCVEKNSKARVSTFTRTAA VLFTGIVALVIJAGAKGTCVCVEKNSKARVSTFTRTAA VLTTGIVSTVISGULTLPVCWTAHAVIRDVKVGCKVYDSLAAA PRODAFAKKGLLALALVSLUPVAGASHCKOTCCGOQCKYDISLALA PODLQARAALCVALLALAFGLUPVAGASHCKOTCCGOQCKYDISLALA PRODAFKKGLLALALVSLUPVAGASHCKOTCCGOQCKYDISLAAA TRISSSPSGCSFTNLAMASAGMILGVVLATLGWKGNAVSTALD RENGPESTYTNIV CHARACSCLLLAGGLLCTCTCSGSGGGDSHWARVSTATAD TRISSSPSGCSFTYNNY CHARACSCLLLAGGLLCTCTCSGSGGGDSHWARVSTATAD TRISSSPSGCSFTYNNY CHARACSCLLLAGGLLCTCTCSGSGGGGSHWARVSTATADY TRISSSPSGCCSFTNLAMASAGMALLAGGGGLKYCKCALLA		sequence		1
PPDLFLPTPTPAREAUTISRTAGEWICKMEVPILDEALINGSTOR EEVIKILSLANIOLORDORINGSOSJARMEELTYPHINTISINI TCDSFKISHEMDSKSKDRITHYFIDLNKKENKNSKFKHKDVPT KLVAKAVELPMTVRCHHFISPTTSTVAVOTASKQVOGDYVVSE WSEITEPCTADVSKVHUTOLLEKENEVISROKHESPYFRONGKE YFDYVERHHGNAMOJPSVKDNSGSIGSPISGKLEGIFPSCSTER TIGKPPODSPYGKTREILARELKJPHNILYTEDFYCMYTAYHYV LIVIAPVSSPODEPCKORLPOLNSKDNKRICTCEEDGVLVYHTHYY LIVIAPVSSPODEPCKORLPOLNSKDNKRICTCEEDGVLVYHTHYY LIVIAPVSSPODEPCKORLPOLNSKDNKRICTCEEDGVLVYHTHYY LIVIAPVSSPODEPCKORLPOLNSKDNKRICTCEEDGVLVYHTHYY LIVIAPVSSPODEPCKORLPOLNSKDNKRICTCEEDGVLVYHTHYY ADALLEVITTOPUDSLIGATVAETIGGLMSISTAANAKDPSCKT CNISVGR 6653 170 1910 FPLEPPELRPFPASRARFYPARTRSPLHPCCFCFEGGSMLSPQ RVAAAASRGADAMESSKOPVQVVILVOKDOHSFELDEKALASI LLQUHTEDLDVVVSVAGARRKSSFILDPHLSYKSKSGHS NILLODBEBLTQFSNRGGSDPETTGLQIVSEVFTVEKRGGKSVA VVLMDTQGAFDSQSTVKDCATIFALSTHTSVOJYNLSQKSGHS NILLODBEBLTQFSNRGGSDPETTGLQIVSEVFTVEKRGGKSVA VVLMDTQGAFDSQSTVKDCATIFALSTHTSVOJYNLSQKSGHS NILLODBEBLTQFSNRGGSDPETTGLQIVSEVFTVEKRGGKSVA VVLMDTQGAFDSQSTVKDCATIFALSTHTSVOJYNLSQKSGHS SKVTCKGLLEFFKAYIKIVQGBDLPFPKSMAKAFING SKVTCKGLLEFFKAYIKIVQGBDLPFPKSMAKAFINGSKAVFSTTFTPA VLFTGIVAPINGSKRUSHGSFRGVALFTFTGLEVARSKRVFSTTFTY VLFTGIVAPINGSKRUSHGSFRGVALFTSTHTSVOJYNLSKAKEING SKVTCKGLLEFFKAYIKIVQGBDLPFPKSMAKAFINGSKAVFSTTFTYPA VLFTGIVAPINGSKUTGGGRFYLSFBLIEBKHCFKCALLITHLTKGY FENDKKAQ FSMSKRAQ 6654 1 705 FSSLSPSCSSFRLAMASAGMGILGVVLTLIGWVRILITALITAGY TRYSGOYRELGGARJULCAASSHULTIAGVKNINGSKAVFSTTFTYSAP AIRSGSPSSFYTNNY NCHANAGKALDAAVALROGSKYDSLOGMOCKYVDSLLIAL PODLQAARALCVILLIVALGGLLLYTLAGKKCTTCVEEKDSKAKEL ASIJTLGWARAGALLLIGGGLLCCTCPGGSSQCPSHTMARTSTSAP AIRSGSPSSFYTNNY THYMAGGLADAPKXG TELEPFRANLAIOPPLSFRALAAPLPEKKGAVPPPQKRAKAVK KSCSCENELTSDLEDDKKIGKLLMDSKYSTITARVKGGDGIHK TRINGSLSPSKYVNINV THENBAGGLADAPKYKG LEPPROKKNINLGOLGSRAVALGCKTCSGFPSHSKRKICKSC KSSCENELTSDLEDDKKIGKLLMDSKYSTITARVKGGDGIHK THENBAGRANGHANGHANFRHYVCKSCECGLISGRAVITKGLLCPT CSKKSKS 110657 830 2120 LLTCGGRAGDCLLSASTMKEVVVNSPKKVADMILLENAMPEYCEF LEHTTOOLINITGCDFKKKPLLAGGGISGRAVILEGIHMINGHLINGHLINGHLINGHLINGHLINGHLINGHLINGHL				FENNGILVTDVNNFIENIEKIAAPFRSSYW
EEVIKILSLEAIGLCDROMSODSGIAEMEELEVPENTKISINI TCDSFKISHEMDSKSKDEITHYPIOLINKEKNINSKEKKHOUPT KLVAKAVPLPMTVEGUMELSPRTETTVAVOTASKOVDGDVVVSE WSEIISFCTADYSKYHLTOOLLEKARVIGGMLKESVYPKROKKE YFDYVREHHONAMGPSVKUDSGSHGSPISKLEGIFFSCSTEPN TGKPPGDSPYGRIFFELARKLENINTNINIFGDFYCMYTHAHY IILVIAPVGSPGDBPYGRIFFELARKLENINTNINIFGDFYCMYTHAHY IILVIAPVGSPGDBPYGRIFFELARKLENINTNINIFGDFYCMYTHAHY IILVIAPVGSPGDBPYGRIFFELARKLENINSKEKTCTEEDGULVHHA QDVILEVIYTDPVDISLATVAEITGHGMSLSTANAKADSCKT CNISVGR 6553 170 1910 FFLEPRIRFFSRARFVPARTEPSPLHPCCFYCEGGGSMLSPQ RVAAAASRGADDAMESSKPGPVQVVLVQKOQHSFSLDEKALASI LLODHIRDLDVVVVSVAGAFRKKSSFILDFMLRYLYSQKESGHS NMLGDEBELTGFSPRMGGSDSPETTGIQTMSEVTERPGGKKVA VVIMDTOGAFDSGSTVKDCATIFALSTMTSSVQIYNLSGRIGED DLOQLGLFFEGRIAMDBIFGCHPOTIMPLIVERPGGKKVA VVIMDTOGAFDSGSTVKDCATIFALSTMTSSVQIYNLSGRIGED LQOGMAPLDKRLOVERBGIEDONVRNHHSGFSDVTCFLHPEG LQVATSPDFDGKKLDIAGEFREQLGALIPFVKHPSKIMKEEING SKVTCRGLLEVFKAYIKIYQGBDLPPKSMLQATAEAYNLAAA SAKNIYYNMAMEVCGGERPYLSDDLLEEKKEGLALDHFKKH KNMGGKDPSFFYQORLEEEIKELY SEPCKUNGSKAVSTSTPTPA VLFFGIVALYIASGLTOFICLEVVAQLFNCMVGLLLAHLAWGY IRYSQYRELGGADIFGAATVLEQASSHIONSTQATVROAVCH WKVTAFIGNSIVVAQVWEGLMNSCVVOSTGOMCKVYDSLLAL PODLQAARRACCYTALVLVALFSDSDLLEEKKEGLALDHFKKT VLTSGIVTELISGJTETLIJVVCAGASSHIONSTQATVROAVCH MKVTAFIGNSIVVAQVWEGLMNSCVVOSTGOMCKVYDSLLAL PODLQAARRACCYTALLVLVALFGLVVLAGSSHIONSTQATVROAVCH WKVTAFIGNSIVVAQVWEGLMNSCVVOSTGOMCKVYDSLLAL VLTSGIVFUSGVLTILIPVCWTAHAVTRDFYNPLVAREAGKRIGA ASLYLGMAASGLLLLGGGLLCCCTCSGGSGSPSHMARYSTSAP AISRGPSEYPYKNYV AISRGPSEYPYKNYV THYENAGGLUGCCTCTSGGSGSPSHMARYSTSAP AISRGPSEYPYKNYV THYENAGGLUGCCTCTSGGSGSPSHMARYSTSAP AISRGPSEYPYKNYV THYENAGGLUGCCTCTSGGSGSPSHMARYSTSAP THOSUSDPSKANGALLLALDYFSLERALAPLPEKPGAVPDPOCKRAKVAK DLNDGVKKNSBLALLALDYFSLERALAPLPEKPGAVPDPOCKRAKVAK THYENAGGLUGCTATGTGGTGCTGCTGSGFHTMATYSTSAP THYENAGGLUGCTATGTGTGTGTTTTWAGAGGGGTTGTTTATTTATTATTATTATTATTATTATTAT	6652	2	1343	IPGSTISCSCHSRRLRGGSPAPRLSLGAASPRPRPPSLPLPLPL
TCDSFKISHENDSKSKDRITHYPILDINKENNISSKEPKHRUPT KLWAKAVPLPHYRGHHEIGSPRETYTWAVGTASKUPGDIYVOSE MSEIISPCTADYSKYRLTOLLEKABVINGEMLKFSVYSTROGKE YPFDYREHHGNAMQPSVKDNSGSHGSPISGKLEGIFFSCSTEPN TGRPPODSPYGRTRFEIAARKLFNNYNLIPGDPYCMYTAHNY IIVIAPVGSPODSPYGRTRFEIAARKLFNNYNLIPGDPYCMYTAHNY IIVIAPVGSPODSPYGRTRFEIAARKLFNNYNLIPGDPYCMYTAHNY IIVIAPVGSPODSPYGRTRFEIAARKLFNNYNLIPGDPYCMYTAHNY IIVIAPVGSPODSPYGRTRFEIAARKLFNNYNLIPGDPYCMYTAHNY IIVIAPVGSPODSPYGRTRFEIAARKLFNNYNLIPGDPYCMYTAHNY IIVIAPVGSPODSPYGRTRFEITHAGKELSTIAMGKKUPSCKT CNISVGR 6653 170 1910 PFLEPRLRFFFASRRFVPARTRFSPLHPCCFCFEGGGSMLSPQ RVAAAASRGADDAMESSKPGPVQVVLVQKDGHSFELDEKALASI LLQHTRIDLDVVVSVAGARFKGKSFILDFMKTJASGKKVA VULMDTQGAFSSGSTVENGAKSKSFILDFMKTJASGKKVA VULMDTQGAFSSGSTVENGATTALSIATHSVOJVNILSQNIGGED DLQOLQLPTEVGRLANDEIFCKFPGTIMPILVRDMSPFYESVGL QCGMAFLDKRILQVERGHGEERDWARHHISESVJOYNLISANDISON SKVTCKGLLEFFRGYIKITYGGEDLPHFKSMLGATAGANIAAAA SAKDIYYNNHESVCGGERPTISDDILEEKEKGIALDHFKKT KRMGGKDFSFRYQGBLBEEIKELYBPICHKNGSKNVESTFRTPA VLFTGIVALIYASGLTGFILGEVVAQLFMCMVGLLLIBLTMGY IRYSGGYRELGGAIDFGAAVULEQASSHIGNSTQATVRDAVVGR PSMMKKAQ 6654 1 705 RTSLSPSQCSSFNLAMASAGMQILGVVLTILLGWVNGLVSCALPM WVTAFIGNS IVVAQVWEGLENKSCVVOSTGOMQCKVYDSLLAL PODLQAARALCVIALLVALFGLLVTLABARCTTCVEKINSKARL VLTSGIVPFILGSVLTLIPVCVAHAAVIRGPVARAQKERGLA ASIVLGMAASGLLLLGGGLLCCTCPSGGSQGPSHYMARYSTSAP AISRGPSEYPTKNV 4 KNAMPKKGLLATALVALFGLLVYLAAGARCTTCVEKINSKARL VLTSGIVPFILGSVLTLIPVCVAHAAVIRGPVARAQKERGLA ASIVLGMAASGLLLLGGGLLCCTCPSGGSQGPSHYMARYSTSAP AISRGPSEYPTKNV 6655 2 1212 RELSPRANLAIGPBLAGGLARGKVCVOSTGEPPBSMRKICKSC CKSCEDHCLTSDLEDDRXIGKLLMDSKYSTLTARVKGGGGIRIY KRNMMINTBIATAGKDPTPTTYRWAPPOVYLARAQKGRCLIFI KRNMMINTBIATAGKDPTPTTYTRWAPPOVYLARAQKGRCLIFI KEKOPVTCTECAFYRRRQLMROPPTYTRWAPPOVYSDRAGYMKOMHP TCFVCAKCSEPILVDLIYPMCDGAPMCGRYYCESLEYRGGDLI IFRADTQRVKMSLGOLGARGTGGGGGGCPERGBATTAG TTNGSLSDPSKEVEYVCHLCKGRAPPOSPVVYSDRAGYMKOMHP TCFVCAKCSEPILVDLIYPMCDGAPMCGRYYCESLEYRGHMINGHT TCFVCAKCSEPILVDLIYPMCDGAPMCGRYYCESLUKSHWEW VPPREVOPPLEDGTFSTHMMCHGLIAVHVTROTYDFVCSP LEGHTQODLINLTQGDFKKPPLCRVSSDNOQALLDMETILMEH HLEHMNGHGARGHLINGTDTTJFDSSFSTKIKH		1		PFPLFLPTRPAERAWIRSRRASEWVGKMEVPRLDHALNSPTSPC
KLUAKAVPLEMTVSKRULTOLLERABVIORGENIK, KEVEYPYRNÖKKE WSETISPCTADYSKRULTOLLERABVIORGENIK, KEVEYPYRNÖKKE YPTOYVREHHGNAMQPSVKDNSGSHGSPISGKLEGIFFSCSTEPN TGKPPQDSPYGRYRFEIAAEKLENINYTNLIFFGDYCMYTHAHYV ILVIAPVOS PEDEPKCQRLEQUINSKONFLITCTEEDGULVYHHA QDVILEVIYTDPUDLSLGTVAETTHOLMSLSTANAKAPSCKT CNISVGR		1		EEVIKNLSLEAIQLCDRDGNKSQDSGIAEMEELPVPHNIKISNI
MSELIEPCTADYSKVELTQLEKRABVLAGEMLKPSVEYRNQHKE YPDVVEHHRAMMOPSVKINSGSHOSPISCHE FPSCSTEP M TGKPPODSPYGRYFEIAAEKLFNPNTNLYFGDFYCMYTAYHYV IIVIAPVGSPODSPYGRYFEIAAEKLFNPNTNLYFGDFYCMYTAYHYV IIVIAPVGSPODSPYGRUPGLINSKONKFLTCTEEDGULYHHA QDVILEVYTTPVDUSLSLTVAGEMLETTHAGMSLSTANAKKADPSCKT CNISVGR 170 1910 PFLEPELRFPFASRAFVPARTRPSPLHPCCFCFEGGGSMLSPQ RVAAAASRGADDAMESSKPGPVQVVLVQKDQHSFELDEKALASI LLQDHTRDLDVVVVSVGASRFKGKSFILDFMYYSGKESGKS NKLGDPEBPLTGFSMRGGSDPETTGIQTMSEVFTVEKPGGKVA VVLMDTOGAFISOSTYNCATIFALSITMTSVJGYNGSKOS UNLDDEBPLTGFSMRGGSDPETTGIQTMSEVFTVEKPGGKVA VVLMDTOGAFISOSTYNCATIFALSITMTSVJVINLSONIOGD DLQQLQLPTEVGRLANDEIPCKFPGTUTMPLVRDMSFPYEYSGL QGGMAFLDKRIQVENGHGEISTGAVKNHTHASFVJVINLSONIOGD DLQQLQLPTEVGRLANDEIPCKFPGTUTMPLVRDMSFPYEYSGL QGGMAFLDKRIQVENGHGEISTGAVRNHTHASFYTSYSGL QGGMAFLDKRIJVSHENGUSPTRAJVINLSDAMSFPYEYSGL QGGMAFLDKRIJVSHENGUSPTRAJVINLSDAMSFPYEYSGL QGGMAFLDKRIJVSHENGUSPTRAJVINLSDAMSFPYEYSGL QGGMAFLDKRIJVSHENGUSPTRAJVINLSDAMSFPYEYSGL QGGMAFLDKRIJVSHENGUSPTRAJVINLSDAMSFPYEYSGL QGGMAFLDKRIJVSHENGUSPTRAJVINLSDAMSFPYETSYGL QGGMAFLDKRIJVSHENGUSPTRAJVINLSDAMSFPYETSYGL QGGMAFLDKRIJVSHENGUSPTRAJVINLSDAMSFPYETSYGL LOVATSPDFDGKKAQ SKYTCKGLLEFTRAJVINLSGALFFRANKANAL SKATUTANSGLIPSTRADA SANDIYNMBEVCGGERPTISDTLEERICHFRQASKARL VLTGGTUPFI JASGLTGTIGGAVUTLELGWVAGLFRANGSLLLLIGWTGLIDVSALDAM VVATSTIGNS IVVAQVVWEGLENGANSCVVOSTGOMGCKVYDSLLAL PODLQAARALCVIALLVALFGLLVTLAAGAKCTTCVEEKSKARL VLTGGTUPFI JASGLTGTLAGVAGAKELLESMA TVATSGUSPTRVYV KRAMPAKKGLALALAVFSLPVFAAEHNIDVRVPEQYQQEHVQGA AINFLKEVSERTATAVPOKADTVKVYCAAGROSGGAKELLESMA TVATSGUSPTRVAVY 6655 341 16 KDAYMFKKGLLALALVFSLPVFAAEHNIDVRVPEQYQQEHVQGA INTILKEVSERIATAVPOKADTVKVYCAAGROSGGAKELLESMA TVATSGUSPTRAVVY KRAMPATRAJSGLOGSAGAGAGAGCATGCGGGGGGGGGGGGGGGGGGGGGGGGG	-			TCDSFKISWEMDSKSKDRITHYFIDLNKKENKNSNKFKHKDVPT
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IQVATSPDFDGKLKDIAGGEFK8QLQALIPYTAINPSKLMEKEING SKYTCRGLLEYFRAYIKIYQGBDLPHPKSMLQATAEAYNLAAAA SAKDIYYNNMEVCGGGKPYLESDILEEKHCEFKQLALDHFKKT KKMGGKDFSFRYQOBLEEIKKLYENFCKHNGSKNVFSTFRTPA VLFTGIVALYIASGLTGFIGLEVVAQLFNCMYGLLIALLTWGY IRYSGQYRBLGGAIDFGAAYVLAQASSHIGNSTQATVRDAVVCR FSMDKKAQ 6654 1 705 RTSLSPSQCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM WKVTAFIGNSIVVAQVVWBGLMMSCVVQSTGQMQCKVYDSLLAL PQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARL VLTSGIVFVISGVLTLIPVCWTHAAVIRDFYNPLVAEAQKRELG ASLYLGMAASGLLLLGGGLLCCTCPSGGSQGPSHYMARYSTSAP AISKGPSEYPTKNYV 6655 341 16 KDAYMFKKGLLALALVFSLPVFAAEHWIDVRVPEQYQQEHVQGA INIPLKEVKBRIATAVPDKNDTVKYYCVAGRQSGGAKBILSEMS YTHVENAGGLKDIAMPKVKS 6656 2 1212 TELPPRPANLAIQPFLSPLRALAPLPEKPGAVPPPQKRMAKVAK DLNFGVKKMSLGQLQSARGVACLGCKGTCSGFEPHSWRKICKSC KCSQEDHCLTSDLEDDRKIGRLLMDSKYSTITARVKGGGGIRIY KRNRMIMPNPLATACKDPTFDTTTYEMAPPGVYQKLGLQYMELIP KEKQPVTGTEGAFYRRQLMHQLPTYDQDPSRCRGLLENELKLM EEFVKQYKSBALGYGEVALPGQOGLPKEGKGGTGSGGETTAA TTNGSLDPSKEWEYVCBLCKGAPPDSFVVYSDRAGYNKQWHP TCFVCAKCSEPLVDLIYFMKDGAPWCGRHYCESLRPRCSGCDEI IFABDYGRVEDLAWHRKHFVCEGCEQLLSGRAYIVTKQQLLCPT CSKSKRS 6657 830 2120 LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP LEHFTGGDLINLTQCEDFKKPPLCRVSSDNGGRLDMIETLMMEH HLEAHKNGHANGHLNIGVDIPPDGSFSIKKTPKNGMPHGYRKEM IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER VPPKEVQPPLDFTFPHFNRVQWAFSICEINGMLLVGLMLJQWL LLKKYKSIISRFFCIVGTLIYLTRCTMYTTLPVGMFFNGSPK LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYHMICWLLSVVGIFCILLAHDHYTVDVVV AYYITTRIFFWHYMANQQVLYRASGOMILLARVWYRFFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT	ĺ			DLQQLQLFTEYGRLAMDEIFQKPFQTLMPLVRDWSFPYEYSYGL
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SAKDIYYNNMEEVCGGEKPYLSPDILEEKHCEFKQLALDHFKKT KKMGGKDFSFRYQQBLEEEIKELYENFCKHNGSKNPSTFRTPA VLFTGIVALIYASGLTGFIGLEVVAQLFNCMVGLLITALITWGY IRYSGQYRBLGGAIDFGAAYVLEQASSHIGNSTQATVRDAVVGR FSMKKAQ 6654 1 705 RTSLSPSGCSSFNLAMASAGMQILGVVLTLLGWVNGLVSCALPM WKVTAFIGNSIVVAQVWEGLWMSCVVQSTGQMQCKVYDSLLAL PQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARL VLTSGIVVISGVLTLIPVCTNAHAVIRDFYNDLVABAQKRELG ASLYLGWAASGLLLLGGGLLCCTCPSGGSQGPSHYMARYSTSAP AISRGPSEYPTKNYV 6655 341 16 KDAYMPKKGLLALLVFSLPVFAAEHWIDVRVPEQYQQEHVQGA INIPLKEVKERIATAVPDKNDTVKVYCNAGRQSGQAKEILSEMG YTHHENAGGLKDIAMPKVKG KCSQEDHLTSDLEBDRKIGRLLMDSKYSTLTARVKGGDGIRIY KRNKMIMTNPLATGKDPTPTITTEWAPPGTYQKGLGLYWELIF KEKQPVTGTEGAFYRRQLMHQLPIYDQDPSRCRGLLENELKLM EEFVKQYKSBALGVGEVALPGQGGLPKEGKQGEKPGABTTAA TINGSLSDPSKVEYVCGLCKGAAPPDSPVVYSDRAGYNKQWHE TCFVCAKCSEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI IFAEDYGRVEDLAWHRKHFVCEGCEQLLSGRAYIVTKGQLLCPT CSKSKRS 6657 830 2120 LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP LEHFTGQDLINLTQEDFKKEPLCRVSSDNGGRLDMIETLKMEH HLEAHKNGHANGHLNIGVDIJPTPDGSFSIKIKPNGMPMSYRKM IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER VPPKEVQPPLEDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL LLKKYSIISRRFFCIVGTILYRGITMYVTTLPVPGMHFNCSPK LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYKFICKLSSONNILARAWWYRPFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT				LQVATSPDFDGKLKDIAGEFKEQLQALIPYVLNPSKLMEKEING
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IFAEDYQRVEDLAWHRKHFVCEGCEQLLSGRAYIVTKGQLLCPT CSKSKRS 6657 830 2120 LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLIDMIETLKMEH HLEAHKNGHANGHLNIGVDIPTPDGSFSIKIKPNGMPNGYRKEM IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT				TTNGSLSDPSKEVEYVCELCKGAAPPDSPVVYSDRAGYNKQWHP
CSKSKRS 6657 830 2120 LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLDMIETLKMEH HLEAHKNGHANGHLMIGVDIPTPDGSFSIKIKPNGMPNGYRKEM IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVYHER VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT				TCFVCAKCSEPLVDLIYFWKDGAPWCGRHYCESLRPRCSGCDEI
6657 830 2120 LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLKMEH HLEAHKNGHANGHLNIGVDIPTPDGSFSIKIKPNGMPNGYRKEM IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT				IFAEDYQRVEDLAWHRKHFVCEGCEQLLSGRAYIVTKGQLLCPT
LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLKMEH HLEAHKNGHANGHLNIGVDIPTPDGSFSIKIKPNGMPNGYRKEM IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT				CSKSKRS
LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLKMEH HLEAHKNGHANGHLNIGVDIPTPDGSFSIKIKPNGMPNGYRKEM IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT	6657	830	2120	LLTCQERAGDCLLSASTMKEVVYWSPKKVADWLLENAMPEYCEP
HLEAHKNGHANGHLNIGVDIPTPDGSFSIKIKPNGMPNGYRKEM IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLIAHDHYTVDVVV AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT				LEHFTGQDLINLTQEDFKKPPLCRVSSDNGQRLLDMIETLKMEH
IKIPMPELERSQYPMEWGKTFLAFLYALSCFVLTTVMISVVHER VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT				
VPPKEVQPPLPDTFFDHFNRVQWAFSICEINGMILVGLWLIQWL LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT				
LLKYKSIISRRFFCIVGTLYLYRCITMYVTTLPVPGMHFNCSPK LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT			1	1
LFGDWEAQLRRIMKLIAGGGLSITGSHNMCGDYLYSGHTVMLTL TYLFIKEYSPRRLWWYHWICWLLSVVGIFGILLAHDHYTVDVVV AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT	1			
TYLFIKEYSPRRLWWYHWICWLLSVVGIFCILLAHDHYTVDVVV AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT				
AYYITTRLFWWYHTMANQQVLKEASQMNLLARVWWYRPFQYFEK NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT				1
NVQGIVPRSYHWPFPWPVVHLSRQVKYSRLVNDT				
6658 35 HCCALGAPGSPYRGLYFSSAAPCTAPRKAKHQSTLEGLTKRMLM	L		-	
	6658	35	855	HCCALGAPGSPYRGLYFSSAAPCTAPRKAKHQSTLEGLTKRMLM

		1 8 3 3 3 3 3 3	
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	1
!	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
l	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\-possible nucleotide insertion)
			FDPVPVKQEAMDPVSVSYPSNYMESMKPNKYGVIYSTPLPEKFF
			QTPEGLSHGIQMEPVDLTVNKRSSPPSAGNSPSSLKFPSSHRRA
1			SPGLSMPSSSPPIKKYSPPSPGVQPFGVPLSMPPVMAAALSRHG
			IRSPGILPVIQPVVVQPVPFMYTSHLQQPLMVSLSEEMENSSSS
			MQVPVIESYEKPISQKKIKIEPGIEPQRTDYYPEEMSPPLMNSV
			SPPQALLQE
6659	18	523	EPORGDCETWFONCSLPKFVCFFCWGFWLWRAHSMSNLHSLPGL
			RGLTSISRNQLQCTNAMRVINNYQRRWKNQNTFLLATFANVVNV
1			CGNPTITCPHNRTLNNCHHSGVQVPLMYCNLTTPSPQNISNCRY
1			AQTPANMFYIVACDNRDQRRDPPQYPVVPVHLHTII
6660	514	1707	CAASLDCRHHLCEPDMKLVWPSAKLLQAAAGASARACDSVTSNV
		ļ	LPLLLEQFHKHSQSSQRRTILEMLLGFLKLQQKWSYEDKDQRPL
1			NGFKDQLCSLVFMALTDPSTQLQLVGIRTLTVLGAQPDLLSYED
			LELAVGHLYRLSFLKEDSQSCRVAALEASGTLAALYPVAFSSHL
			VPKLAEELRVGESNLTNGDEPTQCSRHLCCLQALSAVSTHPSIV
			KETLPLLLQHLWQVNRGNMVAQSSDVIAVCQSLRQMAEKCQQDP
E			ESCWYFHQTAIPCLLALAVQASMPEKEPSVLRKVLLEDEVLAAM
			VSVIGTATTHLSPELAAQSVTHIVPLFLDGNVSFLPENSFPSRF
		}	QPFQDGSSGQRRLIALLMAFVCSLPRNVSEHIWEVLLFNLDKVT
ļ			PG
6661	179	430	GVHAASGTLSATWLAEAKMFDSLAKAGKYLGQAAKLMIGMPDYD
ļ			NYVEHMRVNHPDQTPMTYEEFFRERQDARYGGKGGARCC
6662	185	423	RSLPKPAPAQPASIHCARFSGVTPPTAKTAMSDGNTAFNALMYC
			GPKADDGNIFSACAPASSAVKASVSVAQPGQAVIP
6663	3	1005	RPVLSSRVDDFVPPLPETSGRRKKLERMYSVDRVSDDIPIRTWF
ļ			PKENLFSFQTASTIMQAISNFRKHLRMVGSRRVKAQTFAERRER
ļ			SFSRSWSDPTPMKADTSHDSRDSSDLQSSHCTLDEAFEDLDWDT
Ì			EKGLEAVACDTEGFVPPKVMLISSKVPKAEYIPTIIRRDDPSII
			PILYDHEHATFEDILEEIERKLNVYHKGAKIWKMLIFCQGGPGH
ļ			LYLLKNKVATFAKVEKEEDMIHFWKRLSRLMSKVNPEPNVIHIM
			GCYILGNPNGEKLFQNLRTLMTPYRVTFBSPLELSAQGKQMIET
			YFDFRLYRLWKSRQHSKLLDFDDVL
6664	58	968	PRLLRLPRSVVVMDSPWDELALAFSRTSMFPFFDIAHYLVSVMA
1			VKRQPGAAALAWKNPISSWFTAMLHCFGGGILSCLLLAEPPLKF
	1		LANHTNILLASSIWYITFFCPHDLVSQGYSYLPVQLLASGMKEV
}	1		TRTWKIVGGVTHANSYYKNGWIVMIAIGWARGAGGTIITNFERL
			VKGDWKPEGDEWLKMSYPAKVTLLGSVIFTFQHTQHLAISKHNL
			MFLYTIFIVATKITMMTTQTSTMTFAPFEDTLSWMLFGWQQPFS
			SCEKKSEAKSPSNGVGSLASKPVDVASDNVKKKHTKKNB
6665	171	1278	DERRLACROVVTQQRSELYPGFQKRQRFLPKAGEEAAAQGGRHL
			PGRWLGPGCTQNPCSVHTATGPEPRKLPLLPPDSPNSGYPKEPA
			ALCPGIPSPCRMTHQDLSITAKLINGGVAGLVGVTCVFPIDLAK
1		1	TRLONOHGKAMYKGMIDCLMKTARAEGFFGMYRGAAVNLTLVTP
			EKAIKLAANDFFRRLLMEDGMQRNLKMEMLAGCGAGMCQVVVTC
			PMEMLKIOLODAGRLAVHHOGSASAPSTSRSYTTGSASTHRRPS
		1	ATLIAWELLRTQGLAGLYRGLGATLLRDIPFSIIYFPLFANLNN
			LGFNELAGKASFAHSFVSGCVAGSIAAVAVTPLDVLKTRIQTLK
			KGLGEDMYSGITDCAR
6666	498	2868	MTTFLPVPOMMAGFSFGTFGNPPMESPSAWOTIHOPFIVSCLTL
""	1 200		WSPGCWPOPIQKEGVGLWDIRKPQSSLLRYGGNLSLQSAMSVRF
			NSNGTQLLALRRRLPPVLYDIHSRLPVFQFDNQVYFNSCTMKSC
			CFAGDRDOYILSGSDDFNLYMWRIPADPEAGGIGRVVNGAFMVL
1			KGHRSIVNQVRFNPHTYMICSSGVEKIIKIWSPYKQPGCTGDLD
			GRIEDDSRCLYTHEEYISLVLNSGSGLSHDYANQSVQEDPRMMA
			FFDSLVRREIEGWSSDSDSDLSESTILQLHAGVSERSGYTDSES
			SASLPRSPPPTVDESADNAFHLGPLRVTTTNTVASTPPTPTCED
L	<u> </u>		OUR TENT AND OUR THAT I THE TANK A LITTLE OF THE TA

SĒQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
110.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	sequence	\=possible nucleotide insertion)
	sequence		AASROORLSALRRYODKRLLALSNESDSEENVCEVELDTDLFPR
			PRSPSPEDESSSSSSSSSSSEDEELNERRASTWORNAMRRROKT
			TREDKPSAPIKPTNTYIGEDNYDYPQIKVDDLSSSPTSSPERST
			STLEIQPSRASPTSDIESVERKIYKAYKWLRYSYISYSNNKDGE
			TSLVTGEADEGRAGTSHKDNPAPSSSKEACLNIAMAQRNQDLPP
		Í	
			EGCSKDTFKEETPRTPSNGPGHEHSSHAWAEVPEGTSQDTGNSG
			SVEHPFETKKLINGKALSSRAEEPPSPPVPKASGSTLINSGSGNCP
			RTQSDDSEERSLETICANHNNGRLHPRPPHPHNNGQNLGELEVV
			AYSSPGHSDTDRDNSSLTGTLLHKDCCGSEMACETPNAGTREDP
			TDTPATDSSRAVHGHSGLKRORIELEDTDSENSSSEKKLKT
6667	171	1310	ABEVERLAAMRSDSLVPGTHTPPIRRRSKFANLGRIFKPWKWRK
			KKSEKFKHTSAALERKISMROSREELIKRGVLKEIYDKDGELSI
	i		SNEEDSLENGQSLSSSQLSLPALSEMEPVPMPRDPCSYEVLQPS
			DIMDGPDPGAPVKLPCLPVKLSPPLPPKKVMICMPVGGPDLSLV
			SYTAQKSGQQGVAQHHHTVLPSQIQHQLQYGSHGQHLPSTTGSL
			PMHPSGCRMIDELNKTLAMTMQRLESSEQRVPCSTSYHSSGLHS
i			GDGVTKAGPMGLPEIRQVPTVVIECDDNKENVPHESDYEDSSCL
		*	YTREEEEEEBDEDDDSSLYTSSLAMKVCRKDSLAIKPSNRPSKR
			ELEEKNILPROTDEERLELROOIGTKL
6668	714	358	TLAVATGPALTLRCHVCTSSSNCKHSVVCPASSRFCKTTNTVEP
			LRGNLVKKDCAESCTPSYTLQGQVSSGTSSTQCCQEDLCNEKLH
			NAAPTRTALAHSALSLGLALSLLAVILAPSL
6669	459	1207	KDEETRKDYDYMLDHPEEYYSHYYHYYSRRLAPKVDVRVVILVS
	1		VCAISVFQFFSWWNSYNKAISYLATVPKYRIQATEIAKQQGLLK
	ļ	1	KAKEKGKNKKSKEEIRDEEENIIKNIIKSKIDIKGGYQKPQICD
1			LLLFQIILAPFHLCSYIVWYCRWIYNFNIKGKEYGEEERLYIIR
	1		KSMKMSKSQFDSLEDHQKETFLKRELWIKENYEVYKQEQEEELK
			KKLANDPRWKRYRRWMKNEGPGRLTFVDD
6670	184	594	VARI+GEAAKMSSEPPPPYPGGPTAPLLEEKSGAPPTPGRSSPA
			VMQPPPGMPLPPADIGPPPYEPPGHPMPQPGFIPPHMSADGTYM
1			PPGFYPPPGPHPPMGYYPPGPYTPGPYPGPGGHTATVLVPSGAA
			TTVTV
6671	1	763	LPAEKPRSAPNMAGGRCGPQLTALLAAWIAAVAATAGPEEAALP
1	_		PEQSRVQPMTASNWTLVMEGEWMLKFYAPWCPSCQQTDSEWEAF
1			AKNGEILQISVGKVDVIQEPGLSGRFFVTTLPAFFHAKDGIFRR
			YRGPGIFEDLONYILEKKWOSVEPLTGWKSPASLTMSGMAGLFS
İ			ISGKIWHLHNYFTVTLGIPAWCSYVFFVIATLVFGLSMDLVL*V
			ISOCNWDPPYRHVS*/RPSTNLGVHTAHTSEHLRL
6672	304	1089	APGSKPVQFMDFEGKTSFGMSVFNLSNAIMGSGILGLAYAMAHT
55,2			GVIFFLALLCIALLSSYSIHLLLTCAGIAGIRAYEQLGQRAFG
1			PAGKVVVATVICLHNVGAMSSYLFIIKSELPLVIGTFLYMDPEG
			DWFLKGNLLIIIVSVLIILPLALMKHLGYLGYTSGLSLTCMLFF
			LVSVIYKKFQLGLCYRATMKQQWESEALVGTPQPRDSTAAVKAQ
			MFHS*LTGVLTQWPIMAFAFVCHPGGAGPSITELCRAFQAQD
6673	1116	1963	LQIQTHHTHHGARVTHLGSHQLLANAGTMLCRQQSSSMAPAFSQ
00/3	1110	1303	SVTCGPSPCVRKOESATKCLHIGACGSDLWARGWEQG*G*GLNV
			WLCPCVAFHRGARPQAEEGGARWNSLVSSPWIPPNP*HSSIGAE
1			
1			NAVPRP*QG*KVNPSGQERQS\WVLPLPVPGEPLKLPGLPG*NK
			SFSRV/SGSKGKWILPRQLM*AS*R\TPRFVPGTQWVPITW/PL
}			ITWH*SAPTPPLKACPAPRPSDPCSSCLSCPCVTQHPRFSDTGW
			FGAGHCHSSCDFTRKGAAGGPG
6674	1	440	LEFDYMCQYDYVEVRDGDNRDGQIIKRVCGNERPAPIQSIGSSL
Į	1	1	HVLFHSDGSKNFDGFHAIYEEITACSSSPCFHDGTCVLDKAGSY
1	1	1	KCACLAGYTGQRCENLLEERNCSDPG/WPSQWVPENNRGPWAYQ
Ì	}	l.	PTPC*IGTRVAFFLT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	1	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		\=possible nucleotide insertion/
6675	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
			LEKIHPPSMPGDSGSBIQGSNGETQGYVYAQSVDITSSWDFGIR
]	RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
	1		KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
		İ	GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
	1		YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
		1	GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
			KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
		İ	KETDERAVARRAGSQRVSGSRADGVI EEDGQIDIMI VQDIIDGII
	İ		HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
			ADTWRQEQIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
			KASTKFWIKQKPISIDSDLLCAC\DLAEE
6676	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
5378	1		LEKIHPPSMPGDSGSEIOGSNGETQGYVYAQSVDITSSWDFGIR
1		ļ	RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
1	1		KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
			GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
	Į.	}	YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNEPIHKF
ĺ			YTSEGREPALNONVSAICDNIABODGEVOIDI FI DOONDI TIMA
			GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
	1		KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
l			HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
	i	i	ADTWRQEQIGCCGAACAALRS+DSHKC+EGISGDKVEIDPVTNQ
ļ			KASTKFWIKQKPISIDSDLLCAC\DLAEE
6677	277	1678	GNWPTERMAFLDNPTIILAHIRQSHVTSDDTGMCEMVLIDHDVD
6677	277	1070	LEKIHPPSMPGDSGSEIQGSNGETQGYVYAQSVDITSSWDFGIR
	1	ì	RRSNTAQRLERLRKERQNQIKCKNIQWKERNSKQSAQELKSLFE
l			KKSLKEKPPISGKQSILSVRLEQCPLQLNNPFNEYSKFDGKGHV
1			GTTATKKIDVYLPLHSSQDRLLPMTVVTMASARVQDLIGLICWQ
			GTTATKKIDVYLPLASSQDRLLPMIVVIPASARVQDDIGDICAQ
1		1	YTSEGREPKLNDNVSAYCLHIAEDDGEVDTDFPPLDSNBPIHKF
			GFSTLALVEKYSSPGLTSKESLFVRINAAHGFSLIQVDNTKVTM
			KEILLKAVKRRKGSQKVSGSRADGVFEEDSQIDIATVQDMLSSH
1			HYKSFKVSMIHRLRFTTDVQL/GCALFPGVLRKRAAPVDCLRPS
	1	Į.	ADTWROEOIGCCGAACAALRS*DSHKC*EGISGDKVEIDPVTNQ
			KASTKFWIKQKPISIDSDLLCAC\DLAEE
		865	GPSNQSSGSLSLIVTGCSSYWS*INDTCTILRVLSSNFGRQ*LR
6678	221	1 005	PFPCSQLPMSQGCLWHLDCCCPWVPYIPGQQWRKGRQRMRN*QS
			LLGSDQESVGLEDLCVFVNFLLHVLLGLFP*PHELFLLPVVDLG
	1		FLFPLLLQGGCHCLVLPANLVSQAPQIGKLSCRLQTHDLEGSRN
			FPRAPPPOGGCHCPAPAMPASOWA TOWNSOWED LINDS
	1		HHPLFLVVGRWDAVKHLETVQSGLASLGFVGQHTSHGPP
6679	2	786	LEFARGAMPFLGQDWRSPGQNWVKTVDGWKRFLDEKSGSFVSDL
	1	1	SSYCNKEVYNKENLFNSLNYD/SCSQEEKEGHAE*QNQNS\DFH
			QEKWIYVHKGSTKERHGYCTLGEAFNRLDFSTAILDSRRFNYVV
1	1		RLLELIAKSOLTSLSGIAQKNFMNILEKVVLKVLEDQQNITLIR
l			ELLQTLYTSLCTLVKRVGKSVLVGNINMWVYRMETILHWQQQLN
	1	1	NIQITRVSGQAQPPPGSGSLHRDTGQTRQDFEFTPVTEESGLF
			PLCTLPLMPSALPGWAGERWEKQWPLA/PGPGTWQTPVGSISEE
6680	1498	2951	P\RKNEPDTHCPRGEAR PEV*HLPKPHSPGSEGAEIQTSA*ALP
			F /KWATATUCKGOWKADA - UDAKAMTAGORGWI ATAW WATA
1			/NOVSPPOPM*GAEENGDQRGGKERAGEELHRSSSGLTAAPGFP
			EVHRNLQTFPGLPSRGGGP/GGAGTQGSWAPGEQPP/SPLLPAS
			MORSQAGLPGWEAGLVESPTHHIPALRPSGTNATGEAFPSTTCS
			SGP\PAPPGPTGLRPGGGSSSGGHG**PGLPVGKV\GALGAAQD
			POSOGRGPTOGTVGTEMLLSGLGSAKACPAARPAVP*LPSDPAS
			TIPKKGTRGFGEGPGVLQERNRWVVGRAQGFTSADAAGTAPPGV
1			*LPAPLSQPPGATEPQVRACGMAPPSPGTSGRLVAWGRHPGPQV
1			AQGCPPGAGCWGSQPRGSQRCPRTYTHSPLGHGRAPCPRRCWH*
1			AUGCEPGAGCWGSQFKGSQKCFKIIINSFLGNOKAFCFKKCWA
	1		WODPPSSPRTGCLPGIPARQAYSAPRTRSRPGIRTGRAAYGFIR
			FQGGGGG

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
l	amino acid	residue of	S=Serine, T=Threonine, V=Valine, .
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
6681	1169	511	INYIYYNQQQRAFHELK\EKLMSAPALGLPDLTKLFTLHVSERE
			KMTVGVLTQTVGPWSRPGAYLSKQLDGVSKGWPPCPRALAATAL
i	1		LAQEADELTLRQNLNRKSPHA\VVTLINTKGHH*LINARLTRYQ
1			TLLCENPHKTIEVSNT/LNPATLLLVTESPVKHNCLEVLDSVYS
			SRPNLRDHP*TSVDWELYVDGSGFANPCKVTLKKETSPAPVTPR
1			S
6682	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
1			VRRRIELIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
			YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIEFHSQSG
		1	FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
	1	1	PLQTDAABNNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL
			D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
1			DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK
1		1	NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
	<u> </u>		GPAPRWCSFLDNLTBELEENPBSNE
6683	109	1238	TVLCGAMQVSSLNEVKIYSLSCGKSLPEWLSDRKKRALQKKDVD
		:	VRRRIELIQDFEMPTVCTTIKVSKDGQYILATGTYKPRVRCYDT
			YQLSLKFERCLDSEVVTFEILSDDYSKIVFLHNDRYIBFHSQSG
1			FYYKTRIPKFGRDFSYHYPSCDLYFVGASSEVYRLNLEQGRYLN
1			PLQTDAAENNVCDINSVHGLFATGTIEGRVECWDPRTRNRVGLL
1			D\AP*TVSQQIQR*TSLPTISALKFN\GALTMAVGTTTGQVLLY
			DLRSDKPLLVKDHQYGLPIKSVHFQDSLDLILSADSRIVKMWNK NSGKIFTSLEPEHDLNDVCLYPNSGMLLTANETPKMGIYYIPVL
1			
6684	123	527	GPAPRWCSFLDNLTEELEENPESNE GLRGGTSRGRAGREPEFAAGVLCVVAGFCQSPCPPGGRGREAPA
0004	111	""	PP\SGRRHA*RPA*WLGGPGGDSGREEGGS/GELQRAMESKMG
			ELPLDINIQEPRWDQSTFLGRARHFFTVTDPRNLLLSGAQLEAS
		1	RNIVONYR
6685	258	1473	KLLGDNFEGFCNKFELSDSENGSNS*QSPL\FDRLFDPDPQKVL
*****	250		OGVIDMKNAVIGNNKOKANLIVIGAVPRLLYLLOOETSSTELKT
			ECAVVLGSLAMGTENNVKSLLDCHIIPALLQGLLSPDLKFIEAC
1		1	LRCLRTIFTSPVTPEELLYTDATVIPHLMALLSRSRYTQEYICQ
		1	IFSHCCKGPDHQTILFNHGAVQNIAHLLTSLSYKVRMQALKCFS
		1	VLAFENPQVSMTLVNVLVDGELLPQIFVKMLQRDKPIEMQLTSA
1		1	KCLTYMCRAGAIRTDDNCIVLKTLPCLVRMCSKERLLEERVEGA
]	ETLAYLIEPDVELQRIASITDHLIAMLADYFKYPSSVSAITDIK
			RLDHDLKHAHELRQAAFKLYASLGANDEDIRKKVSLGEGRPPVL
			TASRQGVTST
6686	310	927	DSVTFDDLAVDFTPKEWTLLDPTQRNLYRDVMLENYKNLATVGY
1			QLFKPSLISWLEQEESRTVQRGDFQASEWKVQLKTKELALQQDV
1		1	LGEPTSSGIQMIGSHNGGEVSDVKQCGDVSSEHSCLKTHVRTQN
1	1		SENTFECYLYGVDFLTLHKKTSTGEQRSVFSHVWKKPSSLNPDV
			VCQKNRCTRKKKAF*LQLTLGKSFH*SIHT
6687	181	915	EAMLEAPYKKEEDEQQRKEVKKDYPSNTTSSTSNSGNETSGSST
		1	IGETSNRSRDRDRYRRRNSRSRSPGRQCRHRSRSWDRRHGSESR
			SRDHRREDRVHYRSPPLATGEPVDNLSPEERDARTVFCMQLAAR
1			IRPRDLEDFFSAVGKVRDVRIISDRNSRRSKGIAYVEFCEIQSV
			PLAIGLTGQRLLGVPIIVQASQAEKNRLAAMANNLQKGNGGPMR
	100-		LYVGSLHFNITEDMLRGIFEPFGKV
6688	1025	1	AEVPNYPRVFHKCPDSCWRFKFQPIQLQPYILLSFSSEKPPISF
		1	SEPGLPR/SATARMATAAAPPNSSIDLPSDSGMGFISPAGDSLD
		1	LPSDGGTGFFSLAGDSSSTRLSSLAFISFSLSSVSVGSSAGTTS
		1	STSVGSVVAAFTSSSSSSTNRDVAGLDFSTVITSVSGSLVPSRE
			VAVICGSKGAGASGSASCSSRAGKTTRATAASSMPSGTSSFSTC
			TMSELEELFSLPSPAPILISKLFTSSGSIAICCQDSGPSDTGRLS
L	L	1	VCQLWLADSDTGKLSDCQEVVTVGDSGGLTCPELSLGRM*MSLL

	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ		nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location		H=Histidine, I=Isoleucine, K=Lysine,
1		corresponding to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first	residue of	S=Serine, T=Threonine, V=Valine,
1 1	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	residue of	•	Codon, /=possible nucleotide deletion,
! !	amino acid	sequence	\=possible nucleotide insertion)
	eedneuce		SSAVIPGYSSSDSRLNTVPTVDLLCPFOTKSST
6689	640	1299	SSSASYATSATSISDTAFSGSLKLKHGLLSALDSSSRTS*STSS
			AEDSTFRICSPSVSDTSSDSSGSKDNVLILFSKVSI*SCFSLSS
			FFSDSISFCFSSSSFCKR*FVSSKVSQNALLSSRLSNGPGGSSK
1			QRNSLTARQLAMSL*ATKF*RNACNPNCLSSKKSAL*LSLNQRF
1			GGSASRKPGNISFNSQKCSALSYCCNFVIKPREVSVSSENYPAF
6690	1	442	GTRGKMAATLGPLGSWQQWRRCLSARDGSRMLLLLLLLGSGQGP
ļ		:	QQVGAGQTFEYLKREHSLSKPYQGVGTGSSSLWNLMGNAMVMTQ
			YIRLTPDMQSKQGALWNRVPCFLRDWELQVHFKIHGQGKKNL\H
	ł		GDGLAIWYTKDRMQP
6691	287	1401	LKTETSEBKARRYKDRPSQLNAVFQEQKKMIQAQESITLEDVAV
		J	DFTWEEWQLLGAAQKDLYRDVMLENYSNLVAVGYQASKPDALFK
		1	LEQGEQLWTIEDGIHSGACSDIWKVDHVLERLQSESLVNRRKPC
			HEHDAFENIVHCSKSQFLLGQNHDIFDLRGKSLKSNLTLVNQSK
	İ	1	GYEIKNSVEFTGNGDSFLHANHERLHTAIKFPASQKLISTKSQF
			ISPKHQKTRKLEKHHVCSECGKAFIKKSWLTDHQVMHTGEKPHR
į į			CSLCEKAFSRKFMLTEHQRTHTGEKPYECPECGKAFLKKSRLNI
	1		HQKTHTGEKPYICSECGKGFIQKGNLIVHQRIHTGEKPYICNEC
]		/GKGFIQKTCLIAHQRFHTER
6692	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE
			RQEGHSQGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
			DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
			IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
			DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
			SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
6693	178	939	WIKEGELSLWERFCANIIKAGPMPKHIAFIMDGNRRYAKKCQVE
1			ROEGHSOGFNKLAETLRWCLNLGILEVTVYAFSIENFKRSKSEV
1			DGLMDLARQKFSRLMEEKEKLQKHGVCIRVLGDLHLLPLDLQEL
ł			IAQAVQATKNYNKCFLNVCFAYTSRHEISNAVREMAWGVEQGLL
1		1	DPSDISESLLDKCLYTNRSPHPDILIRTSGEVRLSDFLLWQTSH
ŀ			SCLVFQPVLWPEYTFWNLFEAILQFQMNHSVLQK
6694	292	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR
			EVHSLGQILPQDGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
			LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
1			NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
6695	292	813	SLLLHLAPPGAYTPSQPLSSVSTETASSVRRQAAESRQHELPVR
""		1	EVHSLGOILPODGLTAEAGPPEAQDPWGSPGISLPAAHIGFAAA
			LAVGPSGCHTEP\FDEVWPSLFLGDAYAARDKSKLIQLGITHVV
1			NAAAGKFQVDTGAKFYRGMSLEYYGIEADDNPFFDLSVYFLP
6696	1	782	PRVRGRVGERWAFLSVPAAMSSEMEPLLLAWSYFRRRKFQLCAD
0030	1	, 52	LCTOMLEKSPYDQAAWILKARALTEMVYIDEIDVDQEGIAEMML
			DENAIAQVPRPGTSLKLPGTNQTGGPSQAVRPITQAGRPITGFL
1			RPSTOSGRPGTMEQAIRTPRTAYTARPITSSSGRFVRLGTASML
			TSPDGPFINLSRLNLTKYSQKPKLAKALIEYIFHHENDVKTALD
1			LAALSTEHSQYKDWWWK/DQIEKCYYRVGMYRBAEKQIKSS
6607		782	PPLFLRRLNSRALRPGSRKVMAVVPASLSGQDVGSFAYLTIKDR
6697	3	104	IPOILTKVIDTLHRHKSEFFEKHGEEGVEAEKKAISLLSKLRNE
			LOTDKPFIPLVEKFVDTDIWNQYLEYQQSLLNESDGKSRWFYSP
			WLLV/ECYMYRRIHEAI/IQSPPIDYFDVFKESKEQNFYGSQES
			IIALCTHLQQLIRTIEDLD\ENQLKDEFFKLLQISLWGEISVDL
	1		SL\SGGESSQNTNVLNSLEDLKPFILLNDMEHLWSLLSNCK
1		1	I SP/SCOESSSONINA PUSTENDY LA I DENOMEMPASTISMON
6698	668	754	VGSCACAGSCKCKECKCTSCKKSECRAFP
6698	668	754 492	VGSCACAGSCKCKECKCTSCKKSECRAFP EGELP/PARRVLPRAMTASAQPRGRRPGVGVGVVVTSCKHPRCV
	·		VGSCACAGSCKCKECKCTSCKKSECRAFP

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
110.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
	bequeen		ESKRIIYNHAFFFQESKWSGGILQ
6700	1098	1392	TOCWRSSTPGMRTHFRTQP/RLECGQGFSQQENGHCMDTNECIQ
6700	1050		FPFVCPRDKPVCVNTYGSYRCRTNKKCSRGYBPNEDGTACVERT
	L		LLIGLCNLIGK
6701	2	1485	AAAGPRTRVRRAAAFEGQPSPSPGLGPTSDKAAAAPRTPKRRRLW
			RQRQ/HPAMLCYVTRPDAVLMEVEVEAKANGEDCLNQVCRRLGI
			IEVDYFGLQFTGSKGESLWLNLRNRISQQMDGLAPYRLKLRVKF
			FVEPHLILQEQTRHIFFLHIKEALLAGHLLCSPEQAVELSALLA
			QTKFGDYNONTAKYNYEELCAKELSSATLNSIVAKHKELEGTSQ
			ASAEYQVLQIVSAMENYGIEWHSVRDSEGQKLLIGVGPEGISIC
		1	KDDFSPINRIAYPVVQMATQSGKNVYLTVTKESGNSIVLLFKMI
		1	STRAASGLYRAITETHAFYRCDTVTSAVMMQYSRDLKGHLASLF
			LNENINLGKKYVFDIKRTSKEVYDHARRALYNAGVVDLVSRNNQ
		1	SPSHSPLKSSESSMNCSSCEGLSCQQTRVLQEKLRKLKEAMLCM
			VCCEBEINSTFCPCGHTVCCESCAAQLQVGESAAHFCLQPHLSL
			LLTGSRSQVLAR
6702	397	1971	PLAKFLKLDLVNVLCLPMEDVFLFYRTCFCSMGLGSSCHLSLPK
			RAEALLCSRKATVVRDLVAVRMAEEQEFTQLCKLPAQPSHPHCV
			NNTYRSAQHSQALLRGLLALRDSGILFDVVLVVEGRHIEAHRIL
			LAASCDYFKGMFAGGLKEMEQEEVLIHGVSYNAMCQILHFIYTS
		4	ELELSLSNVQETLVAACQLQIPEIIHFCCDFLMSWVDEENILDV
			YRLAELFDLSRLTEOLDTYILKNFVAFSRTDKYRQLPLEKVYSL
			LSSNRLEVSCETEVYEGALLYHYSLEQVQADQISLHEPPKLLET
		ì	VRFPLMEAEVLQRLHDKLDPSPLRDTVASALMYHRNESLQPSLQ
			SPOTELRSDFQCVVGFGGIHSTPS\MSSATRPKYLNPLLGEWKH
			FTASLAPRMSNQGIAVLNNFVYLIGGDNNVQGFRAESRCWRYDP
		ļ	RHNRWFQIQSLQQEHADLSVCVVGRYIYAVAGRDYHNDLNAVER
			YDPATNSWAYVAPLKREVYAHAGATLEGKMYITCGRKGRIT
			GVGPRAAAMPLELELCPGRWVGGQHPCFIIAEIGQNHQGDLDVA
6703	45	1244	KRMIRMAKECGADCAKFQKSELEFKFNRKALERPYTSKHSWGKT
		'	YGEHKRHLEFSHDQYRELQRYAEEVGIFFTASGMDEMAVEFLHE
	}		LNVPFFKVGSGDTNNFPYLEKTAK/TRGWHSVLRDVCGVQLNDE
	1		TWALLER CONDUCTION AND THE DATE OF THE PARTY
	ì		TSSWDVLGRVRTSKEKVLMVLVLDYSGRPMVISSGMQSMDTMKQ
	1		VYQIVKPLNPNFCFLQCTSAYPLQPEDVNLRVISEYQKLFPDIP
			IGYSGHETGIAISVAAVALGAKVLERHITLDKTWKGSDHSASLE
			PGELAELVRSVRLVERALGSPTKQLLPCEMACNEKLGKSVVAKV
			KIPEGTILTMDMLTVKVGEPKGYPPEDIFNLVGKKVLVTVEEDD
			TIMEE
6704	82	1007	TMNTRNRVVNSGLGASPASRPTRDPQDPSGRQGELSPVEDQREG
			LEAAPKGPSRESVVHAGQRRTSAYTLIAPNINRRNBIQRIAEQE
			LANLEKWKEQNRAKPVHLVPRRLGGSQSETEVRQKQQLQLMQSK
			YKQKLKREESVRIKKEAEEABLQKMKAIQREKSNKLEEKKRLQE
			NLRREAFREHQQYKTAEFL/RQTEHRIARQKCLSKCCLWPTILN
			MGQKLGLQ\DSLKAEENRKLQKMKDEQHQKSELLELKRQQQEQE
			RAKIHQTEHRRVNNAFLDRLQGKSQPGGLEQSGGCWNMNSGNSW
			GI
6705	2	786	RLCRNSARVPCGWSASRSLGEGAGFIGPLRGPHPRAGGTGTSFT
0,03			SYKRKGGIMSTIAAFYGGKSILITVATGFLGKELMEKLFRTSPD
1			LKVIYILVRPKAGQTLQHRVFQILDSKLFEKVIEVRPNVHEKIR
			AIYADLNONDFAISKEDMQELLSCTNIIFHCAATVRFDDTLRHA
1			VQLNVTATRQLLLMASQMPKLEAFIHISTAYSNCNLKHIDEVIY
			PCPVEPKKIIDSLEW\LDDAIIDEITPKLIRDWPNIYTYTK
ļ_ <u></u> _			PCPVEPKKIIDSEW\BDDAIIDEIIPKBIKDAFKIIIIK PTHSSSSHSQEMLGKLNMLRNDGHFCDIIIRVQDKIFRAHKVVL
6706	130	531	PTHSSSSHSQEMLGKLNMLKNDGHFCDIIIRVQDKIFRAHKVVI AACSDFFRTKLVGQAEDENKNVLDLHHVTVTGFIPLLEYAYTAT
			AACSDEEKTKLVGQAEDENKIVEDDIKVIVIGETEDDEIKITAT
	1	I	LSINTENIIDVLAAASYMQMFSVASTCSEFMKSSILWNTPNSQP
	}	1	EK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
_	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
6707	2233	1343	YWSGIGYELQHFHWRKFHFEKKGPPSTCQERLYESRSRWPCIS*
0.0.		· ·	GMVVVGWTAVNGSW*GGQLRCVCVCTSHSSDSTRSSQRASKCHS
			FFILSQ*KT*SSWENWVFAKYSRIYSYGHSCSKGRGD*DFK*NV
	Ì	ł	SQAR*SRFCGLCNPCGHCGLDINLRGGSSPWTDKHSCVHNNLLC
			NRRVFSLLCEGPGHCYQGAVCREACAAASPGLDSAAEPHRLCEH
			TD*LPK*GPGYIQHFHCDSNILCILYNISFNLFSYSF*GVARYA
			C*RCHWYFEWLLYNHCGDILVACL*RRQL*SSQ
6708	115	1729	TVGSWSRSGRSPPVGRQLLLTGRGAQAAGSPQGGMALQVELVPT
6700			GEIIRVVHPHRPCKLALGSDGVRVTMESALTARDRVGVQDFVLL
			ENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQIYSR
			QHMERYRGVSFYEEPPHLLAVADTVYRALRTERRDQAVMISVES
			GAGKTDATKRLLQLYAETCPAPQRGGAVRDRLLQSNPVLEAFGN
		1	AKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKSRVVHQ
			NHGERNFHIFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAK
			VSSINDKSDWKVVRKALTVIDFTEDEVEDLLSIAASVLHLGNIH
			FAANEESNAQVTTENQLKYLTRLLSVEGSTLREALTHRKI IAKG
			EELLSPLNLEQAAYARDALAKAVYSRTFTWLVGKINRSLASKDV
			ESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFI
			ELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGII\SI
			LDE\ECLRPGE
		894	PPHEHLFPSGERGPFSFLVSRRGLGPGKMGKKGKKEKKGRGAEK
6709	3	034	TAAKMEKKVSKRSRKEEEDLEALIAHFQTLDAKRTQTVELPCPP
			PSPRLNASLSVHPEKDELILFGGEYFNGQKTFLYNELYVYNIRK
			DTWTKVDIPSPPPRRCAHQAVVVPQGGGQLWVFGGEFASPNGEQ
			FYHYKDLWVLHLATKTWEQVKSTGGPSGRSGHRMVAWKRQLILF
			GGFHESTRDYIYYNDVYAFNLDTFTWSKLSPSGTGPTPRSGCQ\
			IPSLPRAASSVYGGYSKQRVKKDVDKGTRHSDMF
	150	980	RHKMTNYRVESSSGRAARKMRLALMGPAFLAAIGYIDPGNFATN
6710	158	360	IQAGASFGYQLLWVVVWANLMAMLIQILSAKLGIATGKNLAEQI
	1		RDHYPRPVVWFYWVQABIIAMATDLAEFIGAAIGFKLILGVSLL
			QGAVLTGIATFLILMLQRRGQKPLEKVIGGLLLFVAAAYIVELI
			FSQPNLAQLGKGMVIPSLPTSEAVFLAAGVL\GATIMPHVI/YI
	•	1	WHSSLTQHLHGGSRQQRYSATKWDVAIAMTIAGFVNLAIMATAA
			SELNFYGHTGVA
		347	VTECKTMTCKMSQLERNI*TMINTLHHYSVKLGHPDTLIHGEFK
6711	3	341	ELVRTDLHNILMKENKNDQAI*HIMEDLDTNAHMQIIFKELIML
		1	MAMLTWSYHDNMHDADYGPGQQHRPG
L	 	578	PHGQKRTRYPQVRAPGQQPQAQLAMALCLKQVFAKDKTFRPRKR
6712	118	3/6	FEPGTQRFELYKKAQASLKSGLDLRSVVRLPPGENIDDWIAVHV
			VDFFNRINLIYGTMAERCS*TSCPVMAGGPRYEYRWQDERQYRR
!			PAKLSAPRYMALLMDWIESLI
			QARGSDSEDGEFEIQAEDDARARKLGPGRPLPTFPTSECTSDVE
6713	2485	3	PDTREMVRAQNKKKKKSGGFQSMGLSYPVFKGIMKKGYKVPTPI
			QRKTIPVILDGKDVVAMARTGSGKTACFLLPMFERLKTHSAQTG
ì			QRKTIPVILLGKDVVAMARTGSGKTACFLLPMFEKDKTASAQTG ARALILSPTRELALQTLKFTKELGKFTGLKTALILGGDRMEDQF
1	•		ARALILSPTRELALQTLKFIREIGKFIGHKIADILGGDKMEDQF AALHENPDIIIATPGRLVHVAVEMSLKLQSVEYVVFDEADRLFE
1			MGFAEQLQEIIARLPGGHQTVLFSATLPKLLVEPARAGLTEPVL
1			IRLDVDTKLNEQLKTSFFLVREDTKAAVLLHLLHNVVRPQDQTV
İ			TKPDADAKTAKOPK MMC K MMCDAGGSATA AGST DDMSDATAM S AEMI
1	1		VFVATKHHAEYLTELLTTQRVSCAHIYSALDPTARKINLAKFTL
			GKCSTLIVTDLAARGLDIPLLDNVINYSFPAKGKLFLHRVGRVA
			RAGRSGTAYSLVAPDEIPYLLDLHLFLGRSLTLARPLKEPSGVA
1	ĺ		GVDGMLGRVPQSVVDEEDSGLQSTLEASLELRGLARVADNAQQQ
1			YVRSRPAPSPESIKRAKEMDLVGLGLHPLFSSRFEEEELQRLRL
1	1		VDSIKNYRSRATIFEINASSRDLCSQVMRAKRQKDRKAIARFQQ
1		1	· · · · · · · · · · · · · · · · · · ·
			GQQGRQEQQEGPVGPAPSRPALQEKQPEKEEEEEAGESVEDIFS EVVGRKRQRSGPNRGAKRRREEARQRDQEFYIPYRPKDFDSERG

	I B	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		1 -	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first		S=Serine, T=Threonine, V=Valine,
1	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		/=possible indirection insertion/
			LSISGEGGAFEQQAAGAVLDLMGDEAQNLTRGRQQLKWDRKKKR
			FVGQSGQEDKKKIKTESGRYISSSYKRDLYQKWKQKQKID*S*L
ļ		ļ	GRRRGILTRRPRTEEVGEARPLAQAGCIPGPHAPRHPLQAESA
		<u> </u>	LELKTKQQILKQRRRAQKAALSLQRWWPQAALCPQ
6714	169	1416	NNCQELLPPPPAPMAHIPSGGAPAAGAAPMGPQYCVCKVELSVS
			GQNLLDRDVTSKSDPFCVLFTENNGRWIEYDRTETAINNLNPAF
		ĺ	SKKFVLDYHFEEVQKLKFALFDQDKSSMRLDEHDFLGQFSCSLG
1			TIVSSKKITRPLLLLNDKPAGKGLITIAAQBLSDNRVITLSLAG
			RRLDKKDLFGKSDPFLEFYKPGDDGKWMLVHRTEVIKYTLDPVW
}			KPFTVPLVSLCDGDMEKPIQVMCYDYDNDGGHDFIGEFQTSVSQ
		!	MCEARDSVPLEFECINPKKQRKKNYKNSGIIILRSCKINRDYS
			FLDYILGGCQLMFTVGIDFTASNGNPLDPSSLHYINPMGTNEYL
		1	SAIWAVGQIIQDYDSDKMFPALGFGAQLPPDWKVSHEFAINFNP
J	1	1	TNPFCSGVDGIAQAYSACLP
6715	32	493	GPAGAESGSLHCLPATVQALAGAAHSPHGGQPPRRGPLIGSGMP
-	1		GKPKHLGVPNGRMVLAVSDGELSSTTGPQGQGEGRGSSLSIHSL
İ	•		PSGPSSPFPTEEQPVASWALSFERLLQDPLGLAYFTEFLKKEFS
	Ì		AENVTFWKACERFQQIPASDT
6716	1	176	GAGGPAPRSFGSEEPRAALERDKMSARAAAKSTAMEETAIWEQ
1	_		HTVTLHRVSLCCSK
6717	115	896	LFAMSGFENLNTDFYQTSYSIDDQSQQSYDYGGSGGPYSKQYAG
0,1,	113		YDYSQQGRFVPPDMMQPQQPYTGQIYQPTQAYTPASPQPFYGNN
Į.			FEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGSIMNETDLAG
			PMVFCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCLLNLMSMT
1			GVSFGCVASVLGYCLLPMILLSSFAVIFSLQGMVGIILTAGIIG
1			WCSFSASKIFISALAMBGQQLLVAYPCALLYGVFALISVF
6718	290	599	KQSSTVPGTILPSLKWHNSGLCKFPETGGKMTTFKEGLTFKDVA
0,10	1		VIFTEEELGLLDPVQRNLYQDVMLENFRNLLSVGHHPFKHDVFL
i			LEKEKKLDIMKTATQ
6719	1	691	PTRPEEODREDGKCHKMEMNPISGNLNCDPIAMSQCSSDHGCET
6/13	<u> </u>	05.	DLDSDDDKIEKPNNFMKDSASQDNGLSRKISRKRVCSSDSDSSL
1			OVVKKSSKARTGLLRITRRCAATAANKIKLMSDVEDVSLENVHT
			RSKNGRKKPLHLACTTAKKKLSDCEGSVHCEVPSEQYACEGKPP
			DPDSEGSTKVLSQALNGDSDSEDMLNSEHKHRHTNIHKIDAPSK
			RKSSVTSSG
6720	3	822	HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA
6/20	3	022	VPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY
}		1	QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
			LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG
			IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
			VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM
	1		
			SVVTLISE HEVAEEAGGTVYPQRGTMPGTKRFQHVIETPEPGKWELTGYEAA
6721	3	822	WPITEKSNPLTQDLDKADAENIVRLLGQCDAEIFQEEGQALSTY
1	1		
1			QRLYSESILTTMVQVAGKVQEVLKEPDGGLVVLSGGGTSGRMAF
	1		LMSVSFNQLMKGLGQKPLYTYLIAGGDRSVVASREGTEDSALHG
1		1	IEELKKVAAGKKRVIVIGISVGLSAPFVAGQMDCCMNNTAVFLP
	1		VLVGFNPVSMARHPFPPPRILRSLTVFPSLRAPHYQITSLLFSM
1			SVVTLISE
6722	1	390	RSWSKRTWQALPMAVLFLLLFLCGTPQAADNMQAIYVALGEAVE
			LPCPSPSTLHGDEHLSWFCSPAAGSFTTLVAQVQVGRPAPDPGK
			PGRESRLRLLGNYSLWLEGSKEEDAGRYWCAVLGQHHNYQNW
6723	173	659	VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT
	j		GNEGRVSVENIKQLLQSAHKESSFDIILSGLVPGSTTLHSAEIL
1			AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL
L			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
			VEVKELQREPLTPREVQSVREHLGHESDNL
6724	173	659	VCQYCTARMADFGISAGQFVAVVWDKSSPVEALKGLVDKLQALT
		1	GNEGRVSVENIKOLLOSAHKESSFDIILSGLVPGSTTLHSAEIL
			AEIARILRPGGCLFLKEPVETAVDNNSKVKTASKLCSALTLSGL
		İ	VEVKELQREPLTPEEVQSVREHLGHESDNL
6725	356	722	RRRTPPVILATMDDDLMLALRLQEEWNLQEAERDHAQESLSLVD
0,23	330		ASWELVDPTPDLQALFVQFNDQFFWGQLEAVEVKWSVRMTLCAG
			ICSYEGKGGMCSIRLSEPLLKLRPRKDLVEVFFV
6726	98	714	HLQKMERKINRREKEKEYEGKHNSLEDTDQGKNCKSTLMTLNVG
0,20]	/	GYLYITQKQTLTKYPDTFLEGIVNGKILCPFDADGHYFIDRDGL
			LFRHVLNFLRNGELLLPEGFRENQLLAQEAEFFQLKGLAEEVKS
			RWEKEQLTPRETTFLEITDNHDRSOGLRIFCNAPDFISKIKSRI
		1	VLVSKSRLDGFPEEFSISSNIIQFKYFIK
6727	1 .	831	FRÖMGDERPHYYGKHGTPQKYDPTFKGPIYNRGCTDIICCVFLL
0/2/	1 .	, 631	LAIVGYVAVGIIAWTHGDPRKVIYPTDSRGEFCGQKGTKNENKP
1		}	YLFYFNIVKCASPLVLLEFQCPTPQICVEKCPDRYLTYLNARSS
ļ		ļ	RDFEYYKOFCVPGFKNNKGVAEVLRDGDCPAVLIPSKPLARRCF
1			PAIHAYKGVLMVGNETTYEDGHGSRKNITDLVEGAKKANGVLEA
		}	ROLAMRIFEDYTVSWYWDIISLGIAMAMSLLFIILLRFLAGIMG
}			RGMIIMGILVLGY
6728	486	935	FCSSWLRSLADSSLSWKMFLVGLTGGIASGKSSVIQVFQQLGCA
6728	486	935	
			VIDVDVMARHVVQPGYPAHRRIVEVFGTEVLLENGDINRKVLGD LIFNQPDRRQLLNAITHPEIRKEMMKETFKYFLREPRTSPRGKK
1	1	1	HVPSALKEADSLMRRDT
6729	259	1191	VGLTGAQSGRTASMGRDQRAVAGPALRRWLLLGTVTVGFLAQSV
6/29	259	1191	LAGVKKFDVPCGGRDCSGGCQCYPEKGGRGQPGPVGPQGYNGPP
			GLQGFPGLQGRKGDKGERGAPGVTGPKGDVGARGVSGFPGADGI
		,	
1			PGHPGQGGPRGRPGYDGCNGTQGDSGPQGPPGSEGFTGPPGPQG PKGQKGEPYALPKEERDRYRGEPGEPGLVGFQGPPGRPGHVGQM
İ			GPVGAPGRPGPPGPPGPKGQQGNRGLGFYGVKGEKGDVGQPGPN
)	
			GIPSDTLHPIIAPTGVTFHPDQYKGEKGSEGEPGIRGISLKGEE GIM
6730	204	1015	NMVDYYEVIGLQRYASPEDIKKAYHKVALKWHPDKNPENKEEAE
6/30	784	1013	RKFKEVAEAYEVLSNDEKRDIYDKYGTEGLNEF
6731		446	GIRKRLHGAVVPRVEVGCPWETRESEGVHLERPTSPLKNNDEGS
6/31	1	446	·
1		1	LDIYAGLDSAVSDSASKSCVPSRNCLDLYEEILTEEGTAKEATY
			NDLQVEYGKCQLQMKELMKKFKEIQTQNFSLINENQSLKKNISA LIKTARVEINRKDEEI
6732	102	1205	GRWORRPPPPSPPLWCLOPGGGSDPOOLTOLRHCLSHSPODTPW
0/32	102	1205	
		1	AQRQVCYTAATTQAAAPATRNCLPDHSGHRPTPPRSHRHHRQEN LGSIKPSSRSTKATSTTMAGDGRRAEAVREGWGVYVTPRAPIRE
		1	
			GRGRLAPQNGGSSDAPAYRTPPSRQGRREVRFSDEPPEVYGDFE
1			PLVAKERSPVGKRTRLEEFRSDSAKEEVRESAYYLRSRQRRQPR
}		1	PQETEEMKTRRTTRLQQQHSEQPPLQPSPVMTRRGLRDSHSSEE
		1	DEASSQTDLSQTISKKTVRSIQEAPAVSEDLVIRLRRPPLRYPR
		1	YEATSVQQKVNFSEEGETEEDDQDSSHSSVTTVKARSRDSDESG
(733	 	 	DKTTRSSSQYIESFW
6733	613	1311	RSCRQVGMRSRNQGGESASDGHISCPKPSIIGNAGEKSLSEDAK
	1	1	KKKKSNRKEDDVMASGTVKRHLKTSGECERKTKKSLELSKEDLI
	1		QLLSIMEGELQAREDVIHMLKTEKTKPEVLEAHYGSAEPEKVLR
			VLHRDAILAQEKSIGEDVYEKPISELDRLEEKQKETYRRMLEQL
	1	1	LLAEKCHRRTVYELENEKHKHTDYMNKSDDFTNLLEQERERLKK
653.	<u> </u>	ļ	LLEQEKAYQARKE
6734	189	551	SAAMFPVFSGCFQELQEKNKSLELVSFEEVAVHFTWEEWQDLDD
L		1	AQRTLYRDVMLETYSSLVSLGHCITKPEMIFKLEQGAEPWIVEE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	554	\=possible nucleotide insertion)
	sequence		TLNLRLSGGSKKOVFSGICHRSLVELQEVHLV
6735	280	558	KSRRAGVTKMSNPFLKOVFNKDKTFRPKRKFEPGTORFELHKKA
0,33	200	330	QASLNAGLDLRLAVQLPPGEDLNDWVAVHVVDFFNRVNLIYGTI
}	ļ		XDGCT
6736	195	808	MNYELNFKREMPNIKSLGLTNLNFLLKRLSSVLPLITDYVYFBN
0/30	1,33	""	SSSNPYLIRRIEELNKTASGNVEAKVVCFYRRRDISNTLIMLAD
			KHAKEIEBESETTVEADLTDKOKHOLKHRELFLSRQYESLPATH
ļ			IRGKCSVALLNETESVLSYLDKEDTFFYSLVYDPSLKTLLADKG
			EIRVGPRYQADIPEMLLEGTFFCVFAVL
	3.50	1200	PVIMPLHFSPGDIVRPSCCVSSSPKLRNAHSRLESYRPDTDLS
6737	150	1209	
		1	REDTGCNLQHISDRENIDDLNMEFNPSDHPRASTIFLSKSQTDV
	1		REKRKSLFINHHPPGQIARKYSSCSTIFLDDSTVSQPNLKYTIK CVALAIYYHIKNRDPDGRMLLDIFDENLHPLSKSEVPPDYDKHN
1			
1	1 .	1	PEQKQIYRFVRTLFSAAQLTAECAIVTLVYLERLLTYAEIDICP
			ANWKRIVLGAILLASKVWDDQAVWNVDYCQILKDITVEDMNELE
			RQFLELLQFNINVPSSVYAKYYFDLRSLAHANNLSFPLEPLSRE
			RAHKLEAISRLCEDKYKDLRRSARKRSASADNLTLPRWSPAIIS
6738	148	653	CACAEQPARAEVGAATALPVRWASGEMAPSGSLAVPLAVLVLLL
	ļ.,		WGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
1			QPEWESFABWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHC
		<u> </u>	KDGEFRRYQGPRTKKDFINFISDKEWKSIBPVSSWF
6739	3	631	SWPDMAEEBVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
ļ	Į.		ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
			VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
1			REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
			TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6740	3	631	SWPDMAEEEVAKLEKHLMLLRQEYVKLQKKLAETEKRCALLAAQ
ļ			ANKESSSESFISRLLAIVADLYEQEQYSDLKIKVGDRHISAHKF
l			VLAARSDSWSLANLSSTKELDLSDANPEVTMTMLRWIYTDELEF
l			REDDVFLTELMKLANRFQLQLLRERCEKGVMSLVNVRNCIRFYQ
			TAEELNASTLMNYCAEIIASHWVSEVEGVNKAL
6741	141	960	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
			HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
			YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
			WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
		1	DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
			PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ
	<u></u>		LIPKTKIP
6742	141	960	PLTLPFSSRARAGHTMNTSPGTVGSDPVILATAGYDHTVRFWQA
	1		HSGICTRTVQHQDSQVNALEVTPDRSMIAAAVQPVSLGYQHIRM
Ì		1	YDLNSNNPNPIISYDGVNKNIASVGFHEDGRWMYTGGEDCTARI
			WDLRSRNLQCQRIFQVNAPINCVCLHPNQAELIVGDQSGAIHIW
i			DLKTDHNEQLIPEPEVSITSAHIDPDASYMAAVNSTLVPFSCLL
			PLAIGILQEGEFESLARRGLLFLACQGNCYVWNLTGGIGDEVTQ
Ì			LIPKTKIP
6743	1	412	MHSTQDKSLHLEGDPNPSAAPTSTCAPRKMPKRISISKQLASVK
			ALRKCSDLEKAIATTALIFRNSSDSDGKLEKAIAKDLLQTQFRN
1			FAEGQETKPKYREILSELDEHTENKLDFEDFMILLLSITVMSDL
		†	LONIR
6744	95	1343	RTPARNRCAGCEVLSRFSSPNKASSFALQSAGGGLPAVRALRRD
	1		ROKVSTVGYGMDEVEQDQHBARLKELFDSFDTTGTGSLGQBELT
Ì	į		DLCHMLSLEEVAPVLQQTLLQDNLLGRVHFDQFKEALILILSRT
			LSNEEHFQEPDCSLEAQPKYVRGGKRYGRRSLPEFQESVEBFPE
	1	1	VTVIEPLDEEARPSHIPAGDCSEHWKTQRSEEYEAEGQLRFWNP
1	i	1	DDLNASQSGSSPPQDWIEEKLQEVCEDLGITRDGHLNRKKLVSI
		1	- EDDENASUSGSSPPODWIEGKLOEVCEDEGITRIGHENRKKLVSI

SEQ Predicted Predicted end nucleotide location location corresponding to first amino acid residue of amino acid residue of amino acid sequence se
NO: nucleotide location corresponding to first amino acid residue of amino acid residue of amino acid sequence Sequence
location corresponding to first to first amino acid residue of residue of amino acid residue of amino acid residue of amino acid sequence codon, /=possible nucleotide deletion, codon, /=possible nucleotide deleti
Corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, amino acid sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, *=Stocom, S=Serine, T=Threonine, V=Valine, V=Dogmine, Sequence V=Tryptophan, Y=Tyrosine, X=Unknown, *=Stocom, S=Serine, T=Threonine, V=Valine, V=Dogmine, V=Dog
to first amino acid residue of residue of amino acid residue of amino acid sequence ### Typtophan, Y=Tyrosine, X=Unknown, *=St- Codon, /=possible nucleotide deletion, _=possible nucleotide merition) ### Codon, /=possible nucleotide deletion, _=possible nucleot
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, amino acid sequence Codon, /=possible nucleotide deletion, \- possible nucleotide deletion, \- possible nucleotide insertion) CEQYGLQNVDGEMLEEVFHINLDPDGTMSVEDFFYGLFKNGK.
residue of amino acid sequence
amino acid sequence Codon, /=possible nucleotide deletion, /=possible nucleotide insertion (
Sequence Sequence
CEQYGLQNVDGEMLEEVFHNLDPDGTMSVEDFFYGLFKNGK. PSASTEYRQLKRHLSMQSFDESGRRTTTSSAMTSTIGFRVF. DDGMGHASVERILDTWQEEGIENSQBILKALDFGLDGNINL. TLALEBELLVTKNSIHQACI 6745 1 588 TFRDQGWAQRRRWLLGCASWESWEAAIAAGPGLPSSTARQQ. AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERR. ELPVTSFDCAVCLEVLHQPVRTRCGHVYCRSCIATSLKNNK. PYCRAYLPSEGVPATDVAKRMKSEYKNCAECOTLVCLSEMR. RTCQKYIDKYGPLQELEETA 6746 110 492 GATGAMAESAPARHRKKRRSTPLTSSTLPSQATEKSSYFQT SLWTVVAAIQAVEKMESQAARLQSLEGRTGTAEKKLADCE VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN 6747 247 484 EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLS QPFHRDTFHFLREKFWMMDIATQREGNSYVAGVC 6748 201 665 MTTFKEAVTFKDVAVVFTEEELGLLDDAQRKLYRDVMLENF LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISVQQXPYRCNECKQ 6749 95 719 RREVKGGDGVCPRARGSPQSQCPPSCAGGGEGLQQSGEALD SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPDQADITTEGRGKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSELTTGAEKVVLEKEVHDQLLQLHSIQ HAATGGSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRPGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCMMDNKDLVWLEEIQBEABRM EFSKEPELMPKTPSQKNRRKKRRISYVQDBSRDPIRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVARVVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYMSTTSPEDINYASQKQVYRDIGE QHAFFEGNVCIFAYGGTGAGKSYTMMGKQBKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
PSASTPYRQLKRHLSMQSFDESGRRTTTSSAMTSTIGFRVF. DDCMGHASVERILDTWQEEGI ENSQEILKALDFGLDGNINL: TLALENELLVTKNSIHQACI 6745 1 588 TFRDQCWAQRRWLLGCASWESWEAAIAAGPGLPSSTARQQI AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERR. ELPVTSFDCAVCLEVHHQPVERRCGHVFCRSCIATSLKNNK PYCRAYIPASEGVPATDVAKRMKSEYKNCAECDTLVCLSEMR. RTCQKYIDKYGPLGELEETA 6746 110 492 GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFQT SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCE VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLENRN 6747 247 484 EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLS QFFHRDTFHFLREEKFWMMDIATQREGNSYVAGVC 6748 201 665 MTTFKEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENF LSYGNQPFHQDTFHFLGKEKFWKKTTSQREGNSGGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQQXPYRCNECKQ 6749 95 719 RREVKGGDGVCPRARGSPQSQQFPSCAGGEGLQQSGEALD SAGGPCPAAAGGGFGGASCSVGAPGGVSMFRNLEVLEKEFD VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGGSADGSTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVWASGALPRDTTGLGSEQFSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEARM EPSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSGRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYMSHTSPEDINYASQKQVYRDIGE QHAFEGNVCIFAYGGTGAGKSYTMMGKQEKDQGGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
DDGMGHASVERILDTWQEEGIENSQEILKALDFGLDGNINL' TIALEMELLVTKNSIHQACI 1 588 TFRDQWAQRRRWLLGCASWESWEAAIAAGPGLPSSTARQQI AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERR: ELPVTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNK PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMR RTCQKYIDKYGPLQELEETA 6746 110 492 GATGAMAESAPARHRKRRSTPLTSSTLPSQATEKSSYFQT SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCE VEFGNQLEGKWAVLGTLLQEYGLLQRRLERVENLLRNRN 6747 247 484 EAVTFKDVAVVFTEELIGLLDLAQRKLYRDVMLENFRNLLS QPFHRDTFHFLISEEKFWMMDIATQREGNSYVAGVC 6748 201 665 MTTFKEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENF LSVGNQPFHQDTFHFLISKEKFWKMKTTSQREGNSGGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSQFFKEGD QIEARLSISXVQXYYRCNECKQ 6749 95 719 RREVKGGDGVCPRARGSPQSQQFPSCAGGGEGLQQSGEALD SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSBLTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWWASGALPRDTTGLGSEQPSGDVAGNRAT TAPGPIHLLELCDQKLMEFLCNMDNKGUVWLEEIQEEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRLLSR RSSQLSSRR 6751 152 1417 PTKATEMGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGGTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
TLALENELLVTKNSIHQACI 6745 1 588 TFRDQGWAQRRWILGCASWESWEAAIAAGPGLFSSTARQQI AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERR. ELPVTSPDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNK PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMR RTCQKYIDKYGPLQELEETA 6746 110 492 GATGAMAESAPARHRRKRSTPLTSSTLPSQATEKSSYFQT SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCE VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN 6747 247 484 EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLS QPFHRDTFHFLREEKFMMDLATQREGNSVYAGVC 6748 201 665 MTTFKEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENFRNLLS LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQQXPYRCNECKQ 6749 95 719 REEVKGGDGVCPRARGSPQSCQFFSCAGGGEGLQCSGEALD SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPDQADITYSGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSBLTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLWLEEIQEEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVKVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWHITSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGTGAGKSYTMMGKQBKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
TFRDQGWAQRRWLLGCASWESWEAATAAAGPGLPSSTARQQ AAGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERR ELPVTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNK PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMR RTCQKYIDKYGPLQELEETA 6746 110 492 GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFQT SLMTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCE VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN 6747 247 484 EAVTFKDVAVVFTBEELGLLDLAQRKLYRDVMLENFRNLLS QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC 6748 201 665 MTTFKEAVTFKDVAVVFTBEBLGLLDPAQRKLYRDVMLENFRNLLS LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKLQIF VPERGPHEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQQXPYRCNECKQ 6749 95 719 RREVKGGDGVCPRARGSPQSQQFFSCAGGGEGLQQSGEALD SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRMLEVLEKEF VDVDLLLGEIDPDQADITYEGRGKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVVAVRPFNSREMSRDSKCIIQMSGST NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE GHAFEGYNVCIFFAYGGTGAGKSTTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
AGGTECFAAVWARGTAMGSVLSTDSGKSAPASATARALERR. ELPYTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNK PYCRAYLPSEGVPATDVAKRMKSEYKNCAECUTLVCLSEMR. RTCQKYIDKYGPLQELEETA 6746 110 492 GATGAMAESAPARHRRKRSTPLTSSTLPSQATEKSSYFQT SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCE VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN 6747 247 484 EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLS QPFHRDTFHFLREEKFMMDIATQREGNSVYAGVC 6748 201 665 MTTFKEAVTFKDVAVVFTEEBLGLLDPAQRKLYRDVMLENF LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQQXPYRCNECKQ RREVKGGGGVCPRAARGSPQSQQFPSCAGGGEGLQQSGEALD SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRNLEVLEKEFD VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGFSVEELERELKAN 6750 3 428 SCESRRFGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQBEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAPEGYNVCIFAYGQTGAGKSYTMMGKQBKDQGGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
ELPVTSFDCAVCLEVLHQPVRTRCGHVFCRSCIATSLKNNK PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMR RTCQKYIDKYGPLQELETA 6746 110 492 GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFQT SLMTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCE VEFGNQLEGKWAVLGTLLQEYGLLQRKLENVENLLRNRN 6747 247 484 EAVTFKDVAAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLS QPFHRDTFHFLREEKFMWMDIATQREGNSVYAGVC 6748 201 665 MTFFKEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENF LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQQXPYRCNECKQ VDVDLLLGEIDPDQADITYEGRGKMTSLSSCFAQLCKKAQS INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQBEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE GHAPFGGYNVCIFAYGQTGAGKSYTMMGKQBKDQGGIIPQLC GHAPFGGYNVCIFAYGQTGAGKSYTMMGKQBKDQGGIIPQLC GHAPFGGYNVCIFAYGQTGAGKSYTMMGKQBKDQGGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
PYCRAYLPSEGVPATDVAKRMKSEYKNCAECDTLVCLSEMR RTCQKYIDKYGPLQELEETA 6746 110 492 GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFQT SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCE VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN 6747 247 484 EAVTFKDVAVVFTEELIGLLDLAQRKLYRDVMLENFRNLS QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC 6748 201 665 MTTFKEAVTFKDVAVVFTEEBLGLLDPAQRKLYRDVMLENF LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQQXPYRCNECKQ 8AGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCKKAQS INHKLEAQLVDLKSBLTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRPGARWWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQBEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFFGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
RTCQKYIDKYGPLQELEETA 6746 110 492 GATGAMAESAPARHRKKRSTPLTSSTLPSQATEKSSYFQT SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCE VEFGNQLEGKWAVLGTLLQEYGLLQRKLENVENLENRN 6747 247 484 EAVTFKDVAVVFTEELGLLDLAQRKLYRDVMLENFRNLLS QPFHRDTFHFLREBKFWMMDIATQREGNSVYAGVC 6748 201 665 MTTFKEAVTFKDVAVVFTEEBLGLLDPAQRKLYRDVMLENF LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQQXPYRCNECKQ 6749 95 719 RREVKGGGGVCPRARGSPQSQCFPSCAGGGEGLQQSGEALD SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQBEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
6746 110 492 GATGAMAESAPARHRRKRRSTPLTSSTLPSQATEKSSYFQT SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCE VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLENRN 6747 247 484 EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLS QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC 6748 201 665 MTTFKEAVTFKDVAVVFTEEBLGLLDPAQRKLYRDVMLENF LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQQXPYRCNECKQ 6749 95 719 RREVKGGDGVCPRARGSPQSQGFPSCAGGGEGLQQSGEALD SAGGPCPAAAGGGPGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSBLTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGFSVEELERELKAN 6750 3 428 SCESRRFGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKGTPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
SLWTVVAAIQAVEKKMESQAARLQSLEGRTGTAEKKLADCE VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN 6747 247 484 EAVTFKDVAVVFTBEELGLLDLAQRKLYRDVMLENFRNLLS QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC 6748 201 665 MTTFKEAVTFKDVAVVFTBEBLGLLDPAQRKLYRDVMLENF LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQQXPYRCNECKQ 6749 95 719 RREVKGGDGVCPRARGSPQSQQFPSCAGGGEGLQQSGEALD SAGGPCPAAAGGGPGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPQADITYEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSBLTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQBEAERM EFSKEPELMPKTPSQKNRRKKRISYVQDENRDPIRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
VEFGNQLEGKWAVLGTLLQEYGLLQRRLENVENLLRNRN 6747 247 484 EAVTFKDVAVVFTEEELGLLDLAQRKLYRDVMLENFRNLLS QPFHRDTFHFLKEEKFMMMDLATQREGRSVYAGVC 6748 201 665 MTTFKEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENF LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQXXPYRCNECKQ 6749 95 719 RREVKGGDGVCPRARGSPQSQQFPSCAGGGEGLQQSGEALD SAGGPCPAAAGGGPGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPDQADITTEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRPGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
6747 247 484 EAVTFKDVAVVFTEELGLLDLAQRKLYRDVMLENFRNLLS QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC 6748 201 665 MTTFKEAVTFKDVAVVFTEEELGLLDPAQRKLYRDVMLENF LSVGNOPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQXXPYRCNECKQ 6749 95 719 RREVKGGDGVCPRARGSPQSQQFPSCAGGGEGLQQSGEALD SAGGPCPAAAGGGPGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVMASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQBEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRFFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
QPFHRDTFHFLREEKFWMMDIATQREGNSVYAGVC 6748 201 665 MTTFKEAVTFKDVAVVFTEEBLGLLDPAQRKLYRDVMLENF LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQXPYRCNECKQ QIEARLSISXVQXPYRCNECKQ FREVKGGDGVCPRARGSPQSQFFSCAGGEGLQQSGEALD SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLIGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVWASGALPRDTTGLGSEQFSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCMMDNKDLVWLEEIQEEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
6748 201 665 MTTFKEAVTFKDVAVVFTEEBLGLLDPAQRKLYRDVMLENF LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIBARLSISXVQQXPYRCNECKQ QIBARLSISXVQQXPYRCNECKQ FREVKGGDGVCPRARGSPQSQFPSCAGGEGLQQSGEALD SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPDQADITYBGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSBLTETQABKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGFIHLLELCDQKLMEFLCNMDNKDLVWLEEIQBEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
LSVGNQPFHQDTFHFLGKEKFWKMKTTSQREGNSGKIQIE VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQQXPYRCNECKQ 6749 95 719 RREVKGGDGVCPRARGSPQSQCFPSCAGGGEGLQQSGEALD VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQBEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLNPKNKGNLR
VPEAGPHEEWSCQQIWEQIASDLTRSQNSIRNSSQFFKEGD QIEARLSISXVQQXPYRCNECKQ 6749 95 719 RREVKGGGGVCPRARGSPQSQGFPSCAGGGEGLQQSGEALD SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
QIEARLSISXVQXXPYRCNECKQ 6749 95 719 RREVKGGGGVCPRARGSPQSQFFSCAGGGEGLQQSGEALD SAGGPCPAAAGGGPGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPQADITYEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSBLTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQBEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
6749 95 719 RREVKGGDGVCFRARGSPQSQGFPSCAGGGEGLQQSGEALD SAGGPCPAAAGGGPGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPDQADITYBGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQBEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRFFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
SAGGPCPAAAGGGPGGASCSVGAPGGVSMFRWLEVLEKEFD VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSBLTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRPGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQBEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
VDVDLLLGEIDPDQADITYEGRQKMTSLSSCFAQLCHKAQS INHKLEAQLVDLKSBLTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQBEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVPFPNSREMSRDSKCIIQMSGSTT NPKQPEMETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
INHKLEAQLVDLKSELTETQAEKVVLEKEVHDQLLQLHSIQ HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVMASGALPRDTTGLGSEQFSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCMMDNKDLVMLEEIQEEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPEMETPKSFSFDYSYMSHTSPEDINYASQKQVYNDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
HAKTGQSADSGTIKAKLSGPSVEELERELKAN 6750 3 428 SCESRRFGAKWVWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQBEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVPFNSREMSRDSKCIIQMSGSTT NPKQPEMERSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
6750 3 428 SCESRRFGAKWWASGALPRDTTGLGSEQPSGDVAQSNRAT TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
TAPGPIHLLELCDQKLMEFLCNMDNKDLVWLEEIQEEAERM EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
EFSKEPELMPKTPSQKNRRKKRRISYVQDENRDPIRRRLSR RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
RSSQLSSRR 6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCI I QMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCI FAYGQTGAGKSYTMMGKQEKDQQGI I PQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
6751 152 1417 PTKATEMAGASVKVAVRVRPFNSREMSRDSKCIIQMSGSTT NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
NPKQPKETPKSFSFDYSYWSHTSPEDINYASQKQVYRDIGE QHAFEGYNVCIFAYGQTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
QHAFEGYNVCIFAYGOTGAGKSYTMMGKQEKDQQGIIPQLC FSRINDTTNDNMSYSVEVSYMEIYCERVRDLLNPKNKGNLR
FSRINDTTNDNMSYSVBVSYMEIYCERVRDLLNPKNKGNLR
HPLLGPYVEDLSKLAVTSYNDIQDLMDSGNKARTVAATNMN
SRSHAVFNIIFTQKRHDAETNITTEKVSKISLVDLAGSERA
GAKGTRLKEGANINKSLTTLGKVISALAEMDSGPNKNKKKK
FIPYRDSVLTWLLRENLGGNSRTAMVAALSPADINYDETLS
YADRAKQIRCNAVINEDPNNKLIRELKDEVTRLRDLLYAQG
ITDMTNALVGMSPSSSLSALSSRNV
6752 24 1834 RNCVPPLGCYRSRVKFHSDIKMQYSHHCEHLLERLNKQREA
CDCTIVIGEFQFKAHRNVLASFSEYFGAIYRSTSENNVFLD
VKADGFOKLLEFIYTGTLNLDSWNVKEIHQAADYLKVEBVV
KIKMEDFAFIANPSSTEISSITGNIELNOOTCLLTLRDYNN
SEVSTDLIQANPKQGALAKKSSQTKKKKKAFNSPKTGQNKT
PSDILENASVELFILDANKLPTPVVEOVAQINDNSELELTSV
TFPAQDIVHTVTVKRKRGKSQPNCALKEHSMSNIASVKSPY
NSGEELDORYSKAKPMCNTCGKVFSEASSLRRHMRIHKGVK
CHLCGKAFTQCNQLKTHVRTHTGEKPYKCELCDKGFAQKCQ
HSRMHHGEEKPYKCDVCNLQFATSSNLKIHARKHSGEKPYV
CGORFAQASTLTYHVRRHTGEKPYVCDTCGKAFAVSSSLIT
KHTGEKPFICELCGNSYTDIKNLKKHKTKVHSGADKTLDSS
HTLSEODSIOKSPLSETMDVKPSDMTLPLALPLGTEDHHML
TDTQSPTSDTLLRSTVNGYSEPQLIFLQQLY
6753 2 1305 VPSLPYPPQKVVAHTEFTTSSDSETANGIAKPDPVMPGGEB
PFGIKLRRTNYSLRFNCDQQAEQKKKKRHSSTGDSADAGPP

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Glucamic Acid, Farnenylalanine, Gastycine,
į .	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Ì	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
! '	sequence	00425	\=possible nucleotide insertion)
ļ	Bequence	 	PLSKLSRPYLVELLSRRAGRPDPEPSEPSKEDQESSDRRPPSPP
			GPEERKGQKRDEEEEATERKPASPPLPATQQEKPSQTPEAGRKE
			KPMLQSRHSLDGSKLTEKVETAQPLWITLALQKQKGFREQQATR
1	1		KPMLQSRHSLDGSKLTERVETAQPDWITHADQRQRGFREQQAIR
ŀ	l	Į	EERKQAREAKQAEKLSKENVSVSVQPGSSSVSRAGSLHKSTALP
ļ	\		EEKRPETAVSRLERREQLKKANTLPTSVTVEISYSSPAAPLVKE
		1	VSKRFSSPDDAPVSSEPAWLALAKRKAKAWSDCPLIIK
6754	2	413	FVRRRRRLGGPEVNTMSSLHKSRIADFQDVLKEPSIALEKLRE
. 0,51	1 -	{	LSFSGIPCEGGLRCLCWKILLNYLPLERASWTSILAKQRELYAQ
İ	1	1	FLREMIIOPGIAKANMGVSREDVTFEDHPLNPNPDSRWNTYFKD
1	ì	1	NEALT
L	<u> </u>		PGLQLQVALEADWFLDMPGGRRGPSRQQLSRSALPSLQTLVGGG
6755	298	1343	
1			CGNGTGLRNRNGSAIGLPVPPITALITPGPVRHCQIPDLPVDGS
1			LLFEFLFFIYLLVALFIQYINIYKTVWWYPYNHPASCTSLNFHL
1			IDYHLAAFITVMLARRLVWALISEATKAGAASMIHYMVLISARL
1	1	l .	VLLTLCGWVLCWTLVNLFRSHSVLNLLFLGYPFGVYVPLCCFHQ
ì		1	DSRAHLLLTDYNYVVQHEAVEESASTVGGLAKSKDFLSLLLESL
1			KEQFNNATPIPTHSCPLSPDLIRNEVECLKADFNHRIKEVLFNS
		1	LFSAYYVAFLPLCFVKVSGYLTFMCFLDLCVNYINWVFLV
5755	180	754	IERALGSLPLSIPVSWGSLRTLKYQQQPLRPKVLLCQTRVQCHD
6756	180	/54	LRSLQPQPPGLKQSFCLRVLGLQTGATTPGLRDLTCKELIILTE
	l .	1	REAOKRKKRKEKESGMALTQGPLTFRDVAIEFSQEEWKSLDPVQ
		1	
	t	İ	KALYWDVMLENYRNLVFLGKDNFALEVKICPRVFLYFLCCLSWE
	1		PFHYLTETEALLTHK
6757	2	459	NSRVEAPEAHSRESQGSDAMRKHLSWWWLATVCMLLFSHLSAVQ
-	ì		TRGIKHRIKWNRKALPSTAQITEAQVAENRPGAFIKQGRKLDID
l	i	l .	FGAEGNRYYEANYWQFPDGIHYNGCSEANVTKEAFVTGCINATQ
1	1		AANQGEFQKPDNKLHQQVLW
6758	 	1008	ASGPELPGRRFRDRAPWLPARLLRGVLAVWVSLSALGPGSFCRR
6/36	1 -		RVPSLAQLGHSEAAPSPDDVRWSRVPDRCPEERDRAWPPPPPPS
			LPPSFRRNMANNSPALTGNSQPQHQAAAAAAQQQQQCGGGGATK
		i	PAVSGKQGNVLPLWGNEKTMNLNPMILTNILSSPYFKVQLYELK
	1	1	TYHEVVDEIYFKVTHVEPWEKGSRKTAGQTGMCGGVRGVGTGGI
		Ì	TYMEVVDETTERVIRVEPHERGSRRIAGTOMCGGVRGVGTGGT
		\	VSTAFCLLYKLFTLKLTRKQVMGLITHTDSPYIRALGFMYIRYT
			QPPTDLWDWFESFLDDEEDLDVKAGGGCVMTIGEMLRSFLTKLE
1			WFSTLFPRIPVPVQKNIDQQIKTRPRKI
6759	1	513	RKHNFHSLDGTSTRAFHPQTGLPLLSSPVPQRKTQSGCFDLDSS
1			LLHLKSFSSRSPRPCLNIEDDPDIHEKPFLSSSAPPITSLSLLG
1		1	NFEESVLNYRFDPLGIVDGFTAEVGASGAFCPTHLTLPVEVSFY
1	,	İ	SVSDDNAPSPYMGVITLESLGKRGYRVPPSGTIQVVCVL
6566	239	606	VLSKKKGLSAEEKRTRMMEIFSETKDVFQLKDLEKIAPKEKGIT
6760	233	800	AMSVKEVLQSLVDDGMVDCERIGTSNYYWAFPSKALHARKHKLE
1	1	1	VLESOLSEGSOKHASLOKSIEKAKIGRCETEERT
6761	29	1733	ERTLRGLREVAAPSDVADAAVSRRGRCCCCLHCTQTQVAQDCPS
1			SSSSVQRCELSLFQSLHTMTSKKLVNSVAGCADDALAGLVACNP
			NLQLLQGHRVALRSDLDSLKGRVALLSGGGSGHEPAHAGFIGKG
ļ	1		MLTGVIAGAVFTSPAVGSILAAIRAVAQAGTVGTLLIVKNYTGD
1	1		RLNFGLAREQARAEGIPVEMVVIGDDSAFTVLKKAGRRGLCGTV
1			LIHKVAGALAEAGVGLEEIAKQVNVVTKAMGTLGVSLSSCSVPG
			SKPTFELSADEVELGLGIHGEAGVRRIKMATADEIVKLMLDHMT
1	1		NTTNASHVPVQPGSSVVMMVNNLGGLSFLELGIIADATVRSLEG
1			RGVKIARALVGTFMSALEMPGISLTLLLVDEPLLKLIDAETTAA
			AWPNVAAVSITGRKRSRVAPAEPQEAPDSTAAGGSASKRMALVL
	1		AWYNVAAVSITGKKKSKVAPAEPQEAPUSIAAGGSAGKKAAUVI
	1	t .	BRVCSTLLGLEEHLNALDRAAGDGDCGTTHSRAARAIQEWLKEG
		1	
			PPPASPAQLLSKLSVLLLEKMGGSSGALYGLFLTAAAQPLKAKT

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
		amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	to first	1 -	1
J I	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ł l	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
j k	sequence		\=possible nucleotide insertion)
6762	3	613	ASTISWRLCVAGAEARRPVPVAGERAGGGAMWFMYLLSWLSLFI
i			QVAFITLAVAAGLYYLAELIEBYTVATSRIIKYMIWFSTAVLIG
}		1	LYVFERFPTSMIGVGLFTNLVYFGLLQTFPFIMLTSPNFILSCG
!			LVVVNHYLAFOFFAREYYPFSEVLAYFTFCLWIIPFAFFVSLSA
1		1	GENVLPSTMQPGDDVVSNYFTKGKRGK
6763	2	760	SGPDFPGRRFRGCCCVRPPAGAGMELGGHWDMNSAPRLVSETAE
6763	-	700	RKOEOKTGTEAEAADSGAVGARRFLLCLYLGGFLDLFGVSMVVP
			LLSLHVKSLGASPTVAGIVGSSYGILQLFSSTLVGCWSDVVGRR
			SSLLACILLSALGYLLLGAATNVFLFVLARVPAGIFKHTLSISR
1 1]	ALLSDVVPEKERPLVIGHFNTASGVGFILGPVVGGYLTELEDGF
j [l	YLTAFICFLVFILNAGLVWFFPRREAKPGSTE
6764	80	438	LKKMDTMMLSVRNLFEQLVRRVEILSEGNEVQFIQLAKDFEDFR
, I			KKWQRTDHBLGKYKDLLMKAETERSALDVKLKHARNQVDVEIKR
1			RQRAEADCEKLERQIQLIREMLMCDTSGSIQ
6765	3	550	ARYSRVDHFCRRCRAVARAPRFLLQFPSGPSRHFLAACVARWL
			RGSVLVSEALSGSAMDGIVTEVAVGVKRGSDELLSGSVLSSPNS
			NMSSMVVTANGNDSKKFKGEDKMDGAPSRVLHIRKLPGEVTETE
			VIALGLPFGKVTNILMLKGKNQAFLELATEEAAITNGNYYSAVT
			l i
L			PHLRNQ
6766	1	1287	EGGSFKASLTWLWPLGEMKLHCEVEVISRHLPALGLRNRGKGVR
			AVLSLCQQTSRSQPPVRAFLLISTLKDKRGTRYELRENIEQFFT
1			KFVDEGKATVRLKEPPVDICLSKANSSSLKGFLSAMRLAHRGCN
			VDTPVSTLTPVKTSEFENFKTKMVITSKKDYPLSKNFPYSLEHL
ĺ			QTSYCGLVRVDMRMLCLKSLRKLDLSHNHIKKLPATIGDLIHLQ
1 1	1	l .	ELNLNDNHLESFSVALCHSTLQKSLWSLDLSKNKIKALPVQFCQ
		· ·	LOELKNLKLDDNELIQFPCKIGQLINLRFLSAARNKLPFLPSEF
ļ ļ			RNLSLEYLDLFGNTFEQPKVLPVIKLQAPLTLLESSARTILHNR
			IPYGSHIIPFHLCQDLDTAKICVCGRFCLNSFIQGTTTMNLHSV
! !			AHTVVLVDNLGGTEAPIISYFCSLGCYVNSSDI
6060	226	919	APMICLCSSDLQFRYKBAFLRDRGLQIGYCSVDDDPRMKHFLNV
6767	336	913	
]			GRLQSDNEYKKDFAKSRSQFHSSTDQPGLLQAKRSQQLASDVHY
1	1		RQPLPQPTCDPEQLGLRHAQKAHQLQSDVKYKSDLNLTRGVGWT
		i	PPGSYKVEMARRAAELANARGLGLQGAYRGAEAVEAGDHQSGEV
	Ļ		NPDATEILHVKKKKALLL
6768	2	363	PGSTISCYLLSEGSLPLCMQVACGBEKHRAPTMKTLRARFKKTE
1	į .		LRLSPTDLGSCPPCGPCPIPKPAARGRRQSQDWGKSDERLLQAV
]	1		ENNDAPRVAALIARKGLVPTKLDPEGKSAFHL
6769	284	396	MSTPDFSTAENNQELANEVSCLKAMLTLMLQAMGQAD
6770	1	397	ORNYOVIWSSTMAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEK
1 3,73	1 -	1	ITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKARKSVAGF
1	1	Į.	KIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKS
(55	<u> </u>	ļ	
6771	3	378	APAGTLAMTGKSVKDVDRYQAVLANLLLEEDNKFCADCQSKGPR
			WASWNIGVFICIRCAGIHRNLGVHISRVKSVNLDQWTQEQIQCM
			QEMGNGKANRLYEAYLPETFRRPQIDPYLFWSNLEG
6772	1	1400	AAAFLQGMTVNGFINTVITSL\ERRYDLHSYQSGLIASSYDIAA
1		1	CLCLTFVSYFGGSG\HKPRWLGWGR\VLMGTGSLVFALPHFTAG
}		1	P**GWKLDAGVRTCPANPR\PVCAG\HTSGLSRYQLVFMLGQFL
1	1	1	HGVGATPLYTLGVTYLDENVKSSCSPIYIAIFYTAAILGPAAGY
	1		LIGGALLNIYTEMGRRTELTTESPLWVGAWWVGFLGSGAAAFFT
1			AVPILGYPROLPGSQRYAVMRAAEMHQLKDSSRGEASNPDFGKT
i	i .	1	IRDLPLSIWLLLKNPTFILLCLAGATEATLITGMSTFSPKFLES
		1	
		1	
	į		QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK
			QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK FCLFCTVVSLLGILVFSLHCPSVPMAGVTASYGGSLLPEGHLNL
			QFSLSASEAATLFGYLVVPAGGGGTFLGGFFVNKLRLRGSAVIK

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
		*****	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		PWEAPKEHKYKAEEHTVVLTVTGEPCHFPFQYHRQLYHKCTHKG
6773	1	630	RPGPQPWCATTPNFDQDQRWGYCLEPKKVKDHCSKHSPCQKGGT
	1		RPGPQPWCATTPNFDQDQRWGICHEPRRVRDHCSRHSFCQRGGI
ł		1	CVNMPSGPHCLCPQHLTGNHCQKEKCFEPQLLRFFHKNEIWYRT
	1	1	EQAAVARCQCKGPDAHCQRLASQACRTNPCLHGGRCLEVEGHRL
Ì	į	1	CHCPVGYTGPFCDVGE*GSGASRRPAPRWDGLAR
6774	146	389	LTELSDQQYFLFFILSS/WVPTFLSMDVDGRVIKADSFSKIISS
0 / / 4	140		GLRIGFLTGPKPLIERVILHIQVSTLHPSTFNQLMISQ
	104	614	TCPSQLRVLTARGGRRAPSPQLWTLVLALIEEKWRSHRILRMNS
6775	104	014	GRPETMENLPALYTIFQGEVAMVTDYGAFIKIPGCRKQGLVHRT
Į.			HMSSCRVDKPSEIVDVGDKVWVKLIGREMKNDRIKVSLSMKVVN
	ł		QGTGKDLDPNNV\SLSKKRGGGDPSRITLGRRSPLRLS
	ł	<u> </u>	QGTGKDEDPNNV\SESKRGGGDPSKITEGRRSFERDD
6776	3	1108	HERHERHEGALSQDALLRISIPLDSNMRPEKCRRFVHPQWQLLH
			LNGTFPNTSDADMEPCVDGWVYDRISFSSTIVTEWDLVCDSQSL
1			TSVAKFVFMAGMMVGGILGGHLSDRFGRRFVLRWCYLQVAIVGT
	1	l l	CAALAPTFLIYCSLRFLSGIAAMSLITNTIMLIAEWATHRFQAM
		1	GITLGMCPSGIAFMTLAGLAFAIRDWHILQLVVSVPYFVIFLTS
}	1	1	SWLLESARWLIINNKPEEGLKELRKAAHRSGMKNARDTLTLEIL
	1	l.	KSTMKKELEAAQKKKPFLGERLHMPNICKRISLLPFTKFANFMA
1	1	1	YFGLNLHG/LKHLGNNVFLLQTLFGAV/TPPGQLVLHLGHWGSG
ļ		1	RVSSRGRVNCLGLFVLQVW
	<u> </u>	63	CFFHGPAWRDCEVRATFAKKQGQSGIISCIAFSPAQPLYACGSY
6777	779	53	GRSLGLYAWDDGSPLALLGGHQGGITHLCFHPDGNRFFSGARKD
1.		l l	AELLCWDLRQSGYPLWSLGREVTTNQRIYFDLDPTGQFLVSGST
j	1		AKLLCWDLKQSGIPLWSLGKEVIINQKIIPDHDFIQQIDIOOSI
Į.	ì		SGAVSVWDTDGPGNDGKPEPVLSFLPQKDCTNGVSLHPSLPLLG
	Į.	1	HCLPVSVCFLSPTESGGRRRGAGPSLGSPRRHVHLECRLQLWWC
1		i	GGGARLQHP**SPRARKGR
6778	311	805	IQSITDESRGSIRRKNPANTRLRLNVP\EETAGDSE/ERSPEEE
			VQADPRIRSASPKCPTSSPFPKGRSPEGEGET\DPEKVHFHPGP
Ì	ì	[KDKSVAEKN\KGP\SPVSSEGIKDFFSMKPEWENLNQSNVRRMH
	· ·	1	T\AVRLNEVIVKKSRDAKLVLLNMPGPPRNRNGDENY
	2	535	RALRROPRLLAANGIEPESMAISEPIKGSRKPCVNKEELALKKP
6779	1 2	1 333	MAKCAWKGPREPPQDARAEAESPGGASESDQDGGHESPPKKKAV
-	1	i.	AWVSAKNPAPMRKKKKVSLGPVSYVLVDSEDGRKKPVMPKKGPG
j	1	1	SRREASDQKAPRGQQPAEATASTSRGPKAKPEGSPRRATNESRK
1	1	1	1
-	1		V
6780	3	403	HEVNDNKPBININLMSPGKEEISYIFEGDPIDTFVALVRVQDKD
1	}	i	SGLNGEIVCKLHGHGHFKLQKTYENNYLILTNATLDREKRSEYS
1		1	LTVIAEDRGTPSLSTVKHFTVQINDINDNPPHFQRSRYEFVISE
1			К
6781	 	1269	APTRPVFPTLQDLSSSKEPSNSLNLPHSNELCSSLVHPELSEVS
3,01	1		SNVAPSIPPVMSRPVSSSSISTPLPPNQITVFVTSNPITTSANT
ļ			SAALPTHLQSALMSTVVTMPNAGSKVMVSEGQSAAQSNARPQFI
1	į.		TPVFINSSSIIQVMKGSQPSTIPAAPLTTNSGLMPPSVAVVGPL
ŀ			HIPONIKESSAPVPPNALSSSPAPNIQTGRPLVLSSRATPVQLP
}			SPPCTSSPVVPSHPPVQQVKELNPDEASPQVNTSADQNTLPSSQ
t	1		SEECTSSEAARSULEAAAAAAVERIIAEDEWSEAAAAAAAAAAAA
	1		STTMVSPLLTNSPGSSGNRRSPVSSSKGKGKVDKIGQILLTKAC
	}		KKVTGSLEKGEEQYGADGETEGQGLDTTAPGLMGTEQLSTELDS
1			KTPTPPAPTLLKMTSSPVGPGTASAGPSLPGGALPTSVRSIVTT
	1	1	LVPSELISAVPTTKSNHGGIASESLAG
6782	3	1327	RKPTVIRIPAKPGKCLHEDPQSPPPLPAEKPIGNTFSTVSGKLS
0,82			NVERTRNLESNHPGQTGGFVRVPPRLPPRPVNGKTIPTQQPPTK
			VPPERPPPPKLSATRRSNKKLPFNRSSSDMDLQKKQSNLATGLS
1	1		KAKSQVFKNQDPVLPPRPKPGHPLYSKYMLSVPHGIANEDIVSQ
	ļ		NPGELSCKRGDVLVMLKQTENNYLBCQKGEDTGRVHLSQMKLIT
			PLDEHLRSRPNPFSPPKAPSHAQKPVDSGAPHAVVLHDFPAEQV
L			ADDED DESKRIAL SELECTION OF A DOCUMENT A DUDILLE OF A
		_	

ID b	Predicted Deginning Deginning Degine Decation Decorresponding	Predicted end nucleotide location corresponding to first amino acid residue of amino acid sequence	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E= Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DDINLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
NO: n	nucleotide location corresponding to first amino acid residue of amino acid	location corresponding to first amino acid residue of amino acid	Glutamic Acid, F=Phenylalanine, G=Glycine, H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI DEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
l c t a r	location corresponding to first amino acid residue of amino acid	corresponding to first amino acid residue of amino acid	H=Histidine, I=Isoleucine, K=Lysine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI DEGGNGKRECYSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
c t a x a a	corresponding to first amino acid residue of amino acid	to first amino acid residue of amino acid	L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DDINLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI PEGGNGKRECYSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
t a s s	to first amino acid residue of amino acid	amino acid residue of amino acid	P=Proline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI DEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
t a s e	to first amino acid residue of amino acid	residue of amino acid	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI DEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
3 x 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	amino acid residue of amino acid	residue of amino acid	S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI DEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
r ē	residue of amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DDINLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
5	amino acid	1	Codon, /=possible nucleotide deletion, \=possible nucleotide insertion) DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
		sequence	\=possible nuclectide insertion) DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
	sequence		DDLNLTSGEIVYLLEKIDTDWYRGNCRNQIGIFPANYVKVIIDI PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
6783			PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
6783			PEGGNGKRECVSSHCVKGSRCVARFEYIGEQKDELSFSEGEIII
6783		ļ	
6783		1	LKEYVNEEWARGEVRGRTGIFPLNFVEPVEDYPTSGANVLSTKV
6783		i	PLKTKKEDSGSNSQVNSLPAEWCEALHSFTAETSDDLSFKRGDR
6783			
6783			I SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
	3	1750	SYHHHHAQQSAAASPNDTASQKIVIIISMIIIKIDFDVDIGHIIA
			TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT
			GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
1			LPOVRPKPVAONNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
		1	PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
1			QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
1			QTVQLSKPSLEKQTVKSHTETDEKQTESKTTTFFAAFKFKKEIN
}		1	POKLAFMVSLGLVTHDHLEEIQSKRQERKRRTTANPVYSGAVFE
1		1	PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
1			SHODSPENEKTETTFTFPAPVOPVSLPSPTSTDGDIHEDFCSVC
1		1	RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
1			KEEAIPWPGTLAIVHSYIAYKAAKEBEKQKLLKWSSDLKQEREQ
		1	LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
į		1	PEOKAKOPSUSTRYCWEMKALI PHYGYEMY22DEYAYOTTU
		1	GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
		1	ANCNOGEETK
		1750	SYHHHHAQQSAAASPNLTASQKTVTTTSMITTKTLPLVLKAATA
6784	3	1 1/30	TMPASVVGQRPTIAMVTAINSQKAVLSTDVQNTPVNLQTSSKVT
		1	GPGAEAVQIVAKNTVTLQVQATPPQPIKVPQFIPPPRLTPRPNF
[LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQRPVMLTKFTPTTL
l 1		1	LPQVRPKPVAQNNIPIAPAPPPMLAAPQLIQKFVHLIKFIIII
1		1	PTSQNSIHPVRVVNGQTATIAKTFPMAQLTSIVIATPGTRLAGP
1		1	QTVQLSKPSLEKQTVKSHTETDEKQTESRTITPPAAPKPKREEN
1			POKLAFMVSLGLVTHDHLEEIQSKRQERKRRTTANPVYSGAVFE
1	•		PERKKSAVTYLNSTMHPGTRKRGRPPKYNAVLGFGALTPTSPQS
			SHPDSPENEKTETTFTFPAPVQPVSLPSPTSTDGDIHEDFCSVC
1			RKSGQLLMCDTCSRVYHLDCLDPPLKTIPKGMWICPRCQDQMLK
]			RKSGQLLMCDTCSKVIHLDCLDPPLKTIPKGMITCFRCQDQMIK
1		1	KEEAIPWPGTLAIVHSYIAYKAAKEEEKQKLLKWSSDLKQEREQ
1		ł	LEQKVKQLSNSISKCMEMKNTILARQKEMHSSLEKVKQLIRLIH
1 1			GIDLSKPVDSEATVGAISNGPDCTPPANAATSTPAPSPSSQSCT
1 1			ANCNOGEETK
1 _1			LGNTVLHYCSMYSKPECLKLLLRSKPTVDIVNQAGETALDIAKR
6785	1	528	LKATQCEDLLSQAKSGKFNPHVHVEYEWNLRQEEIDESDDDLDD
		ł	LKATUCEDDESQAASGAFIFTIVAVETEMADAQUETDUGDDDDDD
)			KPSPVKKERSPRPQSFCHSSSISPQDKLALPGFSTPRDKQRLSY
, 1	1		GAFTNQIFVSTSTDSPTSPTTEAPPLPPRNAGKGPTGPPITPHR
	1820	1397	PSDKVLVLAPTRELANHVSRDFKDI\TRKLTVARFYGGTSYQSQ
6786	1870	1331	INHIRNGIDILVGTPGRIKDHLQSGRLDLSKLRHVVLDEVDQML
1	Į.	Į.	DLGFAEQVEDIIHESYKTDSEDNPQTLLFSATCPQWVYTVA\KK
1	Į.		DEGLACIONE DOMESTA SEMESTE A TOURSODD STADISTO
			YMKSRYEQVDLDGKMTQKAATTVEHLAIQCHWSQRPAVIGDVLQ
1	1		VYSGSEGRAIIFCETKKNVTEMAMNPHIKQNAQCLHGDIAQSQR
			FITLKGFREGSFKVLVATNVAARGLDIPEVDLVIQSSPPQDVES
1			YTHRSGRTGRAGRTGICICFYQPRERGQLRYVEQKAGITFKRVG
1			VPSTMDLVKSKSMDAIRSLASVSYAAVDFFRPSAQRLIEEKGAV
1		1	DALAAALAHISGASSFEPRSLITSDKGFVTMTLESLEEIQDVSC
1	1	}	DADAAADAHISCASSI EFRAULISCASI VINIDESBEEST ORD
1		1	AWKELNRKLSSNAVSQITRMCLLKGNMGVCFDVPTTESERLQAE
1	Ì		WHDSDWILSVPAKLPEIEEYYDGNTSSNSRQRSGWSSGRSGRSG
1	1		RSGGRSGGRSGROSROGSRSGSRQDGRRRSGNRNRSRSGGHKRS
1	1		FD*VFYHLVDFLSDFLVDSVYLTGRQIDHLTGLTGLIDHLTSHS
1			l l
1			SVWN
6787	2646	2270	PSSFPKNVPLEELEEPPK*KRSGLGSLTPKSQIQNGP*PQTFFF
1 5,5,			FELGSPSGVISAHCNLRLLGSSDSPAPASRVAGIIGTCHHAWLI
1			LVFLVRMGFHHVGOAGLKLLTL\VIHPPWPPKVLGLQT
L	 	036	GGTVDLR\DMLAVSVLAAVRGGR/ATVRRVRESNVLHEKSKGKT
6788	16	936	REGAEDKMTSGDVLSNRKMFYLLKTAFPSVQINTEEHVD\ELDQ
[l		VERNERALI PROPERTY AND A PROPERTY AN

SEQ Predicted Predicted end nucleotide (A=Alanine, C=Cysteine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart (A=Alanine, D=Aspart	ic Acid, E= G=Glycine,
NO: nucleotide location corresponding corresponding to first location to first location to first location corresponding to first location corresponding to first location location location corresponding location	G=Glycine,
location corresponding to first L=Leucine, M=Methionine, N=Aspart to first amino acid P=Proline, Q=Glutamine, R=Argini	G-Grycrac,
corresponding to first L=Leucine, M=Methionine, N=Aspart to first amino acid P=Proline, Q=Glutamine, R=Argini	ine l
to first amino acid P=Proline, Q=Glutamine, R=Argini	agine
	agine,
	ne,
amino acid residue of S=Serine, T=Threonine, V=Valine, residue of amino acid W=Tryptophan, Y=Tyrosine, X=Unkn.	+-C+on
1 200 200 20 20 20 20 20 20 20 20 20 20 2	own, -=scop
amino acid sequence Codon, /=possible nucleotide del	etion,
sequence _=possible nucleotide insertion)	and the same
EVILWGS*DS*GYPKGK*LLPKEVPSR/RVLL	SGLTPLDATQE
FTEDLSK\YVTTMVCVAVNGKPMLGVIHKPFS	EYTAWAMVDGGS
NVKARSSYNEKTPRIVVSRSHSGMVKQVALQT	FGNQTT11PAGG
AGYKVLALLDVPDKSQEKADLYIHVTYIKKWD	
GHMTTLSGEEISYTGSDGIEGGLLASIRMNHQ	ALVRKLPDLEKT
GHK	
6789 2 678 GNGINVLKIAPESAIKFMAYEQIKRLVW**PG	DS*GF/YERLVA
GSLAGAIAQSSIYPMEVLKTRMALRKTGQYSG	MLDCARRILARE
GVAAFYKGYVPNMLGIIPYAGIDLAVYETLKN	IAWLQHYAVNSAD
PGVFVLLACGTMSSTCGQLASYPLALVRTRMQ	AQASIEGAPEVT
MSSLFKHILRTEGAFGLYRGLAPNFMKVIPAV	'SISYVVYENLKI
TLGVQSR	
DDAGDDDWGAADDAGGGAALLIWTYSSCICD	AWTAPSTSQKCD
6790 2 4068 APPAGKRKMQAAPKAGCGAADDUNIVSSCHCK	
HYQWLQVDFGNRKQISAIATQGRYSSSDWVTQ	YRMLYSDTGRNW
KPYHQDGNIWAFPGNINSDGVVRHELQHPILA	RYVRIVPLDWNG
EGRIGLRIEVYGCSYWADVINFDGHVVLPYRF	RNKKMKTLKDVI
ALNFKTSESEGVILHGEGQQGDYITLBLKKAK	CLVLSLNLGSNOL
GPIYGHTSVMTGSLLDDHHWHSVVIERQGRSI	NITLDRSMOHER
TNGEFDYLDLDYEITFGGIPFSGKPSSSSRKN	JEKOCMESTNYNG
VNITDLARRKKLEPSNVGNLSFSCVEPYTVPV	IF ROCIED IN INC
RLNQDLFSVSFQFRTWNPNGLLVFSHFADNLG	ENTERNITES KVG
RENODERS SPECIAL WARREND ST	MARIADITERIO
VHINITQTKMSQIDISSGSGLNDGQWHEVRFI	WVENLYIBITEG
DEASAVRTNSPLQVKTGEKYFFGGFLNQMNNS	JSHSVLQPSFQGC
MQLIQVDDQLVNLYEVAQRKPGSFANVSIDMO	ATTURCVPNHCE
HGGKCSQTWDSFKCTCDETGYSGATCHNSIYE	SPSCEAYKHLGQT
SNYYWIDPDGSGPLGPLKVYCNMTEDKVWTIV	7SHDLQMQTPVVG
YNPEKYSVTQLVYSASMDQISAITDSAEYCE)YVSYFCKMSRLL
NTPDGSPYTWWVGKANEKHYYWGGSGPGIQKO	CACGIERNCTDPK
YYCNCDADYKQWRKDAGFLSYKDHLPVSQVV	JGDTDROGSEAKL
SVGPLRCQGDRNYWNAASFPNPSSYLHFSTF)GETSADISFYFK
TLTPWGVFLENMGKEDFIKLKLKSATEVSFS	FDVGNGPVEIVVR
SPTPLNDDQWHRVTAERNVKQASLQVDRLPQ)IRKAPTEGHTRL
ELYSQLFVGGAGGQQGFLGCIRSLRMNGVTLI	DLEERAKVTSGFI
SGCSGHCTSYGTNCENGGKCLERYHGYSCDC	SNTAYDGTFCNKD
VGAFFEEGMWLRYNFQAPATNARDSSSRVDN	apdqqnshpdlaq
EEIRFSFSTTKAPCILLYISSFTTDFLAVLVI	KPTGSLQIRYNLG
. GTREPYNIDVDHRNMANGQPHSVNITRHEKT	IFLKLDHYPSVSY
HLPSSSDTLFNSPKSLFLGKVIETGKIDQBI	HKYNTPGFTGCLS
RVOFNOIAPLKAALRQTNASAHVHIQGELVE	SNCGASPLTLSPM
SSATDPWHLDHLDSASADFPYNPGQGQAIRNG	GVNRNSAIIGGVI
A\VVIFTPSLCTP\VLP*SR*HVSPHKGTLP	
KPGRRPSMNNDPPTSQRPIDESKKEWPHLRG	GYLAMG
THE STANDARD CONCENCIAL CONCENCIA	GYPGIPPEL/PGW
6791 1801 1193 TGHEGAKGEKGDKGDLGPRGEKGQHGPKGKK SAVV*SWLTAASTKVQAILLPQPLE*LGLQL	AFMASLATHESNO
NSGIIFSSVETNIGNFFDVMTGRFGAPVSGV	YEETESMMKHEDV
NSG11FSSVEINIGNFFDWIIGRFGAFVSGV EEVYVYLMHNGNTVFSMYSYEMKGKSDTSSN	HAVI KI AKGDEVW
	1124 FILTERIZATION A M
LRMGNGALHGDHQRFSTFAGFLLFETK	WINTE AUDINIVERT
	VI TPWARKNYAPP
6792 33 1073 VRHTNWGVDMYLFSLGSESPKGAIGHIVSTE	ENLAAWGRULUAV
PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTF	
PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTF CPSPTTIVTSGTSTVVCVWELSMTKGRPRGL	KURQALIGHIQAV
PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTF CPSPTTIVTSGTSTVVCVWELSMTKGRPRGL TCLAASVTFSLLVSGSQDCTC1LWDLDHLTH	VTRLPAHREGISA
PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTF CPSPTTIVTSGTSTVVCVWELSMTKGRPRGL TCLAASVTFSLLVSGSQDCTCILWDLDHLTH ITISDVSGTIVSCAGAHLSLWNVNGQPLASI	VTRLPAHREGISA TTAWGPEGAITCC
PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTF CPSPTTIVTSGTSTVVCVMELSMTKGRPRGL TCLAASVTFSLLVSGSQDCTCILWDLDHLTH ITISDVSGTIVSCAGAHLSLWNVNGQPLASI CLMEGPAWDTSOIIITGSODGMVRVWKT/VG	VTRLPAHREGISA TTAWGPEGAITCC CEDVCSWTASRRG
PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTF CPSPTTIVTSGTSTVVCVMBLSMTKGRPRGL TCLAASVTFSLLVSGSQDCTCILWDLDHLTH ITISDVSGTIVSCAGAHLSLWNVNGQPLASI CLMEGPAWDTSQIIITGSQDGMVRVWKT/VG APGSASKPKRPQVGEEPGLESRAGR*HCFDR	VTRLPAHREGISA TTAWGPEGAITCC CEDVCSWTASRRG EAQQNQP\PVTAL
PPLWNRTFSWGFDDFSCCLGSYGSDKVLMTF CPSPTTIVTSGTSTVVCVWELSMTKGRPRGL TCLAASVTFSLLVSGSQDCTCILWDLDHLTH ITISDVSGTIVSCAGAHLSLWNVNGQPLASI	VTRLPAHREGISA TTAWGPEGAITCC CEDVCSWTASRRG EAQQNQP\PVTAL

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	li de la companya	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=	
ID	beginning	nucleotide	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
i	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
Į	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	1	1	
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6793	2340	805	GRKEANY\YGSLTQAGTVSLGLDAEGQEVFVPFSAVLPMVAPND
	ł	1	LVFDGWDISSLNLAEAMRRAKVLDWGLQEQLWPHMEALRPRPSV
!			YIPEFIAANQSARADNLIPGSRAQQLEQIRRDIRDFRSSAGLDK
1	}	+	VIVLWTANTERFCEVIPGLNDTAENLLRTIELGLEVSPSTLFAV
			L Company of the comp
1	1		ASILEGCAFLNGSPQNTLVPGALELAWQHRVFVGGDDFKSGQTK
1	1	ľ	VKSVLVDFLIGSGLKTMSIVSYNHLGNNDGENLSAPLQFRSKEV
!	1		SKSNVVDDMVQSNPVLYTPGEEPDHCVVIKYVPYVGDSKRALDE
		i	YTSELMLGGTNTLVLHNTCEDSLLAAPIMLDLALLTELCQRVSF
			CTDMDPEPQTFHPVLSLLSFLFKAPLVPPGSPVVNALFRQRSCI
)	1	ļ	ENILRACVGLPPONHMLLEHKMERPGPSLKRVGPVAATYPMLNK
	l .		_
1			KGPVPAATNGCTGDANGHLQEEPPMPTT*GPGHTVSRLFLPAAP
			HDPTLKAPTNKGRCHFSPPSTWGSWGL
6794	169	1349	DDVKRKPEASAH*EKPGPPSRPGVRGGRERAGGRGSHGARSCR\
1			EPAPPAPAPPEDHPDEEMGFTIDIKSFLKPGEKTYTQRCRLFVG
1		1	NLPTDITEEDFKRLFERYGEPSEVFINRDRGFGFIRLESRTLAE
İ	1		IAKAELDGTILKSRPLRIRFATHGAALTVKNLSPVVSNELLEQA
1		1	
1	į.	1	FSQFGPVEKAVVVVDDRGRATGKGFVEFAAKPPARKALERCGDG
	i		AFLLTTTPRPVIVEPMEQFDDEDGLPEKLMQKTQQYHKEREQPP
			RFAQPGTFEFEYASRWKALDEMEKQQREQVDRNIREAKEKLEAE
	1		MEAARHEHQLMLMRQDLMRRQEELRRLEELRNQELQKRKQIQLR
j	1	1	HEEEHRRREEEMIRHREQEELRRQQEGFKPNYMENYVCHFLR
6795	1740	1010	GPRROTOVRDHELDSF*DWAAQETDCAQNSGERL*KGV/LENFS
0,33	1740	1010	TMSKSAVKISLDLLSNPLCEQDQDLLNMVTALDTAMKRMDAFNQ
	Į.		
ļ	İ		EKVNQIQKTVIEPLKKFGSVFPSLNMAVKRREQALQDYRRLQAK
1	1		VEKYEEKEKTGPVLAKLHQAREELRPVREDFEAKNRQLLEEMPR
ļ		Ĭ	FYGSRLDYFQPSFESLIRAQVVYYSEMHKIFGDLSHQLDQPGHS
	l.	1	DEQRERENEAKLSELRALSIVADD
6796	48	683	GKEIOIPTIKLAWLLFGLE*PVGALGKGVVSF**SHVALGQLGW
1 0,750	1	1	LTRAVRSSWRWELCVSAQEVVSQRSA*SSPSPVGACPSLNPPET
	1	1	SVOEGRDCWOR*LPRLFSALVGOPGCWPQGAPPERCV*PGRCKW
1		ł	
į		1.	HLQSQVLR*ERRRCCRCLPRFA*GWRRRHQRLGLGIHPAPLGST
L		<u> </u>	SPPHPEGNSQQCRR*GWAAELRLPSSVVL*GKLGC*
6797	1620	211	TERMTPSQPTRGSSCTRPSSMLWTSTWRCLTCHWAGMRMSVVGV
1		j	TLGPMAQGLLSASGTTTEATWTRPTTHLTLIRWWLLTASRVDPP
ļ		1	ERPPPPPSDDLTLLESSSSYKNL/DAQIPQ/DWSMSPSTSG*RP
			LTSRASSIMRSRTAIPSAS*SRLTTKHTVGGSPSAWRPRPTSRS
		1	VSTPVSSSTETTASGSCLTWWSSSPAPCPSSSAPAHSFEASCCK
1			TSLWGSCGGGGGGGSACGSGWNLSMAGTSCSSPAMCSPSRAPS*
1			
			RSASRPRTWRATTSAASSWAPRRCWCGWA*SAT*PSSTTTISSS
ľ			PHCGWPCPASCASAAAWLSSTWATASVAGSCWGPIM*SSAHSPW
1			CLSACSRSSMGTTCL*RSPP\SGASRAAAAWCGSSPSSTFTPSS
1			ASSSTWCSASSSRSSPAPTTPSSIPAAQAQRRASCRPTSHSART
1			APPPASSAAGAARPAAFSAAAEGTPRRSIRCW
6798	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
6/98	3034	1030	
			ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
			VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
			ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
1	1		VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
1			TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
1	1		ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
1			QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
1		1	
1			PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL
1			SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
-{	1	(PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP
	1	1	APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
1	1		DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ
		i contract of the contract of	, - <u>_</u>

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ļ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
			PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
1			RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
			MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
			LTFALGEQLSTEVGEVDQFPPVEQWGNL
6799	3894	1696	STISWESLESWLNKATNPSNRQEDWEYIIGFCDQINKELEG*VS
0,55			ALWGQLRGSGLGRGTTMAKEGQPGSPRLSALECVLLVPQ\PQIA
	1		VRLLAHKIQSPQEWEALQALTYLGDRVSEKVKTKVIELLYSWTM
			ALPEEAKIKDAYHMLKRQGIVQSDPPIPVDRTLIPSPPPRPKNP
			VFDDEEKSKLLAKLLKSKNPDDLQEANKLIKSMVREDEARIQKV
			TKRLHTLEEVNNNVRLLSEMLLHYSQEDSSDGDRELMKELFDQC
			ENKRRTLFKLASETEDNDNSLGDILQASDNLSRVINSYKTIIEG
			QVINGEVATLTLPDSEGNSQCSNQGTLIDLAELDTTNSLSSVLA
	1		PAPTPPSSGIPILPPPPQASGPPRSRSSSQAEATLGPSSTSNAL
			SWLDEELLCLGLADPAPNVPPKESAGNSQWHLLQREQSDLDFFS
	1		PRPGTAACGASDAPLLQPSAPSSSSSQAPLPPPFPAPVVPASVP
			APSAGSSLFSTGVAPALAPKVEPAVPGHHGLALGNSALHHLDAL
l	ì		DQLLEEAKVTSGLVKPTTSPLIPTTTPARPLLPFSTGPGSPLFQ
			PLSFQSQGSPPKGPELSLASIHVPLESIKPSSALPVTAYDKNGF
			RILFHFAKECPPGRPDVLVVVVSMLNTAPLPVKSIVLQAAVPKS
	1		MKVKLQPPSGTELSPFSPIQPPAAITQVMLLANPLKEKVRLRYK
ĺ			LTFALGEQLSTEVGEVDQFPPVEQWGNL
6800	404	1646	RRSPSTGLSPVPQPSSPSLSDYSIPWSLLLSGTIAWATPGK*AG
1			*PQAW*LGLAPAIAFI/GLTRGRKQNKEKMAEGGSGDVDDAGDC
	1	1	SGARYNDWSDDDDDSNESKSIVWYPPWARIGTEAGTRARARARA
			RATRARRAVQKRASPNSDDTVLSPQELQKVLCLVEMSEKPYILE
ł		1	AALIALGNNAAYAFNRDIIRDLGGLPIVAKILNTRDPIVKEKAL
1			IVLNNLSVNAENQRRLKVYMNQVCDDTITSRLNSSVQLAGLRLL
			TNMTVTNEYQHMLANSISDFFRLFSAGNEETKLQVLKLLLNLAE
İ			NPAMTRELLRAQVPSSLG\SLFNKKENKEVILKLLVIFENINDN
}		,	FKWEENEPTQNQFGEGSLFFFLKEFQVCADKVLGIESHHDFLVK
			VKVGKFMAKLAEHMFPKSQE
6801	2	1755	SAEEFESQQASVTMHDVDAESFEVLVDYCYTGRVSLSEANVERL
			YAASDMLQLEYVREACASFLARRLDLTNCTAILKFADAFGHRKL
ļ		1	RSQAQSYIAQNFKQLSHMGSIREETLADLTLAQLLAVLRLDSLD
1	İ		VESEQTVCHVAVQWLEAAPKERGPSAABVFKCVRWMHFTEEDQD
1			YLEGLLTKPIVKKYCLDVIEGALQMRYGDLLYKSLVPVPNSSSS
i	1		/R*QQQLSCICSRKSTPETGYVCQGDGDLLWTPQRSLS\RYDPY
1	İ		SGDIYTMPSPLTSFAHTKTVTSSAVCVSPDHDIYLAAQPRKDLW
		1	VYKPAQNSWQQLADRLLCREGMDVAYLNGYIYILGGRDPITGVK
1			LKEVECYSVQRNQWALVAPVPHSFYSFELIVVQNYLYAVNSKRM
			LCYDPSHNMWLNCASLKRSDFQEACVFNDEIYCICDIPVMKVYN
1	ţ.	Ì	PARGEWRRISNIPLDSETHNYQIVNHDQKLLLITSTTPQWKKNR
1			VTVYEYDTREDQWINIGTMLGLLQFDSGFICLCARVYPSCLEPG
1	Ì		QSFITEEDDARSESSTEWDLDGFSELDSESGSSSSFSDDEVWVQ
1			VAPQRNAQDQQGSL
6802	157	1341	ETFPLFFFLLSKTPGKTASMAHFVQGTSRMIAAESSTEHKECAE
			PSTRKNLMNSLEOKIRCLEKORKELLEVNQQWDQQFRSMKELYE
}		1	RKVAELKTKLDAAERFLSTREKDPHQRQRKDDRQREDDRQRDLT
1			RDRLORERKEKERLNEELHELKEENKLLKGKNTLANKEKEHYEC
			EIKRLNKALODALNIKCSFSEDCLRKSRVBFCHEEMRTEMEVLK
			OOVOIYEEDFKKERSDRERLNQEKEELQQINETSQSQLNRLNSQ
			IKACOMEKEKLEKOLKOMYCPPCNCGLVFHLQDPWVPTGPGAVQ
			KQREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPVCCQAG/PR
			KQREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPVCCQAG/PR TPGLK*SSCLWLPKC*NFRFILSKESPSVEVHTNRERQQATRER
		·	KQREHPPDYQWYALDQLPPDVQHKAN/DWCLAPPPVCCQAG/PR TPGLK*SSCLWLPKC*NFRFILSKESPSVEVHTNRERQQATRER G KLSGRPYRHMGVLGTSKLYDIRKTIFTFTPQFIDQQQFYLALDN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	location	Corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	p=proline, Q=Gidcamine, R=Aiginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		204	\=possible nucleotide insertion)
	sequence		KMIVEMLRTDLSYLCSRWRMTGQPTITFPISHSMLDEDGTSLNS
	,	1	SILAALRKMQDGYFGGARVQTGKLSEFLTTSCCTHLSFMDPGPE
	,	1	SILAALKMODGYFGGARVOIGKLSEFHIISCCIIILSFWD. GI
			GKLYSEDYDDNYDYLESGNWMNDYDSTSHARCGDEVARYLDHLL
	1	1	AHTAPHPKLAPTSQKGGLDRFQAAVQTTCDLMSLVTKAKELHVQ
	ł	1	NVHMYLPTKLFQASRPSFNLLDSPHPRQENQVPSVRVEIHLPRD
	1	1	QSGEVDFKALVLQLKETSSLQEQADILYMLYTMKGPDWNTELYN
	İ		ERSATVRELLTELYGKVGEIRHWGLIRYISGILRKKVEALDEAC
		1	TDLLSHQKHLTVGLPPEPREKTISAPLPYEALTQLIDEASEGDM
			TDLLSHQKHLTVGLPPEPKEKI ISAPIP I KABIQLI DEMORSI.
	1	1	SISILTQEIMVYLAMYMRTQPGLFAEMFRLRIGLIIQVMATELA
			HSLRCSAEEATEGLMNLSPSAMKNLLHHILSGKEFGVERK/SVR
			PTDSNVSPAISIHEIGAVGATKTERTGIMQLKSEIKQVEFRRLS
			ISAESOSPGTSMTPSSGSFPSAYDQQSSKDSRQGQWQRRRRLDG
			ALNRVPVGFYQKVWKVLQKCHGLSVEGFVLPSSTTREMTPGEIK
			FSVHVES\VLNVLLRPEYRQLLVEAILVLTMLADIEIHSIGSII
		1	LOAMARO /ATMADDUKE I KODDA ENTOAD LINDAD TO THE TOP TO THE
	i	ţ	AVEKIVHIANDLFLQEQKTLGP\DDTMLAKDPASG\ICTLR\YD
	1		SAPSGRFGTMTYLS\RAA\ATYVQEFLP\HSICAMQ
6804	 	951	GSPGKKEEKAKNKESLCMENSSNSSSDEDEEETKAKMTPTKKYN
0004	1 -		GLEEKRKSLRTTGFYSGFSEVAEKRIKLLNNSDERLQNSRAKDR
	\	i	KDVWSSIQGQWPKKTLKELFSDSDTEAAASPPHPAPEEGVAEES
			LQTVAEEESCSPSVELEKPPPVNVDSKPIEEKTVEVNDRKAEFP
			SSGSNFSA*IPLPYLHLNRLHQSL*QKGSRQQSSVTVSEPLAPN
			SSGSNFSA*TPDPTDRDRKDRQSD*QxGSRQQSS*T*SBT24*X
			QEEVRSIKSETDSTIEVDSVAGELQDLQSERE*LASRF*CQCEL
	1		KQ**SARTRTS*KSLYRSEKSERCSGRRKFIKKAEKKP*SNSGK
	1	ĺ	QQKEGKRHK
6805	1539	206	ROPDLKYFGKSFDVSVSESSSLLSNDLPKFADGIKARNRNQNYL
6803	1533	1	VPSPVLRILDHTAFSTEKSADIVICDEECDSPESVNQQTQEESP
	ì	l .	IEVHTAEDVPIAVEVHAISEDYDIETENNSSESLQDQTDEEPPA
	1	į.	KLCKILDKSQALNVTAQQKWPLLRANSSGLYKCELCEFNSKYFS
	Į.		KECKIEDKSQAENVIAQQKWFEDRANOBOBIRCOBOBIRCOBOBI
	İ		DLKQHMILKHKRTDSNVCRVCKESFSTNMLLIEHAKLHEEDPYI
	1	i	CKYCDYKTVIFENLSQHIADTHFSDHLYWCEQCDVQFSSSSELY
	1	1	LHFQEHSCDEQYLCQFCEHETNDPEDLHSHVVNEHACKLIELSD
	į		KYNNGEHGQYSLLSKITFDKCKNFFVCQVCGFRSRLHTNVNRHV
		ì	AIEHTKIFPHVCDDCGKGFSSMLE\IAKHLNSHLSEGIYLCQYW
	į.	1	EYSTGQIEDLKIHLDFKHSADLPHKCSDCLMRFGNERELISHLP
			VHETT VALCFPNSDPVMFMDAFYGCLLAELGPVPIEVPLTRKDAGSQQV
6806	272	3794	VALCEPNSDPVMFMDAF IGCHLAEIGPVPTEVPHTRADAGGQQV
		}	GFLLGSCGVFLALTTDACQKGLPKAQTGEVAAFKGWPPLSWLVI
			DGKHLAKPPKDWHPLAQDTGTGTAYIEYKTSKEGSTVGVTVSHA
			SLLAOCRALTOACGYSEAETLTNVLDFKRDAGLWHGVLTSVMNR
			MHVVSVPYALMKANPLSWIOKVCFYKARAALVKSRDMHWSLLAQ
	ļ		RGQRDVSLSSLRMLIVADGANPWSISSCDAFLNVFQSRGLRPEV
	Į.		ICPCASSPEALTVAIRRPPDLGGPPPRKAVLSMNGLSYGVIRVD
			1CPCASSPEALTVAIRRPPDLGGPPPRRAVESTEGES IGVIRVD
			TEEKLSVLTVQDVGQVMPGANVCVVKLEGTPYLCKTDEVGEICV
]	SSSATGTAYYGLLGITKNVFEAVPVTTGGAPIFDRPFTRTGLLG
		1	FIGPDHLVPIVGKLDGLMVTGVRRHNADDVVATALAVEPMKFVY
			PGR LAVESVTVLHDDRIVLVAEORPDASEEDSFQWMSRVLQAID
			SIHQVGVYCLALVPANTLPKAPLGGIHISETKQRFLEGTLHPCN
		1	VLMCPHTCVTNLPKPRQKQPEVGPASMIVGNLVAGKRIAQASGR
			VEHICKTICY INDERENGING FOR STRUCTURE THE STRUCTURE TO THE STRUCTURE TO A DUTY OF THE STRUCTURE TO THE STRUCT
			ELAHLEDSDQARKFLFLADVLQWRAHTTPDHPLFLLLNAKGTVT
ļ			STATCVQLHKRAERVAAALMEKGRLSVGDHVALVYPPGVDLIAA
i .			FYGCLYCGCVPVTVRPPHPQNLGTTLPTVKMIVEVSKSACVLTT
	i		OAVTRLLRSKEAAAAVDIRTWPTILDTDDIPKKKIASVFRPPSP
		1	
	}		DVLAYLDESVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ
			DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ
			DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ IAICLDPYCGLGFALWCLCSVYSGHQSVLVPPLELESNVSLWLS
			DVLAYLDFSVSTTGILAGVKMSHAATSALCRSIKLQCELYPSRQ

			•
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first		S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	S=Serine, Tellifeonine, vevaline,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	_	\=possible nucleotide insertion)
	Bedacuec	 	LOGTAGPDPTTVYVDMRALRHDRVRLVERGSPHSLPLMESGKIL
1			PGVKVIIAHTETKGPLGDSHLGEIWVSSPHNATGYYTVYGEEAL
1			HADHFSARLSFGDTQTIWARTGYLGFLRRTELTDASGGRHDALY
1			VVGSLDETLELRGMRYHPIDIETSVIRAHRSIAECAVFTWTNLL
		1	VVGSLDETLELRGMRYHPIDIETSVIRARRSIAECAVFIWIND
1			VVVVELDGLEQDALDLVALVTNVVLEEHYLVVGVVVIVDPGVIP
1		1	INSRGEKQRMHLRDGFLADQLDPIYVAYNM
	1444	606	VGHDTVHAMFTCFPKCLGFSPPVNVTVSPRSEESHTTTVSGGNG
6807	1444	000	SVFQAGPQLQALANLEARRGSIGAALSSRDVSGLPVYAQSGEPR
1			RLTQAQVAAFPGENALEHSSDQDTWDSLRSPGFCSPLSSGGGAE
i i		•	KULUMUVAAR POEKABERSSDUD INSSERST OF COLDEGISM
1			SLPPGGPGHAEAGHLGKVCDFHLNHQQPSPTSVLPTEVAAPPLE
- !			KILSVDSVAVDCAYRTVPKPGPQPGPHGSLLTEGCLRSLSGDLN
			RFPCGMEVHSGQRELESVVAVGEAMA\LKFPMGAMSYCLRDRSR
1			FLFRLPMGLSCPLQVQ
		737	GVGSGAASALARSRPLASRLSSRRRTRAPRSGAMORLAMDLRML
6808	2063	1 '3'	SRELSLYLEHOVRVGFFGSGVGLSLILGFSVAYAFYYLSSIAKK
l			PQLVTGGESFSRFLQDHCPVVTETYYPTVWCWEGRGQTLLRPF\
		ļ	PQLVTGGESFSRFLQDHCPVVTET11PIVWCWEGRGQ1DDRFF (
1			ITSKPPVQYRNELIKTADGGQISLDWFDNDNSTCYMDASTRPTI
l		1	LLLPGLTGTSKESYILHMIHLSEELGYRCVVFNNRGVAGENLLT
ŀ		\	PRTYCCANTEDLETVIHHVHSLYPSAPFLAAGVSMGGMLLLNYL
1		Ĭ	GKIGSKTPLMAAATFSVGWNTFACSESLEKPLNWLLFNYYLTTC
1		1	LOSSVNKHRHMFVKQVDMDHVMKAKSIREFDKRFTSVMFGYQTI
j		1	DDYYTDASPSPRLKSVGIPVLCLNSVDDVFSPSHAIPIETAKQN
į			PNVALVLTSYGGHIGFLEGIWPRQSTYMDRVFKQFVQAMVEHGH
1	1	1	
	1	1	BLS
6809	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ
0000		1	TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF
1			GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV
	į.	i	EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
		1	VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPPIPTYG
	1	•	AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP
		İ	AVVYQDGFYGAET\LEATQPIDTDSPDQAAQFTATVTABSTQ21
		l	TRTITPSGPRRPTALEPCETFHRFLLGP
6810	939	65	DYSGQTPVPTEHGMTLYTPAQTHPEQPGSEASTQPIAGTQTVPQ
	1	1	TDEAAQTDSQPLHPSDPTEKQQPKRLHVSNIPFRFRDPDLRQMF
	1	1	GQFGKILDVEIIFNERGSKGFGFVTFETSSDADRAREKLNGTIV
i			EGRKIEVNNATARVMTNKKTGNPYTNGWKLNPVVGAVYGPEFYA
ı			VTGFPYPTTGTAVAYRGAHLRGRGRAVYNTFRAAPPPPPIPTYG
i	1		AVVYQDGFYGAEI\LEATQPTDTLSPLQRRQPTATVTAESTQLP
í	Ì		
ł			TRTITPSGPRRPTALEPCETFHRFLLGP
6811	1522	658	DLVTVWSFVDCRVIASTHGH\KSWVSVVAFDPYTTSVEEGDPME
1			FSGSDEDFQDLLHFGRDRADSTQCRLSRRNSTDSRPVSVTYRFG
1			SVGQDTQLCLWDLTEDILFPHQPLSRARTHTNVMNATSPPAGSN
Í		ļ	GNSVTTPGNSVPPPLPRSNSLPHSAVSNAGSKSSVMDGAIASGV
1		Ì	SKFATLSLHDRKERHHEKDHKRNHSMGHISSKSSDKLNLVTKTK
1	1	1	TDPAKTLGTPLCPRMEDVPLLEPLICKKIAHERLTVLIFLEDCI
1			
			VTACQEGFICTWGRPGKVVSFNP
6812	4001	1682	EDAVFSLDLSTIIQGTWFLNGEELKSNEPEGQVEPGALRYRIEQ
1		1	KGLOHRLILHAVKHODSGALVGFSCPGVQDSAALTIQESPVHIL
l .	1		SPODKVSLTFTTSERVVLTCELSRVDFPATWYKDGQKVEESELL
1	1		VVKMDGRKHRLILPEAKVQDSGEFECRTEGVSAFFGVTVQDPPV
			A A ULI DOLUMENT DE EURA Ó DOQUE DOUGLE DO CALLO COLORDO
		1	
			HIVDPREHVFVHAITSECVMLACEV\DR\EDAPVRWYKDGQEVE
			ESDEVVLENEGPHERLVLPATOPSDGGEFQCVAGDECAYFTVTI
			ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGE
			ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGB EVVESPALLLOKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT
			ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGB EVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT VTVTRPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK
			ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGB EVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT VTVTRPPVRIIYPRDEVTLIAVTLECVVLMCELSREDAPVRWYK
			ESDFVVLENEGPHRRLVLPATQPSDGGEFQCVAGDECAYFTVTI TDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPWAEVRWTKDGB EVVESPALLLOKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFT

Deginning		F 500 32 00 03	Predicted end	Amino acid segment containing signal peptide
NO: nucleotide corresponding to first manno acid residue of sanino acid residue of anino acid residue of anino acid adverse company of the co	SEQ	Predicted		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Corresponding to first amino acid residue of amino acid acid amino acid acid acid acid acid acid acid acid	i .	1		Glutamic Acid, F=Phenylalanine, G=Glycine,
Leleucine, Membethionine, Ne-Asparagine, amino acid residue of amino acid residue of amino acid equence acid equence aci	NO:			u_wistidine T=Isoleucine K=Ivsine,
amino acid amino acid		l .		I Lougine M-Methionine N=Asparagine.
amino acid residue of amino acid sequence ##TTP/ptophan, Y=Yprosine, X=Unknown, *=Stop Codon, /=possible nucleotide deletion,				Denetice O-Clutamine P-Arginine
### Tryptophan, Y-Tyrosine, X-Unknown, *-Stop amino acid sequence		to first		peproline, Qediudamine, Realignine,
amino acid sequence Codon, /-possible nucleotide deletion, /-possible nucleotide deletion /-possible nucleotide insertion WSSMORPVOEGSGLEHAESPRYLCTGAASPAHAGIYTCOSG APPCAPSISTYOUGHAGARGATURVESTROGILLUVH ISCRGEDYRRYKTGERLASQSRYOLEGAGARGATURVESTROGILLUVH ISCRGEDYRRYKTGERLASQSRYOLEGAGARGATURVESTROGILLUVH ISCRGEDYRRYKTGERLASQSRYOLEGAGARGATURVESTROGICHOGORGAT CEVENPOADVITHLENGAVUTFOORGCCSVGGENCGORGAGA CEVENPOADVITHLENGAVUTFOORGCCSVGGENCGORGATA CVERROADRAVCHORGACGCVGGENCTTHLACPWFRMOTSTASSS WYSYWTRAPTARARTILAPWGSA 816 SSTOCKPGVPAGPRELDGYLGVADRKPRMOTSTASSS WYSYWTRAPTARARTILAPWGSA GRIERRARDLANVSGGTVPIFWOPSSYMRROCKGOVYNNIHLIS GRIERRARDLANVSGGTVPIFWOPSSYMRROCKGOVYNNIHLIS GRIERRARDLANVSGGTVPIFWOPSSYMRROCKGOVYNNIHLIS GRIERRARDLANVSGGTVPIFWOPSSYMRROCKGOVYNNIHLIS THTIALELCORINVYGGGPPOFCOPHNIESVYHIYYEPFGPDEC THYLSHEGGRISAPHRANGFTIERRYCHAWARTFHIHPFOPWKEPS LAIMPPENKEVF RERROSM/AREENNEMIGLINGALDAHLRAVVPCYSKTQKLSKIFT THIALELCORINVYGGPPOFCOPHNIESVYHIYYEPFGPDEC CLOLARSFILMGGGERAHHTRSTVATYPPHSPELTTPFOGG TLORARSFILMGGGERAHHTRSTVATYPPHSPELTTPFOGG CLOLARSFILMGGGERAHHTRSTVATYPPHSPELTTPFOGG TLORARSFILMGGGERAHHTRSTVATYPPHSPELTTPFOGG GRINGARDANVFIN MSIESKAGETLOVACHNYNYCHMYCOPPSGLAGAAGARFREPDL SHPYDLAHLRSGGLINGDELANVFIN MSIESKAGETLOVACHNYNYCHMYCOPPSGLAGAAGARFREPDL SHPYDLAHLRSGGLINGDELANVFIN MSIESKAGETLOVACHNYNYCHMYCOPPSGLAGAAGAAFREEDLE DVGCDANASFILMGANFINASHERPTVACPGANVCKURCEEN SHPADATHARVACHAGAAGAAGAAFREEDLE SHPYDLAHLRSGGLINGGGRESSRAMAGAAGAAFREEDLE SHPYDLAHLRSGGLINGGGRESSRAMAGAAGAAFREEDLE SHPYDLAHLRSGGLINGGGRESSRAMAGAAGAAFREEDLE SHPYDAARAGAAGAAGAAFREEDLE GRINGARDANAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		amino acid		S=Serine, T=Threonine, v=vailine,
### Sequence Vaposible nucleotide insertion	ŀ	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, -=Stop
Apposible nucleotide insertion	[amino acid	sequence	Codon, /=possible nucleotide deletion,
WSSINGERVOGESGLELHAGGERVALCHAGERIANGSITUGGAS ARDEAPSLSTIVOLAREPPRIVATE PLANGUES LIVE LIGGEGEVENT LIGGEGEVENT LIGGEGEVENT LIGGEGEVENT CUCKENDED AND THE FLAVSVEEP LIVEL VISUALITY LIPERDDATER CEVS PDADUTHLINGAVUT POPORS CCS YGGCENCOGARAT CUCKENDADER FLAVSVEEP LIVEL VISUALITY LIPERDDATER CEVS PDADUTHLINGAVUT POPORS CCS YGGCENCOGARAT CUCKENDADER COLLEGE PLANGUED CANCEL AND TO CHECK THE COLLEGE PLANGUED CANCEL AND THE CANCEL AND THE COLLEGE PLANGUED CANCEL AND THE CA	Ì	1	1	\=possible nucleotide insertion)
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GEYLCDAPQDER IFLUSVEEPLLVIKUSDLTPLTVHERDDAFFR CEVSPPDADVIKURNAVUVTEPGORQSCCSTGGCMGGGRKAGGRAFT CVEKWQAEWVQRGPCAGCEVGSPCPTTLACPPFRMTTSTASS MYSYPTRAPARATITAPPGORA 6813 9 836 SSTQORFGVFAGFRPLDGYLGVADHKPIKMHCRCCALVTSGHL LHSRQGSGILDTROVIRNDAPTRGYGRDVGNATSLRVIAMSSI QRILRARHLINVGCOTPT IFMOPSIMARDKRQVYNNLHLLS QVLBRIKAFMITHRKHLOFDELFKOETTQVNKKISNTWLSTGHF TMTLAELCOR INVYGMOPPOFCOPNINESVPHYTYEPFGPDEC LAIMHEPENEPF 6814 3 737 KRERGERIN JARENRYMHGLINDALDNILRKVVPCYKTQLLSKIET LHAKNYINALSEILRIGKREPDLLTFVONLCKSLSQPTTHLVAG CLQINARSELMOGGGRAHHTRSPYSTFYPPYHSPELTTPGHG TLDNSKSMKPNYNCSAYSEFFSTSPECASPCEGGISPPINY MOISLKOSETLDVGGNYNYGMYCAVPPROPLOGGAMFRLPTD SHEPYDLHLRSQSLTMODELANVEN 6815 906 553 QGLDFASGYRVVELLKDGSGRRGDRSSRDMAGGAGPSSEDLE DVGFTARMNGDGSGSLRRSGSFOKKAGAGPSSEDLE DVGFTARMNGDGSGSLRRSGSFOKKAGAGPSSEDLE SPHSKKRARSSLAPLIKSVERPTORS 6816 1 803 NLLKTHKFYLLGODEDSHBYVVAKOGNYGVYLKTLASPIREID POPERLHTFORPYKOKKAGMIDEADEFVAGQNKVRRGGEN SPHSKRKRARSSLAPLIKSVERPTORS LKPTLVHTDATI HIHGHERMOGGTOFLSKSABSELIK TUDMPPNQVDSLSDDFTSLSKOLLQKGSOPSANFYSYN LKKPTLVHTDATI HIHGHERMOGGTOFLSKSABSELIK TUDMPPNQVDSLSDDFTSLSKOLLQKGSORAFVSRSASSLIN TUDMSPNOVDSLSDDFTSLSKOLLQKGSORAFVSRSASSLIN LEADTVDMATTIDATTUDSTGTREFPONGCTSKLEMPLESK GRSK 6817 172 3457 LOMMSSPKIGNGLFVIGTSSNLPPSNCCTSKLEMPLESK CLOMMSSPKIGNGLFVIGTSSNLPPSSQQNP IRTADELERNEI LEADTVDMATTIDATTUDSTGTREFPONGCTSKLEMPLESK CLOMMSSPKIGNGLFVIGTSSNLPPSSQQNP IRTADELERNEI LEADTVDMATTIDATTUDSTGTREFPONGCTSKLEMPLESK CLOMWSDEIT SLOPQLGCTIGDMES PVARPLLIKLETHIEL FLYSSBUFECSQCGHYQNRIMSLAUTTITN IP EMPLANDE GELVOITSVIGTSSNLPDSSLANSLAUTTITN IP EMPLANDE GELVOITSVIGTSSNLPDSSLANSLAUTTITN IP EMPLANDE GELVOITSVIGTSSNLPDSSLANSLAUTTITN IP EMPLANDE GELVOITSVIGTSSNLPDSSLANSLAUTTITN IP EMPLANDE KREEPPALTVORMATTLATERDESPONGCTSKLEMPLESK CLUMPTER SLANDARDARDARDARDARDARDARDARDARDARDARDARDARD]		ļ	AAPGAPSLSFTVQVAEPPVRVVAPEAAQTRVRSTPGGDLELVVH
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LAINHPENKPVF	1	İ	1	TMYLSHERGRKGSHHRFITEKRVFKNWARTFNIHFFQPDWKPES
RFRQEAN / AREENRHEGINDALDNILKRVVPCYSKTQKISKIFT IRLAKNYI WALSEILRIGKRPDLITFVQNICKGLSQPTTNILVAG CLQLNARSFIMGGGEARHTHSPYSTFYPPYHSPELTTPPGHG TLDNSKSMKPYNYCSAYESFYESTSPECASPCEGFLSPPINY NGIFSLKQESTLDYGNYNYGHYLGAVPPROPIGQGAMPFLETU SHEPYDLHIRSQSLTMQDELNAVPHN GSLDPASQTKVVELLKGSGRRGDRSSRDMAGGAGPRSESDLE DGPTAEWNGDGSGSLRRSGSSRCMLRDALRRSSEMLVKKLQGGT PQEPPNPRMKRASSLMFLMKSVEBTTQPX3 NILKTHKF\LLGQDEDSLHSVDAMGMYGRYLKTLASPIREID PPOPRRHTHFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEN SPMSSKRRRSMSLLLKRPGTPTTVTNHVGGGRPSASMFPSYPN LIKPTLVHTDATITHGHERKMENQGITPDGFISKSAPSEILNM TGDLMPPNQUDSLSDDFTSLSKGGLIQKPGSNAFVGGAKKCSLS VDDKDPVASTLGAMPNTLQITFAMAQGINADIKHQLMKEVRKF GRSK LEMMSPRIGGLEVIGPGTDIGISSLHMVGYLGKNFDSAKVPS GRSK LEMMSPRIGGLEVIGPGTDIGISSLHMVGYLGKNFDSAKVPS GRSK LEMMSPRIGGLEVIGPGTDIGISSLHMVGYLGKNFDSAKVPS GRSK LEMDTUMATTKDPATTUDVSGTGRPSPONGCTSKLEMPLESKC TSFPQALCVQKKNAYALCHLGCISALHNSECHNTVIGLGSKE ESIFWELLTKYNQAMATLLYTSQLGYDDGCKTSKLEMPLESKC TSFPQALCVQKKNAYALCHLGCILSALHNSECHNTVIGLGSKE ESIFWELLTKYNQAMATLLYTSQLGYDDGCKTSKLEMPLESKC TSFPQALCVQKNAYALCHLGCILSALHNSECHNTVIGLGSKE ESIFWELLTKYNQAMATLLYTSQLGYDDGCKTSKLEMPLESKC TSFPQALCVQKNAYALCHLGCILSALHNSELNTVIGLGSKE ESIFWELLTKYNQAMATLLYTSQLASH GPCNNCNSKGJIRKWLEKVSPIPHLHFVELPQNDLQHYAFHF EGCLYQITSVLQYRANNHFITWILDADGSWLECDDLKGPCSBHH KKPEVPASSHIHLVWERKISQVTHASACLIPLKTNOQHALSKE KKPEVPASSHIHLVWERKISQVTHASACLIPLKTNOQHALSKE KKPEVPASSHIHLVWERKISQVTHASACLIPLKTNOQHALSKE VVNTNNQSVQLNTEDTVNTKSVNNTDATIGLIGVKSVEIEKDAQ LKQFLTPKTEQLKPRTVTSGVSLKKETTADSGTTTSKSLQNG LKQFLTPKTEQLKPRTVTSGVSLKKETTADSGTTTSKSLQNG LKQFLTPKTEQLKPRTVTSGVSLKKETTADSGTTTSKSLQNG LKQFLTPKTEQLKPRTVTSGVSLKKKETTADSGTTTSKSLQNG SKNGTAAHPHAHAASEVLEKKSGCAQALHISSTGTTSKSLGNG SKNGTAAHPHAHAASEVLEKKSGCAQALHISSTGTTSKSLGNG SKNGTAAHPHAHAABASEVLEKKSGCAQALHISSTGTTSKSLGNG SKNGTAAHPHAHAABASEVLEKKSGCAQALHISSTGNGGISSANH EDLVEGGIHKLBLURKPTILDELPYPT I DIAMESACTTVPGVSLYSK CTHEBILABLLSPTFVSTBLEBRGGDFRYLGMGSHIPPPVPS EFRIDVSGNITHLRQDHNYCSPTKKNDECDQDDSLTNNACVATILM EPPMKYNTI I DEDEFSSALNALANDECDQ	1	1		LAINHPENKPVF
LELAKNYIWALSEILRIGKPPLLITFVORLIKGLSQPTINLVAG CLQLNARSFLMQGGEAAHTHES PYSTPYPYHS PELTYPPGHG TLDNSKSMKPYNYCSAYESFYESTSPECASPQFEGPLSPPPINY NGIFSLKQBETLDYGKNYNYGHYCAVPPROPLQQAMFRLPTD SHPYDDLHLRSQSLTMQDELNAVPHN OGSPLKDESTLDYGKNYNYGHYCAVPROPLQQAMFRLPTD SHPYDDLHLRSQSLTMQDELNAVPHN OGSPLAEMAGGAGFRESSDLE DWGPTAEMAGGAGFRESSDLE DWGPTAEMAGGAGFRESSDLE DWGPTAEMAGGAGFRESSDLE DWGPTAEMAGGAGFRESSDLE DWGPTAEMAGGAGFRESSDLE DWGPTAEMAGGAGFRESSDLE DWGPTAEMAGGAGFRESSDLE DWGPTAEMAGGAGFRESSDLE DWGPTAEMAGGAGFRESSDLE DWGPTAEMAGGAGFRESSDLE DWGPTAEMAGGAGFRESSDLE DWGPTAEMAGGAGFRESSDLE SHEWLELLAGODEDSLHSVPVAGMGNYGGYLKTLASPLREID POPKRLHTFGNPFKQDKKSMMIDEADEPVACPOMYKAPGEFN SMSSKRRESMSLLLKRPQTPPTVINHVGGKGPPSASWFPSYPN LIKPTLVHTDATIHHGHEEKMENQQITPDGFLSKSASPSELIMM TGDLMPPNQVDSLSDDFTSLSKDLIKPGSANTVAGGAGANCGLS VDDQKDPVASTLGAMPNTLQITFAMAQGINADIKHQLMKEVRKF GRSK LEMPHQNOUTSLSDDFTSLSKDLIKPGSANTVAGAKTENYA DEYCPACKEKGKLKALKTYRISFQSSIFLCEDLQCIYPLGSKSL NNLISFDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTENYA LOGGKYLNSKHINGEVYDETSSNLIPDSSQQFRIRTADSLERNEI LEADTVDMATTKDPATTUVSGTGREPSPONEGCTSKLEMPLESKC TSFPQALCVQKKNAYALCMLDCINPDSSGQFRIRTADSLERNEI LEADTVDMATTKDPATTUVSGTGREPSPONEGCTSKLEMPLESKC TSFPQALCVQKKNAYALCMLDCINPDSSGQFRIRTADSLERNEI CLINEVEDSIFTSLQPQLRCTLIGGMESPVFAFFLLLKLETHIEKL FLYSFSPWDFECSQCGHQYONRHMKSLVYFTNVITGLGKSE SISTMALHTANAVALCMLDCINCHKSLVYFTNVITGLAGKE GESTPRUNCHKSQIRKMVLEKVSPIPMLHFVEGLPQNDLQHXAFHF GPCNNCNSKSQIRKMVLEKVSPIPMLHFVEGLPQNDLQHXAFHF GPCNNCNSKSQIRKMVLEKVSPIPMLHFVEGLPQNDLQHXAFHF GPCNNCNSKSQIRKMVLEKVSPIPMLHFVEGLPQNDLQHXAFHF GPCNNCNSKSQIRKMVLEKVSPIPMLHFVEGLPQNDLQHXAFHF GPCNNCNSKSQIRKMVLEKVSPIPMLHFVEGLPQNDLQHXAFH GPCNNCNSKSQIRKMVLEKVSPIPMLFUNGHANHFITDLQPS VXNTINQSVQLNTEDTVNTKSVNNTDATGLIGGVKSVEIEKDAQ UXTINNQSVQLNTEDTVNTKSVNNTDATGLIGGVKSVEIEKDAQ UXTINNGSVQLNTEDTVNTKSVNNTDATGLIGGVKSVEIEKDAQ UXTINNGSVGLNTEDTVNTKSVNNTDATGLIGGVKSVEIEKDAQ UXTINNGSVGLNTEDTVNTKSVNNTDATGLIGGVKSVEIEKDAQ UXTINNGSVGLNTEDTVNTKSVNNTDATGLIGGVKSVEIEKDAQ UXTINNGSVGLNTEDTVNTKSVNNTDATGLIGGVKSVEIEKDAQ UXTINNGSVGLNTEDTVNTKSVNNTDATGLIGGVKSVEIEKDAQ UXTINNGSVGLNTEDTVNTKSVNNTDATGLIGGVKSVEIEKDAQ UXTINNGS		<u> </u>	727	KERROEAN/ARERNRMHGLNDALDNLRKVVPCYSKTQKLSKIET
CLQLNASSFLMGQGGRAAHTRSPYSTTYPPYBSPELTTPOHG TLDNSKSMKPYNYCSAYESTYBCTSPEGDSPPERSPENTY NGITSLKQESTLDYGKNYNYGMYCAVPPRGPLGQGAMFRLPTD SHPPYDLHLRSQSLTMQDELNAVFIN GLDPASQTKVVELLKDGSGRRGDRSSSRMAGGAGPRSESDLE DWGPTAEMNOBGSGSLRRSGSFGKLRDALRRSSEMLVKKLQGGT PGEPPNPRMKRASSLAFLAKSVEBTTQPXG 6816 1 803 NLLKTHKP\LLGQDEDSLHSVPVAMGMYGGYLKTLASPLREID PQCPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SMSSKRRRSMSLLLKRPQTPFTVTNHVGGKGFPSASMFPSYPN LLKPTLVHTDATITHGHEEKHENQGITPDGFISKSAPSELITM TGDLMPPNQVDSLSDDFTSLSKGGLIQKPGSNAFVGGAKNGSLS VDDQKDFVASTLGAMPNTLQITPANAQGINADIKHQLMKEVRKF GRSK 6817 172 3457 LGMMDSPKIGNGLBVIGPGTDIGISSLHWVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA ILDGKVLNSKHNGBVVDETTSNIPDSSGQVBFIATADSLERNBI LEADTVUMATTXDPATTUVSGTGPSPPQNBGCTSKLEMPLESKC TSFPQALCVQMKNAYALCVLDCILSALVHSEELKNTVTGLCSKE ESIFWRLIKYNQANTLLVTSQLSGVKGODCKKLTSSIFABIBT CLABEVEDEITSISLOPQLKCTLGBMESPVPAFPLLKLETHIERL FLYSFSMDFECSQCGHQYQNRHMKSLVTFTNVIPEMBLMAAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVELPQNDLQHYAFHF EGCLYGITSVJQYRANNHFITATLDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVIDKEAACLPLKKTNOCHALSNE KPYSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGFKGLVNNIHLDLTLEETIQKTASVSQLNSEAFIL\LENTFPSQ VVNTNMQSVQLNTEDTVATKSVNNTDATCLIQCVKSVEIEKDAQ LKQFLTPKTEQLKFERVTSQVSNLKKKETTADSQTTTSKSLONQ SLKENQKKPFVGSWKGLISRGASFMPLCVSAHNRITITDLQFS SKNCTAAHHHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGGIHKLRLKLRKKLKABLKKKLAALMSSPOSRTVRESNLE QVPQDGSPMCES IEDLINBLYCTVPOVSLYSS CTHEBILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPDVS EFFIDVSQNTHLRQDHNTQSPTKKNDCPHYRDSVTRLA	6814	3	'3'	LRIAKNYIWALSEILRIGKRPDLLTFVQNLCKGLSQPTTNLVAG
TIDNSKSMKPYNYCSAVESFYESTSPECASPOFEGFLSPFINY MGIFSLKQEETLDYGKYNYUGMYCAVPPRGPLGQGAMFRLPTD SHPPYDLHIRSQSLTMQDELNAVPHN 6815 906 553 QGLDPASGTKVVELLKKDGGGRGDRRSSEMMGGAGFRSESDLE DVGPTAEMINGDGSGSLRRSGSFKKIRDALRRSSEMLVKKLQGGT FQEPPNPRMKRASSLNPLNKSVERPTOPGG NLLKTHKF\LLGQDEDSLHSVPVAQMGTVGPYLKTLASPLREID PDOPKRLHTFGNPFKQDKKGMIDEADEPVAGFQNKVKRPGEPN SPMSSKRRSMSLLLRRPQTPPTVTNINVGGKGPPSASWFPSYPN LIKPTLVHTDATI I HDGHEEKMENQGI TPDGFLSKSAPSELINM TGBLMPPPNQVDSLSDDTTSLSKDGLI QKPGSNAFVGGAKNGSLS VDDQKDPVASTLGAMPNTLQI TPAMAQGINADI KHQLMKEVRKF GRSK 172 3457 LOMMDSPKIGNGLPVIGFGTDIGISSLHMVGYLGKNFDSAKVFS DEYCPACKEKGKLKALKTYRTSFQBST FLCEDLQCI YPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNP IRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRFSP/ORSGCTSKLEMPLESKC TSFPOALCVGWRAYALCHLOCILSALVHSEELKNTVTCLGSKE ESIFMELLIKYMQANTLLYTSQLSGVKLGDCKKLTSBIFABLBT CLNEVKDEIFISLQPQLRCTLGDMSS PVFAPFLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMSLVTFTNVJ PEWHPLNAAHF GPCNNCNSKGITRKWLEKVSBIFMLHFVBLPQNDLQHYAFHF EGCLYQITSVIQ YRANNIFI TIWHLDADGSWLECDDLKGPCSBEH KKFEVPASBIHVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHRKDI EVAPRTLSOUTAVTHGO HLLSGPKGLVBNILPLTLEETI QKTASVSQLNSEAFL\LENKV AENTGILKTNTLLSQBSLMASSVSAPCNEKLIODGFVDISFPSQ VVNTTMNQSVQLNTEDTVXTKSVNNTDATGLIQCVKSVEIEKDAQ LKGPCTPKTEGLKPREVTSQVSNLKKKETTADSGTTTSKSLQN SKKONKFPVGSWVKGLISRGASFMPLCVSAHRNNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARXSASKPP PISKPPAGPP VKGVNNFGFKTKGINQKASHVSKKARXSASKP PISKPPAGPP SSNCTAAHPHAHAASEVLEKSGSTSCGAQINHSS YGNGISSANH EDLVEGGIHKLRIKLKKKKLKASKKKLAMAMSSPOGRSTVRSENLE OVPQGSPNDCBS IBDLLENG PYPI LI ANESACTTVPGVSLYSS CTHEBILLSETPVSTELSENGEGDFRYLGMGDSHIPPVPS EFFIDVSONTHLRQDHNYCSPTKKNECEVQPDSLTNNACVATLAL ESPHKYTLI FDEPSSSALMALALANDSTLOUSTIVAL	1			CLOLNARSELMGOGGEAAHHTRSPYSTFYPPYHSPELTTPPGHG
MGIFSLKQEETLDYGKNYNYGMEYCAVPPRGPLGQGAMFRLPTD GHPPYDLHIRSQSLTMQDELNAVPHN GHPPYDLHIRSQSLTMQDELNAVPHN GHPPYDLHIRSQSCHMGRSSRCMAGGAGPRSSDLE DUGPTAEMAGGASGSKERSGSFGKLRDALRRSSEMLVKKLQGGT PQEPPNPRMKRASSLNFLNKSVERPTOPGG SULKTHKF\LLGQEDELHSVPVAQMGNYQBYLKTLASPLREID PDOPKRLHTFGNPFKQDKKGMMIDRADEPVAGPMGKVARPGEPN SPMSSKRRSMSLLIRKPQTPPTVTNIVGGKGPSASWFPSYPN LIKPTLVHTDATIIHDGHERMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDTTSLSKDGLIQKPGSNAFVGGAKNGLIS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVKF GRSK GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEVCPACKEKGKLKALKTYRISFGBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLANSKHNGEVYDBTSSNLPDSSGQNPIRTADSLERNEI LEADTOMATTRDPATVDVSGTGRPSPQNBGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFMELLIKKYNQANTLLYTSQLSGVKDGDCKKLTSEIPAELST CLMEWPDEIFISLQPQLECTIGDMESVPFAPPLLLKLETHIEKL FLYSFSWDFCCSQCGHQVQNRHMKSLVYFTNVIPEMPINAAHF GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF GPCNNCNSKSQIRKMVLBKVSPIFMLHFVEGLPQNDLQHYAFHF GPCNNCNSKSQIRKMVLBKVSPIFMLHSCHCDDLKGPCSERH KKFEVPASBIHIVIWERKISQVTNCHAACLFLKKTNOPALISME KKFEVPASBIHIVIWERKISQVTNCHAACLFLKKTNOPALSHM KKPEVASBIHVIWERKISQVTNCHAACLFLKKTNOPALSHM KKPEVASBIHVIWERKISQVTNCHAACLFLKKTNOPALSHM KKPEVASBIHVIWERKISQVTNCHAACLFLKKTNOPALSHM KKPEVASBIHVIWERKISQVTNCHAACLFLKKTNOPALSHM KKPEVASBIHVIWERKISQVTNCHAACLFLKKTNOPALSHM KKPEVASBIHVIWERKISQVTNCHAACLFLKKTNOPALSHM KKPEVASBIHVIWERKISQVTNCHAACLFLKKTNOPALSHM KKPEVASBIHVIWERKISQVTNCHAACLFLKKTNOPALSHM KKPEVASBIHVIWERKISQVTNCHAACLFLKKTNOPALSHM KKPEVASBIHVIWERKISQVTNCHAACLFLKKTNOPALSHTNATITTLLQPS VVNTMQSVOLNTEDTVATKXSVNNTDATGLIQGVKSVEIKKDAQ VVNTMQSVOLNTEDTVATKXSVNNTDATGLIQGVKSVEIKKDAQ VVKTMRGSCHTLEGURGEGTFTVGSOLSLANS SKKTAAHPHAAASEVLEKSGSTSCGAQLNHSSYGNGISSANH DUFGGGIHKLRLKLKKKLKABKKLLAALMSSPOSRTVRSENLE OVPQGSPNOCES IBELLIAUELPYPI DIANESACTTVPGVSLYSS OVPGGSPNOCES IBELLIA	1			TI DNCKCMKDYNYCGAYFGFYESTSPECASPOFEGPLSPPPINY
SHEPYDLHLRSQSLTMQDELNAVPHN	ļ	ì		THE PARTY PACKATUNING MUYCA VPPROPRING AMERIAPTE
G815 906 553 QGLDPASQTKVVELLKDGSGRRGDRRSSRDMAGGAGPRSESDLE DWGPTAEMNGDGSGLRRSGSPKLIRDALRRSSEMLVKKLQGGT POEPPNPRMKRASSLNFLNKSVEBTOPGG 6816 1 803 NLLKTHKF\LLQDEDSLHSVPVAQMGNYGEYLKTLASFLREID PDOPKRLHTFGNFFKQDKKGMAIDEADEFVAGPQNKVKRPGEPN SPMSSKRRRSMSLLLRKPQTPPTVTINHVAGKGPPSASMFPSYPN LIKPTLVHTDATIIHDGHEEKMENQQITPGGFLSKSAPSELINM TGDLMPPNQVBSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK 172 3457 LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKIKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKYRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTUDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQMKNAYALCHLDCILSAUMSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGWKEDGDCKKLTSEIFAELET CLNEVEDEIFISLQPQLGCTLGEMESPVPAFPLLLKLETHIEKL FLYSFSWDFECSQCGRQYQNRHMSSLVTFTNVIPPEMPHLNAAHF GPCNNCNSKGIRKMLERPIPPMLFWGLPONLOKHYAFHF EGGLYQITSVIOYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTUKBAACLPLKKTNDQHALISNE KPVSLTSCSVGDASASATASVTHEKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPY AENTGILKINTTLLSGESLMASSVSARCNEKLIQDGVUSTEIKDAQ VVNTNMGSVQLNTEDTVNTTKSVNNTDATGLIQVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTASQTTTSKSLONG SLKENGKKPFVGSWYKGLISRGASFPPLCVSAHIRMTITTDLGS VKGNNFGGFKTKGINGKASHVSKKARKSASRPPFISKPPAGPP VKGNNFGGFKTKGINGKASHVSKKARKSASRPPFISKPPAGPP SSNCTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSAMH EDLVEGGIHKIRLKLRKKLKAEKKKLAALKKALAKKKLAALKKLABIKKKLAALKKABLKKLALANSFORSTVRSENLE QVPQGSPNCESIEDLLABLPYPIDIFSVSCHINACVRTLNL ESPHKTDIFPOFFSSSALNALANDTLDLPHEDEYLFENY		ŀ	1	
DUGPTAEMNGDGSGSLRRSGSFGKLKADALRRSSEMLVKKLQGGT PQEPPNPRMKRASSLNFLNKSVEEPTQPGG NLKKTHKFYLLGQDEDSLHSVVAQMGMYQEYLKTLASPLREID PDQPKRLHTFGNPFKQDKKGMMIDRADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLRRQTTPPTVTNHVOGKGPPSASWPPSYPN LKRPTLVHTDATTI HEDHEEKMENQQI TPDGFLSKSABSELINM TGDLMPPNQVDSLSDDFTSLSKUGLIQKFGSNAFVGGANCGLS VDDQKDPVASTLGAMPNTLQITFAMAQGINADI KHQLMKEVRKF GRSK 172 3457 LGMMDSPKIGNGLPVIGPGTDIGI SSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKILKALKTYRI ISPGES IFLCEDLQCI YPLGSKSL NNLISPDLEECHTPHKPQ RKSLESSYKDSLLLANSKKTRNYI A IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNP IRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGGTSKLEMPLESKC TSPFQALCVQWKNAYALCHJCILSALVHSEELKNTVTGLGSKE ESSTMELLTKYNQANTLLYTSQLSGVKDGDCKKLTSEI FAEIET CLMEVRDEI FISLQPQLRCTLGGMESPVRAFPELLKLETHIEKL FLYSFSMDFECSQOGHQYQNRHMKSLVTPTNVI PEMPLENAAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAPHF EGCLYQITSVIOYRANNHFITWILDADGSWLECDDLKGPCSHA KKFEVPASEIHIVIWERKISQVTDKERACLPLEKKTNDCHALSNE KPVSLTSCSVGDAASAETASVTHPKDI SVAPRTLSQDTAVTHGD HLLSGPKGLVDNILBLTLLEETIGKTASVSQLNSEATL\LENKFV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDGFVTJSFPSQ VVNTNMGSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTGOLKPERVTSQVSNLKKKETTADSQTTTSKSLONQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGNNNGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYCNGISSANH EDLVEGGIHKLRIKLKKKLKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNCESIEDLLIANSPPCSTVLGMGSHIPPPVS SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYCNGISSANH EDLVEGGIHKLRIKLKKKLKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNCESIEDLLIANLANDTIDLIPHFDEYLFENY CTHEBILAELLSPTPVSTBLSENGEGFRYLGMGSHIPPPVS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPHKTDIFFDFFSSSALNALANDTIDLPHEDEYLFENY	1			SHPPYDLHERSQSLTMQDELINAVFAN
PQEPPNPRMKRASSLMPLNKSVEBPTOPGG NLKYHKF\LIGQDEDSLHSVPVAQMGNYQBYLKTLASPLREID PDOPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN SPMSSKRRRSMSLLLRKPQTPPTVTNHVGGKGPPSASHPPSYPN LIKPTLVHTDATIHDCHERMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDDPTSLSKODLIQKPGSNAFYGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEVCPACKERGKLKALKTYRISFQBSIFLCEBLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVINSKHNGEVYDETSSNLPDSSQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNBGCTSKLEMPLESKC ESIFMRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFABIET CLNEVRDEIFISLQPQLRCTLGDMES PVPAFPLLIKLKETHIEKL FLNSFSMDFECSQCGHQYQNRHMKSLVTPTNVIPEWHPLNAAHP GPCNNCNSKSQIRKMVLEKVSPITMLHFVBGLPQNDLQHYAPHF EGGLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSRCH KKFEVPASEHHIVLWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLUNNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENNGILKTNTLLSGSLSMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKGPLTPKTEQLKPERVTSQVSNLKKKETTASQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHHAHASEVLEKSGSTSCGAQLMISSYCNGGISSANH EDLVEGGIHKLRLKKLKKLKKALMSPSQSTVRSENLE OVPQDGS PNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTBLSENGEGDFFYLKMGDEHIPPPVS EFNDVSONTHLRQDHNYCSPTKKNDCEVQPDSLTNNACVRTLNL ESPMKTDITDPFFSSSLAINALANDTLDLPHFDEYLFENY	6815	906	553	QGLDPASQTKVVELLKDGSGRRGDRRSSRDMAGGAGFRSESDIE
S03 NILKTHKF\LIGQDEDSLHSVPVAQMGNYGEYLKTLASPLREID PDQPKRLHTTGNPFKQDKKGMIDBADEFVAGPQNKVKRPGEPN SPMSSKRRSMSLLLKRPQTPPTVTNHVGGKGPPSASMFPSYPN LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM TGDLMPPNQVDSLSDPTSLSKDGLIGKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVKKF GRSK LCMMDSPKTONGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFGBSIFLCEDLQCIYPIGSKSL NNLISPDLEECHTPHKPQKKKSLESSYKDSLLLANSKKTRNYIA IDGKVLNSKHNGEVYDETSSNLPDSSGQOPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNBEGCTSKLEMPLESKC TSFPQALCVQWKNNYALCMLDCILSALVHSEELKNTVTGLCSKE ESIFWRLITKYNQANTLLYTSQLSGVKDGDCKKLTSEIFABIET CLMEVRDEIFISLQPQLCCTLGDMESPVFAPPLLLKLETHIEKL FLVSFSMPFESQCGHQYQNRHMKSLVTFTNVIPPSWHPLNAAHF GPCNNCNSKSQIRKMVLEKVSFIFMLHFVESLPQNDLCHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEHHIVVERKRISQVTDKEAACLPLKKTNDCHALSNE KKFEVPASEHHIVVERKRISQVTDKEAACLPLKKTNDCHALSNE KKFEVPASEHHIVVERKRISQVTDKEAACLPLKKTNDCHALSNE KKPSVFASEHHIVVERKRISQVTDKEAACLPLKKTNDCHALSNE KKPSVFASEHHIVVERKRISQVTDKTASVSQINSEAFLLVENKPU AENTGILKTNTLLSGESLMASSVSAPCNEKLIQDGFVDISFFSQ VVNTNMGSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTFKTEQLKFPRVTSQVSNLKKKETTADSQTTTSKSLONQ SLKENQKKFFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNISSYGNGISSANH EDLVEGGIHKKLAKKKLKAKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTELSENGEGDFFYLAMGDSHIPPPVPS GTHEBILAELLSPTPVSTELSENGEGDFFYLAMGDSHIPPPVPS EFNUVSONTHLRQDHNYGSPTKKNDCEVQPDSLTNNACVRTLNL ESPMKTDITDPFFSSSALMALANDTLDLPHFDEFYLFENY				
PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGFQNKVKPGEPN SPMSSKRRSMSLLLRKPQTPPTVTNHVGGKGPPSASMFPSYPN LIKPTLVHTDATI IHDGHEEKMENGQITPDGFLSKSAFSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVKKF GRSK LCMMDSFKIGNGLFVIGFGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHINGEVJDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVOWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLUTSEIFABLET CLMEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHKSLVTFTTNVIPEWHPLNAAHF GPCNNCNSKSQIRKNVLEKVSPIFMLHFVBGLPQNDLQHYAFHF EGGLYQTITSVIQYRANNHFITWILDADGSWLECDDLKGPCSSRH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHFKDISVARTLSQDTAVTHGD HLLSGPKGLVDNILPLILEETIQKTASVSQLNSEAFL\LENKFV AENTGILKTNTLLSGESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVBIEKDAQ LKQPLTPRTEGLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGFP SSNKTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRKLKLRKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCSIBDLMBLPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTBLEENGEGFFRYLGMGDSHIPPPVDS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIT DIPPFSSSSALNALANDTILDLPHTPEYLFENY				POEPPNPRMKRASSLNFLNKSVEEPTOPGG
PDOPKRIHTEGNPKQDKKGMMIDEADEFVAGCQNKVRPGEEN SPMSSKRRRSMSLLLRKPQTPPTVTNHVGGKGPPSASHFPSYPN LIKPTLVHTDATI IHDGHEEKMENQQITPDGFISKSAPSELINM TGDLMPPNQVDSLSDDFTSLSKDGLIQKFGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADI KHQLMKEVRKF GRSK LGMMDSPKIGNGLFVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEVCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKATRNYIA IDGGKVLNSKHINGEVYDBTSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVOWKNAYALCHLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTHLYTSQLSGVKDGDCKKLTSEIFABLET CLMEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSNDFECSQCGHQYQNRHMKSLVTFTTNVIPEWHPLINAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF EGGLYQITSVIQYRANNIFITWILDADGSWLECDDLKGPCSBRH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHRKDISVAFRTLSQDTAVTHGD HLLSGPKGLVDNILPLILEETIQKTASVSQLNSEAFL\LENKFV AENTGILKTNTLLSGESLMASSVSAPCNEKLIQDQFVDISFPSQ VWNTNMGSVQLNTEDTVNTKSVNNTDATGLIQGVKSVBIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNENTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISRPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRLKLKKKLKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSSNDCESIEDLLMELPPPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTBLEENGEGFFRYLGMGDSHIPPPVDS EFNDVSONTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFYSSSALNALANDTILDLPHFDEYLFENY	6816	+	803	NLLKTHKF\LLGQDEDSLHSVPVAQMGNYQEYLKTLASPLREID
LIKPTLVHTDATI I HIDGHEKMENGQI TPDGFLSKSAPSELINM TIDIMPPNQVDSLSDDFTSLSKDGLI QKPGSNAFVGGAKNCSLS VDDQKDPVASTLGAMPNTLQI TPAMAQGINADI KHQLMKEVRKF GRSK LGMMDSPKIGRGLPVIGPGTDIGISSLHWVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQBSI FLCEDLQCI YPLGSKSL NNLIS PDLEECHTPHKPQRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQONPIRTADSLERNEI LEADTVDMATTKDPATVUDVGTGRPSPQNEGCTSKLEMPLESK TSFPQALCVQWKNAYALCULDCILSALVHSEELKNTVTGLCSKE ESIFWRLLIKYNQANTLLYTSQLSGVKDGDCKKLTSEI FAEI ET CLNEVRDEI FISLQPQLRCTLGDMES PVFAFPLLIKKETHIEKL FLYSFSNDFECSQCCHQYQNRHMKSLVTPTNVI PEWHPLNAAHF GPCNNCNSKSQIRKMVLEKYSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSEH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDCHALSNE KPYSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFLLLENRPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQQVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLONQ SLKENQKKFFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGFP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRLKLRKKLKABKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEBILAELSPTPVSTELSENGEGDFRYLGMGDSHIPPVDS EFNDVSQNTHLRQDHNYCSPTKKNPCEVVQPDSLTNNACVRTLNL ESPMKTDIFDEFPSSSALNALANDTDLDLPHFDEYLFENY	1 0010	_		PDQPKRLHTFGNPFKQDKKGMMIDEADEFVAGPQNKVKRPGEPN
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TGDLMPPNQVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNGSLS VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHWVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIVPLGSKSL NNLISPDLEECHTPHKPQKRKSLBSSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDETSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLGSKE ESIFWRLLIKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFPLLIKLETHIEKL FLYSFSNDFECSQCGHQYQNRHMSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSEH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENFPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVSIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHRNTTTDLOPS VKGVNNFGGFKTTGINQKASRVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGGIHKLRLKKRKLKAEKKLAALMSSPOSRTVRSENLE QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFPSSSALNALANDTDLDLPHFDEYLFENY	1		l	LIKPTLVHTDATIIHDGHEEKMENGQITPDGFLSKSAPSELINM
VDDQKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF GRSK LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEVCPACKEKGKLKALKTYRISFQESIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLIPDSSQQNPIRTADSLERNEI LEADTVDMATTKDPATTUDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFABIET CLMEVRDEIFISLQPQLRCTLGDMESPVFAFPLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTPTNVIPEWHPLNAAHF EGCLYQITSVIQVRANNHIFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKFV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQQDFVDISFPSQ VVNTNMGSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEGLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGWNNFGGFKTKGINQKASHVSKKARKSASKPPISKPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGGIHKLIKLKLRKKLKAEKKKLAALMSSPQSRTVRSENLE OVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTBLSENGEGDFRYLGMGDSHTPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL	1	1	İ	TGDLMPPNOVDSLSDDFTSLSKDGLIQKPGSNAFVGGAKNCSLS
GRSK 172 3457 LCMMDSPKIGNGLPVIGPGTDIGISSLHWVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFQBSIFLCEDLQCIYPLGSKSL NNLISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNBGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLLTKYNQANTLLTTSQLSGVKDGDCKKLTSEIFABIET CLMEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEMHPLNAAHF GPCNNCNSKSQIRKWLEKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASSIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAFRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASTMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKAKKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLMHSSYGNGISSANH EDLVBGQIHKLRLKLKKKKLKABKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTRLSENGEGDFRYLGMGDSHIPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDFFSSSALNALANDTLDLPHFDEYLFENY	1	1		VDDOKDPVASTLGAMPNTLQITPAMAQGINADIKHQLMKEVRKF
G817 LGMMDSPKIGNGLPVIGPGTDIGISSLHMVGYLGKNFDSAKVPS DEYCPACKEKGKLKALKTYRISFOBSIFLCEDLQCIYPLGSKSL NNIISPDLEECHTPHKPQKRKSLESSYKDSLLLANSKKTRNYIA IDGGKVLNSKHNGEVYDBTSSNLPDSSGQQNPIRTADSLERNEI LEADTVDMATTKDPATVDVSGTGRPSPQNBGCTSKLEMPLESKC TSFPQALCVQWKNAYALCWLDCILSALVHSEELKNTVTGLCSKE ESIFWRLITKYNQANTLLTTSQLSGVKDGDCKKLTSEIFAEIET CLMEVRDEIFISLQPQLRCTLGDMESPVFPFPLLKKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEHPLNANHF GPCNNCNSKSQIRKWVLEKVSPIFMLHFVBGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSGESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGFP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLMHSSYGNGISSANH EDLVEGQIHKLRLKLRKKLKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLNELPPPIDIANESACTTVPGVSLYSS CTHEBILAELLSPTVSTBLSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIPDFFSSSALNALANDTUDLPHFDEYLFENY				
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LEADTVDMATTKDPATVDVSGTGRPSPQNEGCTSKLEMPLESKC TSFPQALCVQMKNAYALCMLDCILSALVHSEELKNTVTGLCSKE ESIFMRLLIKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAELET CLNEVRDEIFISLQPQLRCTLGDMESPVFAFPLLLKLETHIEKL FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVEGLPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAFRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQINSEAFLLENKEV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRLKLKKKKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLINELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL	1	1	1	NNLTSPULBECHTPHRPQRRSSESSTRESSERSTRESSESSTRESSERSTRESSESSTRESSESSTRESSESSTRESSESSTRESSERSTRESSERSTRESSERSTRESSERSTRESSERSTRESSERSTRESSESSTRESSESSTRESSERSTRESSERSTRESSERSTRESSERSTRESSERSTRESSERSTRESSESSTRESSESSTRESSERSTRESSERSTRESSESSTRESSESSTRESSESSTRESSESSTRESSESSTRESSESSTRESSERSTRESSESSTRESSESSTRESSESSTRESSESSTRESSESSTRESSESSTRESSESSTRESSERSTRESS
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FLYSFSWDFECSQCGHQYQNRHMKSLVTFTNVIPEWHPLNAAHF GPCNNCNSKSQIRKMVLEKVSPIFMLHFVBELPQNDLQHYAFHF EGCLYQITSVIQYRANNHFITWILDADGSWLECDDLKGPCSERH KKFBVPASEIHIVIWERKISQVTDKEAACLPLKKTNDCHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTMMQSVQLNTEDTVNTKSVNNTDATGLIQVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP VSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVBGQIHKLRLKLRKKLKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTBLSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY	1	i		ESIFWRLLTKYNQANTLLYTSQLSGVKDGDCKKLTSEIFAEIET
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KKFEVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQTASVTLEKNEV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRLKLKKKKAEKKKLAALMSSPQSRTVRSENLE OVPQDGSPNDCESIEDLLINELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY	1	1	1	EGCLYOITSVIOYRANNHFITWILDADGSWLECDDLKGPCSERH
KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD HLLSGPKGLVDNILPLTLEETIQKTASVSQLINSEAFL\LENKPV AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRLKLRKKLKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLINELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY				KKFRVPASEIHIVIWERKISQVTDKEAACLPLKKTNDQHALSNE
HLLSGPKGLVDNILPLTLEETIQKTASVSQLNSEAFL\LENKPV AENTGILKTNTLLSGESLMASSVSAPCNEKLIQDQFVDLSFPSQ VVNTMMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHIRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVBGQIHKLRLKLRKKLKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLINELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY				KPVSLTSCSVGDAASAETASVTHPKDISVAPRTLSQDTAVTHGD
AENTGILKTNTLLSQESLMASSVSAPCNEKLIQDQFVDISFPSQ VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVBGQIHKLRLKLRKKLKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLINELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTBLSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY	1			HIT.SGPKGLVDNILPLILEETIOKTASVSOLNSEAFL\LENKPV
VVNTNMQSVQLNTEDTVNTKSVNNTDATGLIQGVKSVEIEKDAQ LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCAQLINHSSYGNGISSANH EDLVEGQIHKLRLKLRKKKKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTBLSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY	1			PENECTI MENTIL CORSI MA SSUSA DONEKT TODOF VOTISEDSO
LKQFLTPKTEQLKPERVTSQVSNLKKKETTADSQTTTSKSLQNQ SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVBGQIHKLRLKLKRKKLKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTBLSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY		1		WENTG TRYINI THE SECTION OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CHARGE TO CALL A PROPERTY OF THE CAL
SLKENQKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGGIHKLRLKLKKKKLKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTBLSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY				AAM IMMOAADHI EDIAM TESAMITEN I AM IMMOAA AM IMMOAAAAAAAAAAAAAAAAAAAA
VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP SSNGTAAHPHAHAASEVLEKSGSTSCGAQLMISSYGNGISSANH EDLVEGQIHKLRLKLRKKLKAEKKKLAALMSSPQSRTVRSENLE OVPQDGSPNDCESIEDLLINELPYPIIANAESACTTVPGVSLYSS QTHEBILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY				PKÖLTLKLEÖPKARALZÖASUPKKKELLUDGI LIZKZPÖMÖ
SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH EDLVEGQIHKLRLKLIKKKIKAEKKKLAALMSSPQSRTVRSENLE OVPQDGSPNDCESIEDLLINELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY		1		SLKENOKKPFVGSWVKGLISRGASFMPLCVSAHNRNTITDLQPS
EDLVEGQIHKLRLKLKKKKLKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLINELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTBLSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY		}		VKGVNNFGGFKTKGINQKASHVSKKARKSASKPPPISKPPAGPP
EDLVEGQIHKLRLKLKKKKLKAEKKKLAALMSSPQSRTVRSENLE QVPQDGSPNDCESIEDLLINELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTBLSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY	1			SSNGTAAHPHAHAASEVLEKSGSTSCGAQLNHSSYGNGISSANH
OVPQDGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS QTHEBILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY	1	1		EDLVEGOIHKLELKLEKKLKAEKKKLAALMSSPQSETVESENLE
QTHEBILAELLSPTPVSTELSENGEGDFRYLGMGDSHIPPPVPS EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY		j		OVPODGSPNDCESIEDLLNELPYPIDIANESACTTVPGVSLYSS
EFNDVSQNTHLRQDHNYCSPTKKNPCEVQPDSLTNNACVRTLNL ESPMKTDIFDEFFSSSALNALANDTLDLPHFDEYLFENY	1			OTHERILAELLSPTPVSTRLSENGEGDFRYLGMGDSHIPPPVPS
FSPMKTDI FDEFFSSSALNALANDTLDLPHFDEYLFENY		1		EFNDVSONTHLRODHNYCSPTKKNPCEVOPDSLTNNACVRTLNL
LAPPINIUI POLITICIA DE LA CONTRACTOR DE		1		PCDMWTDIFDERESSSALNALANDTI-DI-PHFDEYLFENY
DODDWY HIT / L CONVEY CHOPED I SPINGEEGYPGELKVWVTYTL				RGFDKVLWT/LSGAVK\CVQFSRISPDGEEGYPGELKVWVTYTL
6819 2 240 RGFDKVLWT/LSGAVK\CVQFSRISPDGEEGIFGEEKVWVTTT	6818	2	240	KOLDVADATA PROMAK (CAŠLRKIRE PORPOTI ORDIVANA 1118

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
[corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
	bequesse		DGGE/LHS/ATTEHKP/VOATPVNLT\TILTSTWQARLPQI
6819	1	961	GIPCTEMGNFDNANVTGEIEFAIHYCFKTHSLEICIKACKNLAY
9913	_		GEEKKKKCNPYVKTYLLPDRSSQGKRKTGVQRNTVDPTFQETLK
ł			YOVAPAOLVTRQLQVSVWHLGTLARRVFLGEVIIPLATWDFEDS
\			TTOSFRWHPLRAKADKYEDSVPQSNGELTVRAKLVLPSRPRKLQ
ļ			EAGEGTDQPSLHGQLCLVVLGAKNLPVRPDGTLNSFVKGCLTLP
	1		DQQKLRLKSPVLRKQACPQWKHSFVFSGVTPAQLRQSSLELTVW
1			DQALFGMNDRLLGGT\RLGSKGDTAVGGDACSQSKLQWQKVLSS
i			PNLWTDMTLVLH
			GDMVYIVGHVPPGFFEKTQNKAWFREGFNEKYLKVVRKHHRVIA
6820	1014	340	GOFFGHHHTDSFRMLYDDAGVPISAMFITPGVTPWKTTLPGVVN
			GANNPAIRVFEYDRATLSLKDMVTYFMNLSQANAQGTPRWELEY
	1		QLTEAYGVPDASAHSMHTVLDRIAGDQSTLQRYYVYNSVSYSAG
1	1		VCDEACSMQHVCAMRQVDIDAYTTCLYASGTTPVPQLPLLLMAL
_			LGLCT EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
6821	1088	518	RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
1		1	RFCVLTLDPETLPATATTEIDVLF ISHSTPREAASSSPEPSST
Ì			FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
1			GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
· ·			GSVIEVLQRRQEGLAS
6822	1088	518	EFDIYR/EVGGEFVPVTRDDSSNGFPRTQHGPSPTVHPIQSPQN
		1	RFCVLTLDPETLPAIATTLIDVLFYSHSTPKEAASSSPEPSSIT
Ì	1		FFAFSLIEGYI\SIVMDAETQKKFPSDLLLTSSSGELWRMVRIG
ì		· ·	GQPLGFDECGIVAQIAGPLAAADISAYYISTFNFDHALVPEDGI
1			GSVIEVLQRRQEGLAS
6823	654	221	PPKLLSRWARMGHGDBIV\LSDLNFPGLLHLPVVGPWRSVQTAC
1		ì	GIPQLLEAVLKLLPLDTYVESPAAVMELVPSDKERGLQTPVWTE
N .	1		YESILRRAGCVRALAKIERFEFYERAKKAFAVVATGETALYGNL
ł		_	ILRKGVLALNPLL
6824	858	104	LLLAQRWGWG\CCFFSLAVSVKMNVLLFAPGLLFLLLTQFGFRG
			ALPKLGICAGLQVVLGLPFLLENPSGYLSRSFDLGRQFLFHWTV
			NWRFLPEALFLHRAFHLALLTAHLTLLLLFALCRWHRTGESILS
1			LLRDPSKRKVPPQPLTPNQIVSTLFTSNFIGICFSRSLHYQFYV
			WYPHTLPYLLWAMPARWLTHLLRLLVLGLIELSWNTYPSTSCSS
1			AALHICHAVILLQLWLGPQPFPKSTQHSKKAH
6825	3	1173	SSGEFGLQASDIMWTISDTGWILIILCSLMEPWALGACTFVHLL
3000			PKFDPLVILKTLSSYPIKSMMGAPIVYRMLLQQDLSSYKFPHLQ
			NCLAGGESLLPETLENWRAQTGLDIREFYGQTETGLTCMVSKTM
			KIKPGYMGTAASCYDVQIIDDKGNVLPPGTEGDIGIRVKPIRPI
			GIFSGYVDNPDKTAANIRGDFWLLGDRGIKDEDGYFQFMGRADD
			IINSSGYRIGPSEVENALMEHPAVVETAVISSPDPVRGEVVKAF
			VILALOFLSHDPEQLTKELQQHVKSVTAPYKYPRKIEFVLNLPK
			TVTGKIORA\KLRDKEWKMSGKAPCAVRHLRDIHLDSPLLSLSF
		}	PEGPLALPMDGYGDSLWEEHEYKFCLALVISTKLYHVRC
	2304	954	LKTESFKPW/VNIALAFHLLGERASPNSFWQPYIQTLPREYDTP
6826	2304	734	LYFEEDEVRYLQSTQAIHDVFSQYKNTARQYAYFYKVIQTHPHA
			NKLPLKDSFTYEDYRWAVSSVMTRQNQIPTEDGSRVTLALIPLW
			DMCNHTNGLITTGYNLEDDRCECVALQDFRAGEQIYIFYGTRSN
1			AEFVIHSGFFFDNNSHDRVKIKLGVSKSDRLYAMKAEVLARAGI
		1	PTSSVFALHFTEPPISAQLLAFLRVFCMTEEELKEHLLGDSAID
			RIFTLGNSEFPVSWDNEVKLWTFLEDRASLLLKTYKTTIEEDKS
			VLKNHDLSVRAKMAIKLRLGEKEILBKAVKSAAVNREYYRQQME
			VLKNHDLSVRAKMATKIRIGERETIBEAVKSAAVKRETTAQQUE EKAPLPKYEESNIGLLESSVGDSRLPLVLRNLEEEAGVQDALNI
			REAISKAKATENGLVNGENSIPNGTRSENESLNQBSKRAVEDAK
		<u>l</u>	GSSSDSTAGVKE

T	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
,	sequence	Beque	\=possible nucleotide insertion) .
6827	sequence	779	SSVVEFGLSVLGGLFLLFVLENMLGLLRHRGLRPRCCRRKRRNL
6827	•	1,7	ETRNLDPENGSGMALQPLQAAPEPGAQGQREKNSQHPPALAPPG
			HQGHSHGHQGGTDITWMVLLGDGLHNLTDGLAIGAAFSDGFSSG
			LSTTLAVFCHELPHELGDFAMLLQSGLSFRRLILLSLVSGALGL
			GGAVLGVGLSLGPVPLTPWVFGVTAGVFLYVALVDMLPALFPSS
		1	GAPAYA\HVLLQGLGLLLGGCLMLAITLLEERLLPVTTEG
	 	1654	KSQHG/WILQLMHSCKEGYVKDLKGNPGLHRAMLDLDNGTRPSE
6828	3	1034	LGHLSQTASLKRGSSFQSGRDDTWRYKTPHRVAFVEKLTKLVLS
			QLPNFWKLWISYVNGSLFSETAEKSGQIERSKNVRQRQNDFKKM
			IQEVMHSLVKLTRGALLPLSIRDGEAKQYGGWEVKCELSGQWLA
			HAIQTVRLTHESLTALEIPNDLLQTIQDLILDLRVRCVMATLQH
			TAEEIKRLAEKEDWIVDNEGLTSLPCQFEQCIVCSLQSLKGVLE
			CKPGEASVFQQPKTQEEVCQLSINIMQVFIYCLEQLSTKPDADI
			DTTHLSVDVSSPDLFGSIHEDFSLTSEQRLLIVLSNCCYLERHT
			PLNIAEHFEKHNFQGIEKITQVSMASLKELDQRLFENYIELKAD
			PIVGSLEPGIYAGYFDWKDCLPPTGVRNYLKEALVNIIAVHAEV
	l.		FTISKELVPRVLSKVIEAVSEELSRLMQCVSSFSKNGALQARLE
			ICALRDTVAVYLTPESKSSFKQALEALPQLSSGADKKLLEELLN
			KFKSSMHLQLTCFQAASSTMMKT
			MRMEAGEAAPPAGAGGRAAGGWGKWVRLNVGGTVFLTTRQTLCR
6829	1	782 .	BOKSFLSRLCQGEELQSDRDETGAYLIDRDPTYFGPILNFLRHG
			KLVLDKDMAEEGVLBEAEFYNIGPLIRIIKDRMEEKDYTVTQVP
		İ	PKHYYRVLQCQEEELTQMVSTMSDGWRFEQLVNIGSSYNYGSED
			QAEFLCVVSKELHSTPNGLSSESSRKTKSTEEQLEEQQQQEEEV
			EBVEVEQVQVEADAQEK/CCYKPEAPGCEAPDHLQGLGVPI
			MEPGSVENLSIVYRSRDFLVVNKHWDVRIDSKAWRETLTLQKQL
6830	1	939	RYRFPELADPDTCYGFRFCHQLDFSTSGALCVALNKAAAGSAYR
			CFKERRVTKAYLALLRGHIQESRVTISHAIGRNSTEGRAHTMCI
			EGSQGCENPKPSLTDLVVLEHGLYAGDPVSKVLLKPLTGRTHQL
			RV\HCSALGHPVVGDLTYGEVSGREDRPFRMMLHAFYLRIPTDT
			ECVEVCTPDPFLPSLDACWSPHTLLQSLDQLVQALRATPDPDPE
}			DRGPRPGSPSALLPGPGRPPPPPTKPPETEAQRGPCLQWLSEWT
ļ		1	LEPDS
		1087	SLFFGSSTPDNKVAEQEDLETQPSPSVEKAVTVIDPEGTIPTNF
6831	3	1007	NVAEKPADHSLSEVKLKTADEPRGTLVKSGDGQNVKEKSMILSN
		į.	VEDLQQPKF1SEVSREDYGKKE1SGDSEEMNINSVVTSADGENL
}			EIQSYSLIGEKLVMEEAKTIVPPHVTDSKRVQKPAIAPPSKWNI
1			SIFKEEPRSDQKQKSLLSFDVVDKVPQQPKSASSNFASKNITKE
1	1	Ì	SEKPESIILPVEESKGSLIDFSEDRLKKEMQNPTSLKISEEETK
		1	LRSVSPTEKKDNLENR\SYTL\ABKKVLAEKQNSV\APLELRDS
			NEIGKTQITLGSRSTELKESKADAMPQHFYQNEDYNERPKIIVG
	1	1	SEKEKDEKKKK
		<u> </u>	MGSGLISGPPQDNSGEALKEPERAQEHSLPNFAGGQHFFEYLLV
6832	1809	412	VSLKKKRSEDDYEPIITYQFPKRENLLRGQQEEEERLLKAIPLF
1			CFPDGNEWASLTEYPRETFSFVLTNVDGSRKIGYCRRLLPAGPG
			PRLPKVYCIISCIGCFGLFSKILDBVEKRHQISMAVIYPFMQGL
	}		REAAFPAPGKTVTLKSFIPDSGTEFISLTRPLDSHLEHVDFSSL
1	1		LHCLSFEQILQIFASAVLERKIIFLAEGLSTLSQCIHAAAALLY
	Ì		PFSWAHTYIPVVPESLLATVCCPTPFMVGVQMRFQQEVMDSPME
	1		PRESENTATION OF THE PROPERTY O
	1		EVLLVNLCEGTFLMSVGDEKDILPPKLQDDILDSLGQGINELKT
			AEQINEHVSGPFVQFFVKIVGHYASYIKREANGQGHFQERSFCK
1		}	ALTSKTNRRFVKKFVKTQLFSLFIQEAEKSKNPPAGYFQQKILE
	1	ì	YEEQKKQ/TETKGKNCEIRAVVNKND
	1	.I	THE PART OF THE PA
6833	1	1129	PLMTLSQCGGIPGHGHSHGGHGHGHGLPKGPRVKSTRPGSSDIN
6833	1	1129	PLMTLSQCGGIPGHGHSHGGHGHGLPKGPRVKSTRPGSSDIN VAPGEQGPDQEETNTLVANTSNSNGLKLDPADPENPRSGDTVEV QVNGNLVREPDHMELEEDRAGQLNMRGVFLHVLGDALGSVIVVV

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning		Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	p=proline, Q=Giucamine, k=Aiginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	- 1	\=possible nucleotide insertion)
	sequence		NALVEYESWKGCSEGDFCVNPCFPDPCKAFVEIINSTHASVYEA
			GPCWVLYLDPTLCVVMVCILLYTTYPLLKESALILLQTVPKQID
			IRNLIKELRNVEGVEEVHELHVWQLAGSRIIATAHIKCEDPTSY
	ţ		MEVAKTIKDVFHNHGIHATTIQPEFASVGSKSSVVPCELACRTQ
			CALKQCCGTLPQAPSGKDAEKTPAVSISCLELSNNLEKKPRRTK
	1	•	CADROCCG TEPOAPSGRDAERT PAVOID COMPANY
			AENIPA\VVIEIKN\IPNK\QPESSL
6834	78	1151	AGQERPAPIWRLLWLPTPSVSRKAEPAHIPINR*GA*B*RGGLP
0051			LCGSSASAYGWH*RLTPWSPGGS*HM*SSKAPVTQAREVLVAGE
	1	l .	CSKLVLSGARGIVGTTVQVLVEAQQPLLLLFTGVWGLNLRAGE
		ļ	SRAL*LIEEVTOVRDAHLGNAVVGCAQCLSQGQVGSALAKALLE
			AAAAVRDCKEVLTVSGDKQQAEVSVRL*VRDVCVEEAGCVEFGQ
		Ì	AHGRPGLALAKGRGGTNEVEEQVQVDGVQKLVLSAHECHELVAC
	ļ		QQDGEDQAARTRLLQAGAHSVAHGRRQGQAPCRPHQEAGVSCHE
			LOOVVGDAL*ARE*APQIIVLLLLEDVAQLRTGKKA*DLVVDVI
	,		
			QLLRQL
6835	1	834	GIPAADR\EASLELIKLDISRTFPNLCIFQQGGPYHDMLHSILC
0032	_		AYTCYRPDVGYVQGMSFIAAVLILNLDTADAFIAFSNLLNKPC
			MAFFRVDHGLMLTYFAAFEVFFEENLPKLFAHFKKNNLTPDIY
			IDWIFTLYSKSLPLDLACRIWDVFCRDGEBFLFRTALGILKLF
			DILTKMDFIHMAQFLTRLPEDLPAEELFASIATIQMQSRNKKW
	1	i	QVLTALQKDSREMREGKSVPPTLRLQREFALGTNQSPMPRPLC
	1	l	
			FRLTPGQPRRTDAL MSCGRPPFDVDGMITLKV\DNLTYRTSPDSLRRVFEKYGRVGD
6836	1	850	MSCGRPPPDVDGMITLKV\DNLTIKISPDSLKKVPEKIGKVD
•	1		YIPREPHTKAPRGFAFVRFHDRRDAQDAEAAMDGAELDGRELR
	1	1	QVARYGRRDLPRSRQGRRHAAGPEAA/RYGRRSRSYGRRSRSP
	1	1	RRHRSRSRGPSCSRSRSRSRYRGSRYSRSPYSRSPYSRSRYSR
		İ	PYSRSRYRBSRYGGSHYSSSGYSNSRYSRYHSSRSHSKSGSST
			SRSASTSKSSSARRSKSSSVSRSRSRSRSRSSSMTRSPPRVSKRK
			KSRSRSKRPPKSPEEEGQMSS
			TDGAAVAGNPGSDYFPGGTAP/GGPRTRRP\SGTSSSGSKASG
6837	1	1369	PNPPAQGDGTSLSPNYTLESTSGNDGKPVSGGGGRGRGRKKRD
			GHVSPGTFFDKYSAAPDSGGAPGVSPGQQQASGAAVGGSSAGE
		,	GHVSPGTFFDKYSAAPDSGGAPGVSPGQQQASGAAVGGSSAGE
	ì		RGAPTPHEKALTSPSWGKGAELLLGDQPDLIGSLDGGAKSDSS
	i		PNVGEFASDEVSTSYANEDEVSSSSDNPQALVKASRSPLVTGS
			KLPPRGVGAGEHGPKAPPPALGLGIMSNSTSTPDSYGGGGGPG
			PGTPGLEOVRTPTSSSGAPPPDEIHPLEILQAQIQLQRQQFSI
			EDOPLGLKGGKKGECAVGASGAQNGDSELGSCCSEAVKSAMST
	1		DLDSIMAEHSAAWYMPADKALVDSADDDKTLAPWEKAKPQNPN
			KEAHDLPANKASASQPGSHLQCLSVHCTDDVGDAKARASVPTW
	1	1	SLHSDISNRFGTFVAALT
			LTDTPPPKTHMIHHSISDYKATLRCWALGFYPMEITLTWQQDE
6838	16	499	PLDIALANT CHOMBON STANDSCORD (V ANACRION
			DQTRDMELVETRPAGDGTFQKWAAVVVPSGEE/Q/RYMCHVQH
			GLPEPLTLRWEQSSQPTIPIVGIVAGLVLLGAVVTGAVVSAVM
			RKKNSDRVSYSEAASSDHAQGSDVSLTACKV
6839		1195	AAPAGGGPDPEALSAFPGRHLSGLSWPQVKRLDALLSEPIPIH
9559		1	PGNFPTLSVOPROIRAGGPOHPGGAG\IHVHRVRLHGSAASHV
			HDESGLGYKDLDLVFRMDLRSEASFQLTKAVVLACLLDFLPAG
			SRAKITPLTLKEAYVQKLVKVCTDSDRWSLISLSNKSGKNVEI
			FVDSVRRQFEFSIDSFQIILDSLLLFGQCSSTPMSEAFHPTVI
	1		FVDSVRRQFEFSTDSFQ1TEDSDEBEQCG5TFFBEAF1F1V
			ESLYGDFTEALEHLRHRVIATRSPEEIRGGGLLKYCHLLVRGI
		1	PRPSTDVRALQRYMCSRFFIDFPDLVEQRRTLERYLEAHFGGA
1			AARRYACI,VTI.HRVVNESTVCLMNHERRQTLDL IAALALQAL
1		1	QGPAATAALAWRPPGTDGVVPATVNYYVTPVQPLLAHAYPTWI
1			CN
L			ELQGDFSVPDVPKSMAWCENSICVGFKRDYYLIRVDGKGSIKI
6840	4254	2061	FPTGKQLEPLVAPLADGKVAVGQDDLTVVLNEEGICTQKCALM
1			

- C20 1	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
]	sequence	1	\=possible nucleotide insertion)
	- Doquoine		TDIPVAMEHQPPYIIAVLPRYVEIRTFEPRLLVQSIELQRPRFI
			TSGGSNIIYVASNHFVWRLIPVPMATQIQQLLQDKQFELALQLA
			EMKDDSDSEKQQQIHHIKNLYAFNLFCQKRFDESMQVFAKLGTD
			PTHVMGLYPDLLPTDYRKQLQYPNPLPVLSGAELEKAHLALIDY
		1	LTQKRSQLVKKLNDSDHQSSTSPLMEGTPTIKSKKKLLQIIDTT
	'		LLKCYLHTNVALVAPLLRLENNHCHIEESEHVLKKAHKYSELII
			LYEKKGLHEKALQVLVDQSKKANSPLKGHERTVQYLQHLGTENL
			HLIFSYSVWVLRDFPEDGLKIFTEDLPEVESLPRDRVLGFLIEN
			PKGLAIPYLEHIIHVWEETGSRFHNCLIQLYCEKVQGLMKEYLL
,		i	SFPAGKTPVPAGEEEGELGEYRQKLLMFLEISSYYDPGRLICDF
			PFDGLLEERALLLGRMGKHEQALFIYVHILKDTRMABEYCHKHY
	ļ		DRNKDGNKDVYLSLLRMYLSPPSIHCLGPIKLELLEPKANLQAA
		1	LQVLELHHSKLDTTKALNLLPANTQINDIRIFLEKVLEENAQKK
			RFNQVLKNLLHAEFLRV\QEERILHQQVKCIITEEKVCMVCKKK
			IGNSAFARYPNGVVVHYFCS\KEVNPADT
6841	1	3206	TPSTTGTKSNTPTSSVPSAAVTPLNESLQPLGDYGVGSKNSKRA
			REKRDSRNMEVQVTQBMRNVSIGMGSSDEWSDVQDIIDSTPELD
			MCPETRLDRTGSSPTQGIVNKAFGINTDSLYHELSTAGSEVIGD
			VDEGADLLGEFSGMGKEVGNLLLENSQLLETKNALNVVKNDLIA
	1		KVDQLSGEQEVLRGELEAAKQAKVKLENRIKELEEELKRVKSEA
			IIARREPKEEAEDVSSYLCTESDKIPMAQRRRFTRVEMARVLME
			RNOYKERLMELQEAVRWTEMIRASREHPSVQEKKKSTIWQFFSR
			LFSSSSSPPPAKRPYPSGNIHYKSPTTAGFSQRRNHAMCPISAG
			SRPLEFFPDDDCTSSARREQKREQYRQVREHVRNDDGRLQACGW
			SLPAKYKQLSPNGGQEDTRMKNVPVPVYCRPLVEKDPTMKLWCA
•			AGVNLSGWRPNEDDAGNGVKPAPGRDPLTCDREGDGEPKSAHTS
			PEKKKAKELPEMDATSSRVWILTSTLTTSKVVIIDANQPGTVVD
		1	QFTVCNAHVLCISSIPAASDSDYPPGEMFLDSDVNPEDPGADGV
,			LAGITLYGCATRCNVPRSNCSSRGDTPVLDKGQGEVATIANGKV
			NPSQSTEEATEATEVPDPGPSEPETATLRPGPLTEHVFTDPAPT PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAPTMWLG
			PSSGPQPGSENGPEPDSSSTRPEPEPSGDPTGAGSSAAFTMAGG AQNGWLYVHSAVANWKKCLHSIKLKDSVLSLVHVKGRVLVALAD
			GTLAIFHRGEDGQWDLSNYHLMDLGHPHHSIRCMAVVYDRVWCG
			YKNKVHVIQPKTMQIEKSFDAHPRRESQVRQLAWIGDGVWVSIR
	1		LDSTLRLYHAHTHQHLQDVDIEPYVSKMLGTGKLGFSFVRITAL
	1		LVAGSRLWVGTGNGVVISIPLTETVVLHRGQ\LLG\LRANKTSP
1	İ		TSGEG\ARPGG\IIHVYG\DDSSDRAARSFIPYCSMAQAQLCFH
ŀ	1		GHRDAVKFFVSVPGNVLATLNGSVLDSPAEGPGPAAPASEVEGQ
		Ì	KLRNVLVLSGGEGYIDFRIGDGEDDETEEGAGDMSQVKPVLSKA
			ERSHIIVWOVSYTPE
-60:0	 	926	RCQQLSATILTDHQYLERTPLCAILKQKAPQQYRTRAKLRSYKP
6842	3	720	RRLFQSVKLHCPKCHLLQEVPHEGDLDIIFQDGATKTPDVKLQN
1			TSLYDSKIWTTKNQKGRKVAVHFVKNNGILPLSNECLLLIEGGT
			LSEICKLSNKFNSVIPVRSGHEDLELLDLSAPFLIQGTVHHYGC
		1	KQWST*RSIQNLNSLVDKTSWIPSSVAEALGIVPLQYVFVMTFT
		1	LDDGTGVLEAYLMDSDKFFQIPASEVLMDDDLQKSVDMIMDMFC
			PPGIKIDAYPWLECFIKSYNVTNGTDNQICYQIFDTTVAEDVI
6040	1	851	NHRKVLSGAKRYECNECGKSFAYTSSLIKHRRIHTGERPYECSE
6843	2	831	CGRSFAENSSLIKHLRVHTGERPYECVECGKSFRRSSSLLQHQR
1			VHTRERPYECSECGKSFSLRSNLIHHQRVHTGERHECGQCGKSF
	1		SRKSSLI IHLRVHTGERPYECSDCGKSFAENSSLI KHLRVHTGE
1			
1		i	PDVECIDCGKSFRHSSSFRRHORVHTGMRPYK*SKFWKFSCPGF
-			RPYECIDCGKSFRHSSSFRRHQRVHTGMRPYK*SKFWKFSCPGF
			LLLQGQRVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE
	244	542	LLLQGQRVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE CNECEKAFSPLSLVTTIFT
6844	244	642	LLLQGQRVHTGSRCYECDKWGIFFS*NASFFT*KSAPTEEVPFE

	- nno - I	Predicted	Predicted end	Amino acid segment containing signal peptide
No:	SEQ			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Corresponding to first anino acid anino acid residue of anino acid ible nucleotide deletion, V-possible nucleotide deletion,		7	*****	Glutamic Acid. F=Phenylalanine, G=Glycine,
L=Leucine, M=Methionine, N=Asparagine, enion acid residue of amino acid residue of amino acid sequence sestine, T=Threonine, V=Valine, amino acid sequence v=TyPtophan, Y=Tyrosine, X=Wuknown, *=stop Codon, /=possible nucleotide deletion, /=vpossible deletion, /=vpossible nucleotide deletion, /=vpossible nucleoti	NO:	Y		u-wistidine Telsoleucine Kelvsine.
to first amino acid amino acid amino acid amino acid sequence Peproline, Q=Glutamine, R=Arginine, R=Stopnan, Y=Tyrosine, X=Unknown, Y=Stopnan, Y=Tyrosine, X=Unknown, Y=Stopnan, Y=Tyrosine, X=Unknown, Y=Stopnan, Y=Tyrosine, X=Unknown, Y=Tyr				I-Laugine M-Methionine N-Asparagine.
amino acid residue of amino acid sequence whytepophan, Y-Tyrosine, X-Unknown, *-Stop Codon, /-possible nucleotide deletion, /-possible nucleotide deletion (D-Droline O-Clutamine P-Arginine
residue of amino acid sequence				
amino acid sequence Codon, /=possible nucleotide deletion, /-possible nucleotide deletion				S=Serine, T=Inreonine, v=valine,
Sequence V-possible nuclectide insertion		residue of	amino acid	W=Tryptopnan, Y=Tyrosine, X=Unknown, ==Scop
FLGEDCTSELREITDECRANDSVRSVOETLIKKLSTESK-CIK 1		amino acid	sequence	Codon, /=possible nucleotide deletion,
1519 VAVEDECVERHVENDODLAMILFILMCHEETARARLE YRIRTLO GALENAQUILGY COLAFFANESAD SCLEVCE PDI YGVOGUNUNGU GLAFELY THITTODLOLF PREAGGND VVRAVAS PRECESTED STATEMENT OF THE COLOR		sequence		\=possible nucleotide insertion)
See				PLGEDCPSELREIIDECRAHDPSVRPSVDEILKKLSTFSK*CIK
GALENA, GLAPEL, YHTTOOL LIPREAGUND VYRAVES FICKSYNSHIPRE KYHLIRGUNG PDEVINGUND VYRAVES FICKSYNSHIPRE KYHLIRGUNG PDEVINGUND VYRAVES FICKSYNSHIPRE KYHLIRGUNG PDEVINGUND VYRAVES FICKSYNSHIPRE KYHLIRGUNG PDEVINGUND VYRAVES FICKSYNSHIP KYRAVITA WARRELLIGAS FARMAD FIR FOR THE WARREN FOR THE WARRE				
GALENA, GLAPEL, YHTTOOL LIPREAGUND VYRAVES FICKSYNSHIPRE KYHLIRGUNG PDEVINGUND VYRAVES FICKSYNSHIPRE KYHLIRGUNG PDEVINGUND VYRAVES FICKSYNSHIPRE KYHLIRGUNG PDEVINGUND VYRAVES FICKSYNSHIPRE KYHLIRGUNG PDEVINGUND VYRAVES FICKSYNSHIP KYRAVITA WARRELLIGAS FARMAD FIR FOR THE WARREN FOR THE WARRE	6845		1519	VAVRDECYWRHVFWDQDLWMLLFILMCHPETARARLEYRIRTLD
GLAPELYHTTOOLOLFREAGGDDVYRAVAEPKGSRAEMSPREE KYHLRGWAN PEVHSGAVNASYYTNIVLVONLAGALAGOLGLEP 1 PSOWLAVADKIKYP POVEON PHPEF DGYZFGEVVKOADVULLG 1 PSOWLAVADKIKYP POVEON PHPEF DGYZFGEVVKOADVULLG 2 YPYPFSS PDVRKKNLEI YEAVTS POGPATHARVOKMEKLD AVRARGLIDASFANMAEPFKWITENAGGSAVNFLTGMGGFLOA VVFGCTGFFVTRAGVTFDPVCLSGISRVSVSGIFYGOKKINFSF SEDSUTVEVTRAGAPHAPHLEALBHSGSGLSELLGGIKKYSFPRS AGRIQMSPPKLPGSSSSEFFGRTFSDVXDDFLGSSSPT TESLTUPPASS'S SCTGASETLEDPSLWFRLIGTLLACHINSSSP TESLTUPPASS'S SCTGASETLEDPSLWFRLIGTLLACHINSSSPT PAARLSGKVHAAMPFFKAFCL 1 LYFKKTIK INKILAEMPY YEMBKITKLRNTIMBOYTRTEESARG 1 LYFKKTROSAVALSQN ITENSKRAEVGVKAHHLIGAGHSSFFKP MYDMECKEVI SKFPTGKINLLATVTAEEGLIKTLACHINSSPFKP MYDMECKEVI SKFPTGKINLLATVTAEEGLIKTLACHINGAUNDFREM WYKAIHCVQNMKEEYAHKILELQMQSIMEKKMKTKRNIAKHKK NNPSLITPICKNCSVLACSGEDIHVIEKMHVMMTPEFKELYIV RENNTLOKKCADYGINGEI CKCGOAMGTMWIKKGLDLCKLR NVVVVFKNSTKKQYKKWELPITFPHLÜSECLIFSBED 6847 1450 348 SKCWNSDRLEMPLIDLALILYPESYPYTTGHLSDDSLERKYLLT WERDALINGUY ARARI OPHCHAGDDMEKKRKYKNIACHING PRAYGTITVRSLLDTTEHCLME PHP PDYSKVAQRENVOLRCF POVVRSLDALGMERGOLALVOCHAGDMEKKRYGYWNKLQCTLRQQ PPAYGTITVRSLLDTTEHCLME PHP PDYSKVAQRENVOLRCF POVVRSLDALGMERGOLALVOCHAGDMEKKRYGYWNKLQCTLRQQ PPAYGTITVRSLLDTTEHCLME PHP PDYSKVAQRENVOLRCF POVVRSLDALGMERGOLALVOCHAGDMEKKRYGYWNKLQCTLRQQ PPAYGTITVRSLLDTEHCLME PHP PDYSKVAQRENVOLRCF POVVRSLDALGMERGOLALVOCHAGDMEKKRYGYWNKLQCTLRQQ PPAYGTITVRSLLDTEHCLME PHP PDYSKVAQRENVOLRCF POVVRSLDALGMERGOLALVOCHAGDMEKKRYGYWNKLQCTLRQQ PPAYGTITVRSLLDTEHCLME PHP PDYSKVAQRENVALRCF POVVRSLDALGMERGOLALVOCHAGDMEKKRYGYWNKLQCTLRQQ PPAYGTITVRSLLDTEHCLME PHP POYSKVAQRENVALACHING REGALDVIL GENGGAVATHYHAALRCCSLKLAVINGCTLRGC POVVRSLDALGMERGOLALVOCHAGARAVATALGALGCT REGALDVIL GENGGAVATHYHAALRCCSLKLAVINGCTLAGAUNA REGALDVIL GENGGAVATHYHAALRCCSLKLAVINGCTLAGAUNA VILTAGAMUNALARCOGGATARLACKERGVACH VYPEAGLQEETH TARKIASLSRPVVSLGKARTFYQLDGOTGSYRC VILTAGAMUNALARCOGGATARLACKERGVACHAGAUNA VYPEAGLQEETH TARKIASLSRPVVSLGKARTFYQLDGOTGSYRC VILTAGAMUNALARCOGGATARLACKERGVACHAGAUNA VYPEAGLQEETH TARKIASLSRPVVSLGKARTGUANGANGAUNA VYPEAGLQEETH TARKIASLSRPVVSLGK	0042	j]	
### AUTOPOST STATEMENT OF THE STATEMENT				GLAFELYYHTTODLOLFREAGGWDVVRAVAEFWCSRVEWSPREE
I PSOMILAVADKIKVP DVEONPHEPETOSTREGEVYKQADVULIG YPVPPSLS PDVERRINEITYEM-TSTOGPARMSVAMBLIAD AVRARGLIDRS FANNAEPPKVMTENADCSGAVAFLTIMGGFLQA VVPGCTIFFRUTRAGYTPDVCLSGISRVEVSGIFT/COMKINEPS SEDSUTVEWTARAGYMAPHLEAELMPSQSELSILLGHKVSFPRS AGRIQMSPPKLPGSSSSEPFGRTFSDVRDPLGSPLMVTLGSSSP TESITUPDASS'S SCHAGESTLEPSLMPRELIGELLIGHTLACHIPS PARLEGKVHAAMPEFKAPCI LYFLKTIK'LBILLELMPYSEMELTRILATULAGHSSEPKP MYDREGKEVISKFFKAPCI LYFLKTIK'LBILLELMPYSEMELTRILATULAGHSSEPKP MYDREGKEVISKFFKAPCI LYFLKTIK'LBILLELMPSGVBLATHLIAGHTSSEPKP MYDREGKEVISKFFKANLLIATUVAHSGSSVISHETVADFREKM MYKAIHCVONMKPBEVAHKILLELQMSSIMEKKHKKKRIKKHK NNPBLITPLCKICOSULAGGBETVLVAHSGSSVISHETVADFREKM MYKAIHCVONMKPBEVAHKILLELQMSSIMEKKHKKKRIKKHK NNPBLITPLCKICOSULAGGBETVLVAHSGSSVISHETVADFREKM MYKAIHCVONMKPBEVAHKILLELQMSSIMEKKHKKKRIKKHK NNPBLITPLCKICOSULAGGBUTHVIEMHUNMTPEFKELYIV RENKTLOKKCADYGINGEITCKGQAMGTMWINKGLIPCLKIR NYVVVFKNNSTKKQYKKWELDITTPFILLDYSECLFSDED SMCWNSDRLEMPLIDLALILYPESYVYTGHLSDDSLERKYCLT WEEDALNGUL'RABAJOHCUNAGDRMEKFRQXYMKLQTLRQC PRAYGTLITVRSILDTREHCLMEPRIPDDYSKCLQESDED YRGFEKKKLQERPHLUDSVSKUQRBNQUALRCF POVVSSLDALGMERGGLALVINGLLAGNVFUMGAKAVSAVLESDE YRGFEKKKLQERPHLUDSVSKUQRBNQUALRCF POVVSSLDALGMERGGLALVINGLLAGNVFUMGAKAVSAVLESDE YRGFEKKKLQERPHLUDSVSKUQRBNQUALRCF POVVSSLDALGMERGGLALVINGLLAGNVFUMGAKAVSAVLESDE YRGFEKKKLQERPHLUDSVSKUQRBNQUALRCF POVVSSLDALGMERGGLALVINGLLAGNVFUMGAKAVAVLESDE YRGFEKKKLQERPHLUDSVSKUQRBNQUALRCF POVVSSLDALGMERGGLALVINGLLAGNVFUMGAKAVURSDLUSGLUSG LINGMINSLLDGTENTLAGNERARVEYVQEBANDVTHSSSLIVAB RAGMDEVVISALBERGILLVINGTSSPENLDLSRLDKALLAGNUBLAG REGADLVVIEGGGRAVVTNYABALRCESLKLAVINNAWLABRIGG GRIFSVIFKYEVPABE MAMMSLDGTRITULSNFKKRNTLSLAMLKSLQSDILHDADSND LKVII 1SAGGPVFSSCHDLKELITEPGSPLSAQGEALLHOLLSKAMM VULFCSTPGVALARAVPRVALENLEFTGEPISAQGEALLHOLLSKAMM VULFCSTPGVALARAVPRVALENLEFTGEPISAQGEALLHOLLSKAMM VULFCSTPGVALARAVPRVALENLEFTGEPISAQGEALLHOLLSKAMM VULFCSTPGVALARAVPRVALENLEFTGEPISAQGEALHON VULFGKSGUCTYFILATULTSTGPFSATUG VULVAKKGUCTYFILATULTSTGPFSATUG VULVAKKGUCTYFILATULTSTGPFSATUG VULVAKKGUCTYFILATULTSTGPFSATUG VULVAKKGUCTYFILATULTSTGPFSATUG RENTELLELIPPEN				
TYPYPSISPDWRRNLETYEAVTSPOGPATMSMRAVGMMELKD AVRARGILLARSFANMAPPERWEADDSGATMTETTOMGGFLOG VYPGCTGFPVTRAGVTFDVCLSGISRVSVSGIFYGGMKINFSF SEDSVTVEVTRAGVTFDVCLSGISRVSVSGIFYGGMKINFSF SEDSVTVEVTRAGVTFDVCLSGISRVSVSGIFYGGMKINFSF SEDSVTVEVTRAGVTFDVCLSGISRVSVSGIFYGGMKINFSF SEDSVTVEVTRAGVTFDVCLSGISRVSVSGIFYGGMKINFSF SEDSVTVEVTRAGVTFDVCLSGISRVSVSGIFYGGMKINFSF AGRICMSPFKLPGSSSSEFFGRTFSDVRDPLQSPLAVTLGSSSP TESLTVDPASF*SGTGASETSLOPSLBFRLHPPLLGTLLAGHSF PAARLSGKVHAAMPEFKAFL BAALLSGKVHAAMPEFKAFL LYFIKKTIK*LARHPYEMEKLTKLRNTIMEQYTRTEESARG TIFKKTGGSAVALSGMTLEMKTAEVGKVHAHLIGAGHSSEFFK MYQMEGKEVISKFTGKKINLLIATTVAEEGLDIKSCHOTKRYGL VINTILAMVQBGRAARDESTVLVAHISGSQISHETVADFREKE MYXAIHCVQNMKPEEVAHKLLELOMGSIMEKKMKKTRNILAKHYK NNFSLITFLCNICSVLAGSGEDIHVIEKMHVNIMTPEFKELJVI VERNALIKCADYGINGSI ICKGGAMGTMWHISGLDLPCLKTR NFVVVFRNSTKKQYKKWVELPITFPNLDVSECCLFSDED ARVENTLOKKCADYGINGSI ICKGGAMGTMWHISGLDLPCLKTR NFVVVFRNSTKKQYKKWVELPITFPNLDVSECCLFSDED PARYGTLTVRSLLDTEHELLARPSPPDYSHGNAVISKOLPLKRI NFVVVFRNSTKKQYKKWVELPITFPNLDVSECCLFSDED PARYGTLTVRSLLDTHEHCLAEPNFPDDYSKOLPLKROVLTRQQ PARYGTLTVRSLLDTHEHCLAEPNFPDDYSHCOLFSREVCLT WEEDALNGVI*RABAGPERLLLVQTGSSSPCLDLSRLDKALDKALSKOLBADVR REAGADLWI*RABAGPENLDATHSPNLOVELARPY PARYGTLTVRSLLDTHEHCLAENFPPDYSHGKAKVLSEDLF REAGADLWI*RABAGRESHLLVQTGSSSPCLDLSRLDKALALVR REAGADLWI*RABAGRESHLLVQTGSSSPCLDLSRLDKALALVR REAGADLWI*RABAGRESHLLVQTGSSSPCLDLSRLDKALALVR REAGADLWI*RABAGRESHLLVQTGSSSPCLDLSRLDKALALVR REAGADLWI*RABAGRESHLLVQTGSSPCLDLSRLDKALALVR REAGADLWI*RABAGRESHLLVQTGSSPCLDLSRLDKALALVR REAGADLWI*RABAGRESHLLVQTGSSPCLDLSRLDKALALVR REAGADLWI*RABAGRESHLLVQTGSSPCLDLSRLDKALALVR REAGADLWI*RABAGRESHLLVGTSSSPCLDLSRLDKALALALVR REAGADLWI*RABAGRESHLLVGTSSSPCLDLSRLDKALALXR REAGADLWI*RABAGRESHLLVGTSSSPCLDLSRLDKALALALALXR REAGADLWI*RABAGRESHLLTBALTKALALALALALALALALALALALALALALALALALAL				T DSOWLAVADKI KVPFDVEONFHPEFDGYEPGEVVKOADVVLLG
AVRARGILDRSFANNAP PKVATENANGSGANTELINGGEFLOA VVPGCTGFEVPTARAGYPDVCLSGISEVSUSGIFYGGNKLNIPSF SEDSVTVEVTARAGPMAPHLRAELMPSGRILSLLDGHKVSPPSS AGRIQMSPPKLIPSSSSSEPFGRTFSDVRDFLOG PLAVTLGSSSP TESLTVDPASE' SGTGASSTSLOPSLMPRIHPPLIGTLLACHES FAARLSGKVHAAWPEFKAPCL 1 STELTVDPASE' SGTGASSTSLOPSLMPRIHPPLIGTLLACHES PAARLSGKVHAAWPEFKAPCL 1 LYFLKTIK' INNLAEHP' VENEKLTKLRNTIMEQYTRTEESARG LYFLKTIK' INNLAEHP' VENEKLTKLRNTIMEQYTRTEESARG 1 LYFLKTIK' INNLAEHP' VENEKLTKLRNTIMEQYTRTEESARG 1 LYFLKTIK' INNLAEHP' VENEKLTKLRNTIMEQYTRTEESARG 1 LYFLKTIK' INNLAEHP' VENEKLTKLLATVAEGLDI IKCNIVITYGL VINE IANVQARGRARADESTYULVAHSGSGVI EHETVMDFREKM MYKAHLVQOMKPEEYAHKI LELDMQS HEKKMKTKIN LACHYK NNPSLITPLCKNCSVLAGSEGHIN' IENGHLSKCHIVTRYGL VINVELCKNISCNLAEGEHIN LATTVAEGLDI IKCNIVITYGL RENNTLCKKCADYQINGEI I CKCGGAMGTMMYHKGHKSHKYK NNPSLITPLCKNCSVLAGSGEHIN LALTVATHERELDI IKCNIVITYGL RENNTLCKKCADYQINGEI I CKCGGAMGTMMYHKGHKSHKYK NNPSLITPLCKNCSVLAGSGEHIN ILDSSCLIFSDED 6847 1450 348 SKCMMSDRLEMELICKNCSULLAGNUFMGAKAVSAVLESDE PRAYGITTVRSLLDTREHCLNEFNFPDPYSKVKQEBNOVALRCE POVVKSLDALGGERRQLAUVKSLLAGNUFMGAKAVSAVLESDE YGGFEERKKRLGERREULDVSTSSENGLUKNGPHKCALIFADNSG IDI ILGVFPTVERLLLROTTSVSTSCLUKSPHKCALIFADNSG IDI ILGVFPTVERLLLROTTSVSTSCLUKSPHKCALIFADNSG IDI ILGVFPTVERLLLROTTSVSTSCLUKSPHKCALIFADNSG GRIEFSVLFKAVEVAB 6848 19 16 RMWNSLDGIRNIVLSNFKKRNTLSLAMLKSLQSDILLIDADSND LKVII ISABGPVFSSGHDLKELITEEQGRDHHAEVTCSSKUM VULFCSTEGVALARAVPRKVALEMLFTCEPISAGSLHIGLLINK VVPERAULGESTMERATAGCQLVASCIDIAVASDKSSFATFGVN VCLFCSTFGVALARAVPRKVALEMLFTCEPISAGSALHIGLLINK VVPERAULGESTMERATAGCQLVASCIDIAVASDKSSFATFGVN VCLFCSTFGVALARAVPRKVALEMLFTCEPISAGSCSHLIGTM VULTAGAMVONLALADGGGGITAFLOKKEVWSHEPV-VEH SKONGSCLEGSFARERGTTST-P VOLTAGATGGEDLYHOGYE VCLVFSVPDKSCLEGSFARERGTTST-P VOLTAGATGGEDLYHOGYE VCLVFSVPDKLEGETMIARATAGCQLVASCHAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG			1	VDVDRST CDDVDDKNI.ETVEAUTSDOGDAMTWSMFAVGWMELKD
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### ITTIKTROSAYALSOWITENEKFAEVGUKARHLIGAGHSSEFKP #### MTQNEGKEVISKFRTGKINLLIATADEGIGIT KECNIVIRYGL VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREM MYKAIHCVQMMKPEEVAHKILELQMQSIMEKKMKTKRITAKHYK NPSLITPICKNCSVLAGGEGEIHVIEMMHVMMTEFRELIVIV RENKTLQKKCADYQINGEIICKCGQAMGTMWYHKGLDLPCLKIR NPVVVFRNNSTRKQYKKWUELFITFPNLDYSECCLFSDED **SCHMISORIEMPLIDLALILYPFSVFYTCHLSDDSLSKRYCLT* WEDDALNGVI**RABAIQPHCVNAGDRMKKPGKYMWKLCTLRQQ PPAYGTLTVRSLLDALILYPSVFYTCHLSDDSLSKRYCLT* WEDDALNGVI**RABAIQPHCVNAGDRMKKPGKYMWKLCTLRQQ PPAYGTLTVRSLLDATHEHCLNEFPDPYSKVXQRENGVALRGF POVVRSLDALGWERQLALVKGLLAGNVFDWGAKAVSAVLESDP YBGFEAKRKLQERPHIVDSYSEMUQRLKWPHKCALIFADNSG IDIILGVFFFYRELLLAGTSVEILAGNSFPHKCALIFADNSG IDIILGVFFFYRELLLAGTSVEILAGNSFPHKSESLIVAB RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAMLAERLG GRLFSVIFKKYEVPB **AMMWSLOGIENTVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGVFFSSGDLKEITERQGRDYHAEVFQTCSEKVMH VUFLFCSTFGVALARAVPRKVALEMFTGEDFISAQEALLHGLINK VVPEABLQEFTMRIARKIASLSFRVVSLGATFYKQLPQDLGTA YYLTSQAMVDHLALRDQGSGITAFLQKSKPWSHEPV*VEH **SLGVDGSCLEGGSPAPRPTOTTSF*PVONMATQQEDLYHQSYEC VCVLPASVPDFKEFYSSSNINHEGLECLRLINEILADFOELISK PKRSGVEKKTIGSTYMAATGLNATSGQDAQDAERSCSHLGTM VEFAVALGSKLDVINKISFNNFFLRVQSLINGFVVAGVIGAQKFQ VINVKGKQQLCTYFLNTDLTRTGPPSATLG **GESTERHHLKILHVKSNITKVPSNITTVAPHITKLVINDSCNITTSPSATLG CHESTERHHLKILHVKSNITKVPSNITTVAPHITKLVIINDGT KLLVINSLKKMMNVAELELQNCELERIPHATFSLSNLQELDLINS NNIRTIEBIISFQHLKRLTCLKUPNINTVIVPSHITTVAPHSLTL **CDHLRCLHVKFTDVAETPAWVILLKILRELYLIGINLNSENNKMI GLESLEERHHLKILHVKSNITKVPSNITTVAPHITKLVIINDGT KLLVINSLKKMMNVAELELQNCELERIPHATFSLSNLQELDLINS NNIRTIEBIISFQHLKRLLTCLKUPNINTVIVPSHITTVAPHSLTL **CPHINCESLEVAVFSLQALGCCRMLKKSGLVVEDHLFDTLPLEVA** **CHINGNCOMPLAGGGGCCMLKKSGLVVEDHLFDTLPLEVA** **CHINGNCOMPLAGGGCCCMLKKSGLVVEDHLFDTLPLEVA** **CHINGNCOMPLAGGGCCCMLKKSGLVVEDHLFDTLPLEVA** **LULNGLKGNCOMPLAGGGCCCMLKKSGLVVEDHLFDTLPLEVA** **CHINGNCOMPLAGGGCCCMLKKSGLVVEDHLFDTLPLEVA** **CHINGNCOMPLAGGGCCCMLKKSGLVVEDHLFDTLPLEVA** **CHINGNCOMPLAGGGCCCMLKKSGLVVEDHLFDTLPLEVA** **CHINGNCOMPLAGGGCCCMLKKSGLVVEDHLFDTLPLEVA** **				PAARLSGKVHAAWPEFKAFCL
IIFTKTRQSAYALSQMITENERFAEVGWKAHHLIGAGHSSEFKP MYONEQKRVISKPTRKINLLIATABEGIDIKECNIVIRYGL VTNEIAMVQARGRARADESTYVLVAHSGSGVIEHETVNDFREMM MYKAIHCVQMMKPEEVAHKILELQMQSIMMEKRHKTKRNIAKHYK NPSLITTPLCKNCSVLAGGEDIHVIEMMHVMMTEFRELIVIV RRNKTLQKKCADVQINGEIICKCGQAWGTMWYHKGIDLPCLKIR NPVVVFNNSTKKQYKKWVELPITFPNLDYSECCLFSDED SMCWNSDRLEMPLIDLALILYPSVFYTCHLSDOSLSRRYCLT WEDDALNGVL*RABAIQPHCVNAGDRMEKRRQKYWNKLQTLRQQ PPAYGTILTVRSLLDTHEHCLNEFPDYSKVKORENGVALRGF PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDP YPGFEAKRKLQERPHLVDSYSEMLQRLKRGPHKCALIFADNSG IDIILGVFFYFRELLLAGTSVILACNSGPALNDVTHSESLIVAE RIAGMDPVVHSALREERLLLVGTGSSSPCLDLERLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRLFSVIFKKEVPAE RIAGMDPVVHSALREERLLLVGTGSSSPCLDLERLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRLFSVIFKKEVPAE AWMWNSLOSIENTVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIISAGGPVFSSGHDLKEITERGGRDYHAEVFOTCSKVMH VVPEABLQEFTMIRTARKIASLSRPVVSLGKAFFKKQLPOOLGTA YYLTSQAWYDHLALRQGQSITAFLQKSKGYDYMSEPY*VEH SIGVIGSCLEQGSPAPRPFOTDTSF*PVGNWATQQEDLYHQSYEC VCVLPASVPDFKEFYSSSNINHEGLECLRLINEIIADFOELLSK PKRSGYEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKISFNNTHEGLECLRLINEIIADFOELLSK PKRSGYEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKISFNNTHEGLECLRLINEIIADFOELLSK PKRSGYEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKISFNNTHEGLECLRLINEIIADFOELLSK PKRSGYEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKISFNNTHEGLECLRLINEIIADFOELLSK PKRSGYEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKISFNNTHEGLECLRLINEIIADRUFTGFERSCH VEFAVALGSKLDVINKISFNNTHEGLECLRLINEIIADRUFTGFERSCH VEFAVALGSKLDVINKISFNNTHEGLECLRLINEINKMI GLESLERHHLKILHVKSNITTVPSHITTVALFISL CLULMSLKKMMNVAELELDNCELERIPHATFSLSNLQELDLKS NNIRTIEBIISFQHLKRLTCLLVSNITKVYPSNITTVAPHHTKLCSL CLULMSLKKMMNVAELELDNCELERIPHATFSLSNLQELDLKS NNIRTIEBIISFQHLKRLTVVSNITTVPSNITTVAHLESL LTULELKGNCLORLPAQLGQCRMLKKSGLVVEDHLFDTLFLEVA LTULELKGNCLORLP	6846	213	1258	LYFLKTIK*LNRLAEHP*YENEKLTKLRNTIMEQYTRTEESARG
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NPYVVFKNNSTKKQVKKWVELPITPPNLDYSECCLFSDED				PRNKTLOKKCADYOINGELICKCGOAWGTMMVHKGLDLPCLKIR
SHOWNSDRLEMPLIDLALILYPPSVYPTGHLSDDSLERKYCLT	•		l l	NEWWYERNOYKKWYELPITEPNIDYSECCLESDED
WFEDALINGUL*RAEAIQPHCVINGGRMEKFROKYWNKLQTIRQC PPAYGTITVRSLLDTREHCLINEFNIPDPYSKVKQRENGVALRCF PGUVRSLDALGWERGILALVKGILAGNVFDWGAKAVSAVLESDP YPGFEEAKRKLQERPWLVDSYSEMLQRLKGPPHKCALIFADNSG IDIILGVFFFVERBLLENGTEVILACNSGPALNDVTHSESLIVAE RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSKLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE 6848 19 16 AMWINSLOGIRIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEQGRDYHAEVPQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQUAS CDIAVASDKSSFATFGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQBEALHGLINK VVPEABLQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YVLTSQAMVDNLALRDGGGGITAFLOKKKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVEDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKPSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTAVLSKIQVTEETAMALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLINEWTFEKLRQHISRNAQDKGLHLEFMLSGVPDAVFDLTD LDVLKLELIPPAKIPAHISQNCELHLICHCPAVVGCTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHIKILHVKSNITKVESNITDVAPHLTKLVILHINGT KLLVLNSLKKMMNVAELBLQNCELERIPHATPSLANQELDLSK NNIRTIEEIISFGHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISNIPIEIGLUNLQ HLHITGNKVDILPKQLFKCI KLRTINLGQNCITSLPEKVQGLSG LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPPANGI VSAQVSAREGENCLGWNLADSSQESYKSLEEAEBCYPPSLLTILD EALNGDINIPPANGI VSAQVSAREGENCLGWNLADSSQESYKSLEEAEBCYPPSLLTILD				CMCMMSDBI FMDI.TDI.MI.TI.VDDSVVDYTGHI.SDDSLSRKYCLT
PRAYGTLTURS.LLDTREHCLNERNFPDPYSKUKQRENGVARGE PGUVRS.LDALGWEERQLALVKGGLAGNVFDWGAKAVSAVLESDP YGFEEAKRKLQERPHLUDGYSEMLQRLKGPPHKCALIFADNSG IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYAGLSGSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYAGLRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE 6848 19 16 AMMWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMI IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLINK VVPEABLQEETMRIARKIASLSRPVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGGGITAFLOKKPVWSEBPV-VEH 6849 70 821 SLGVDGSCLEQGSPAPRPOTDTSF*PVGNWATQQEDLYHQSYEC VCULFASVPDFKEFYSESNINHEGLECLRLINEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKISFNNFRLRVGLNHGFVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTTYFLNTDLTTTGPPSATIG 6850 2 1235 ARGINHEWTFEKLRGHISRNAQDKQELHLFMISGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAETPAWYYLLKNLRELYLIGBLINSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVTHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHATPSLSNLQELDLDS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLSSL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLUNLQ HLHITGNKVDILPKGLECKI KLRTINLGGNCTTSLPEKVGQLSG LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPPANGI VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNOVECQFPLLSCPKAGTDLSWGARREVGWMAAGLMIGAGA	6847	1450	348	MEEDAL NOVI * PARA TORUCINAGOPMEKEROKYWNKT.OTT.ROO
PGVVRSLDALGWEERQLALVKGLLAGNVFDWGAKAVSAVLESDF YPGFEEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE RIAGMDPVVHSALREERILLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIESMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE GRASULVIESMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE 19 16 AMMWNSLDGTRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIANVNGLATAAGCQLVAS CDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLINK VVPEAELQEETMRTARKTASLSRPVVSLGKATTYKQLPQDLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKEVWSHEPV*VEH YYLTSQAMVDNLALRDGQEGITAFLOKRKEVWSHEPV*VEH VVEYAFASLQSESTPRPOTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEILADFDELLSK PKRSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFFLRVGLNHGPVVAGVTGAQKPQ YDIWGNTVNNASRMESTOVLGKTQVTEETAWALQSLGYTCYSRG VIKVKGKQQLCTYPLINTDLTRTGPPSATLG ARGLINEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPBAKIPAKVIGQNTLLKELLRELYLIGNLNSENNKMI GLESLEELERHLKILIHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKKLIHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKKLIHVKSNLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGRKVDILPKGVTLDFKCJOKLSCHLSPRKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNOVEGQFLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				WARDATINGAT COMBRIGO MERKEDDDAKANAKAN UNITED STERAK
YPGFEEAKRKLQERPWLVDSYSEWLQRLKGPPHKCALIFADNSG IDIILGVFFPVRELLLRGTEVILACNSGPALNDVTHSESLIVAE RIAGMDPVVHSALREERILLVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE 6848 19 16 AMWINSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTEGFISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPODLGTA YYLTSQAMVDNLALRDGOEGITAFLQKRKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHGSYEC VCVLFASVPDPKEFYSESNINHEGLECLRILNEIIADFDELLSK PKPSGVEKIKTIGSTYMAATGLNATSGQDAQDAERSCSHLGTM VEFAVALGSKLDVINKHSPNNFRLRVGLNGFVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVILGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG VEFAVALGSKLDVINKHSPNNFRLRVGLNHGFVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVILGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVLLKNLRELPLIGINNENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELBLQNCELBRIPHAIFSLSNLQELDLKS NNIRTIEBIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLEVAVFSLQKLCLDVSYNNISMIPIEIGLLQNLQ HLHHTGRKVDILPKGLJFKCILDVSYNNISMIPIEIGLLQNLQ HLHHTGRKVDILPKGLJFKCIKLKTLNLGGNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 05851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLTILD LRDLFNOVEQGELLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	ł			PAYGIETVKSLEDIKERCENEFNIFDFISKVKQKENGVADKCI
IDIILGVFPFVRELLLRGTEVILACNSGPALMDVTHSESLTVAE RIAGMDPVVHSALRERELLUVQTGSSSPCLDLSRLDKGLAALVR ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRLFSVIFKYEVPAE 6848 19 16 AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKLEUTEEQGRDYHAEVPÇTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VCLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQDPQDLGTA YYLTSQAMVDNLALRDGGEITAFLGKRKVWSHEPVV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSVEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGFVVAGVIGAQKY YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKQQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPBAKIPAKISGMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVHNDGT KLLVLNSLKKMMNVAELELQNCELERIPHAIFSLSNLQELDLKS NNIRTIEBIISFQHLKRLTCLKLMINKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNRVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNOVEOGPILSCPKAGTDLSWGRAREVGWMAAGLMIGAGA				
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ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG GRIFSVIFKYEVPAE 6848 19 16 AMWINSLDGIRRIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLINK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQANVDNLALRDGOGGITAFLOKKKPWSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLINEIIADFDELLSK PKFSGVERIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSPNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTTNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLINHEWTFEKLROHISRNAQDKOELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELDLKCLHVKSPNLTDVAPHLTKLVIHNDGT KLLVINSLKKMMNVAELBLQNCGLERIPHATFSLSNLQELDLKS NNIRTIEBIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL VFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIBIGLLONLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 0 VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLTID LRDLFNOVEGGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				IDIILGVFPFVRELLLRGTEVILACNSGPALNDVTHSESLIVAE
GRLFSVIFKYEVPAE 6848 19 16 AMMWNSLGIRNTVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTFGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGGGITAFLOKRKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLINEIIADFDELLSK PKREGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDLWGNTUNVASRMESTGVLGKTQVTEETAWALQSLGYTCYSRG VIKVKGKQQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKOGLHLEMISGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMI GLESLRELRHLKILHVKSNITKVPSNITDVAPHLTKLVIHNDGT KLLVINSLKKMMNVABLELQNCCLERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLMFINKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPFKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI 6851 1765 660 VSAQVSAREGENCLGWNLADSSQESYKSLEEABCCYPPSLTTLD LRDLFNOVEGGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	ļ			RIAGMDPVVHSALREERLLLVQTGSSSPCLDLSRLDKGLAALVK
6848 19 16 AMWINSLOGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFOTCS KVMMH IRNHPVPVIAMVNGLATAAGCQLVAS CDIAVAS DKSSFATPGW VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLINK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPODLGTA YYLTSQAMVDNLALRDGQEGITAFLOKRKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPOTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLINEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG CHENCHVKFTDVAEIPAWVLLKHLEHLHCHCPAKVEQTAFSFL RDHLRCLHVKFTDVAEIPAWVLLKHLRELYLIGNLINSENNKH GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLINSLKKMMNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNOVCOSPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	1			ERGADLVVIEGMGRAVHTNYHAALRCESLKLAVIKNAWLAERLG
LKVIIISAEGPVFSSGHDLKELTEEQGRDYHAEVFQTCSKVMMH IRNHPVPVIAMVNGLATAAGCQLVASCDIAVASDKSSFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLINK VVPEAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYLTSQAMVDNLALRDGOEGTTAFLOKRKPVMSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLLNEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVKFTDVABIPAWVYLLKNLEELYLIGNLINSENNKMI GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIKTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLEKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNOVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA				GRLFSVIFKYEVPAE
LKVIIISAEGPVFSSGHDLKELTEQQEDYHAEVFOTCS KVMMH IRNHPVPVIAWNOGLATAAGCQLVAS CDIAVASDKS SFATPGVN VGLFCSTPGVALARAVPRKVALEMLFTGEPISAQEALLHGLLNK VVPFAELQEETMRIARKIASLSRPVVSLGKATFYKQLPQDLGTA YYITSQAMVDNLALRDGQEGITAFLQKRKPVWSHEPV*VEH 6849 70 821 SLGVDGSCLEQGSPAPRPQTDTSP*PVGNWATQQEDLYHQSYEC VCVLFASVPDFKEFYSESNINHEGLECLRLINEIIADFDELLSK PKFSGVEKIKTIGSTYMAATGLNATSGQDAQQDAERSCSHLGTM VEFAVALGSKLDVINKHSFNNFRLRVGLNHGPVVAGVIGAQKPQ YDIWGNTVNVASRMESTGVLGKIQVTEETAWALQSLGYTCYSRG VIKVKGKGQLCTYFLNTDLTRTGPPSATLG 6850 2 1235 ARGLNHEWTFEKLRQHISRNAQDKQELHLFMLSGVPDAVFDLTD LDVLKLELIPEAKIPAKISQMTNLQELHLCHCPAKVEQTAFSFL RDHLRCLHVVFTDVAEIPAWVLLKNLRELYLIGNLSENNKN GLESLRELRHLKILHVKSNLTKVPSNITDVAPHLTKLVIHNDGT KLLVLNSLKKMMNVAELBLQNCELERIPHAIFSLSNLQELDLKS NNIRTIEEIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESL YFSNNKLESLPVAVFSLQKLRCLDVSYNNISMIPIEIGLLQNLQ HLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLPEKVGQLSQ LTQLELKGNCLDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVK EALNQDINIPFANGI VSAQVSAREGENCLGWNLADSSQESYKSLEEAEDCYPPSLLTLD LRDLFNOVEQGPLLSCPKAGTDLSMGRAREVGWMAAGLMIGAGA	6848	19	16	AMWWNSLDGIRNIVLSNPKKRNTLSLAMLKSLQSDILHDADSND
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CICATENI I GEODG PICTURE DE CARDON D			1	CYCVYKLTIGRDDSEKLEREGEEEWDDDQELDEREPDIWFDFEI

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		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	I C.C.RATAINA DEARDHILLU ACTUI
ID	beginning	location	las tania baid Emphenylalanine, Gediyeme,
NO: [nucleotide	corresponding	to or all along Telegoleticine, Kebyshie,
1	location		1 - Januara Mamethionine, Namediagric,
ľ	corresponding	to first	n proline O=Glutamine, K=Alginine,
1	to first	amino acid	m mbwoonine V=Valine.
	amino acid	residue of) Warning Varyrogine, X=Unknown, "-but
	residue of	amino acid	Codon, /=possible nucleotide deletion,
l	amino acid	sequence	\=possible nucleotide insertion)
	sequence ,		\=possible nucleotide inscretory
	sequence		The possible The
	ļ	l	MARPWIELGEWIELFGAFOCH LENGTH L
		}	
	}		
			FPLISEGSGCAKVQVLKPLMGLSEKPVLAGELVGAQMLFSFMSL
		1	CNDRILLETTEND
6852	1	407	TOTAL CONTINUES OF THE CONTINUES OF
0032	†		GFIGLNSIAVICINEVNOLABIT IAETLWEQVLKPLGDNLMEENIRQSVTNSIKAGLTDQVSHHARL
	i		IAETLWEQVERPLEDINEMENTAL
	ļ		KTD TOTAL TRANSPORT LINE TO THE TOTAL TOTA
	1	469	GDSCAVCIELYKPNDLVRILTCNHIFHKTCVDPWLLEHRTCPMC
6853	3	1	
		1	ASSGYASVOGTYEPPLEEHVQSTNESDQLVNAEAUSVAVDVIII
	1	l	
			THE PROPERTY OF THE PROPERTY O
6854	1148	585	THE PROPERTY OF THE PROPERTY O
	1		
	Ì	ì	LFHSFEELLLEAHGDYGLRNDYHMNLGQFLEFLKKHKSEHVFQI
		1	
			LFGIESKSSDS GRVGGRVGRICSPLSGANEYIASTDTLKTEEVLLFTDQTDDLAK
	1913	1148	GRVGGRVGRICSPLSGANEYIASIDIDKILADASRF
6855	1 1913		GRVGGRVGRICSFLSGARETTAG EEPTSLFQRDSETKGESGLVLEGDKEIHQIFEDLDKKLALASRF
			YIPEGCIQRWAAEMVVALDALHREGIVCRDLNPNNILLNDRGHI
	}	1	TEDMY (APRVIAL LEGISACE)
		•	ON THE PRICE OF THE PROPERTY O
		1	I TOT AND CORD TECHDEFT PVDWALLING
			THE PROPERTY OF THE PROPERTY O
6856	1617	997	The state of the s
		ł	The state of the s
	1	1	RKFKIGGEWWTWINYNRFQELIQEYEDSGGSKTFSAKDYMARTP
	\ \		I THE STREET OF THE PROPERTY O
1			HWALFGASERGFDFNDTRINGRAM KGPEATAMVCVCSHPNCRQNHIKPSHSAAQTWCGSPTPASAPNH KGPEATAMVCVCSHPNCRQNHIKPSHSAAQTWCGSPTPASAPNH
	- 1	617	KGPEATAMVCVCSHPNCRQNHIRPSASARQIWCGGLESKALWF
6857	1	•	KGPEATAMVCVCShPNCAQMINE KLMAMEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF KLMAMEQGKTLPSATEDAKEEGLEAQISRLAELIGRLESKALWF
Ì			
	ļ	Į.	TOWNOCHITAVRLSDGFTFVIYEFWETEEAWKRILDGFTEEAU
}	1		L CODEST COTT.VDAAWCTVGRU
1			
685	3 2	669	I
	1		
	1		
1		1	IVNTCPQDIGVIDIVSAGSIMDSCINC KIPSLGMCFCEENKEEGKWELVNPPVKTLTHGANAAFNWRNWIS
1	1		•
1	l l		GN CREATER COSCOCYNUSDI I OSPSSTGLLKSG
	9 1	1150	GN GETMFKKAKTKAKKKPRKRSDSSGGYNLSDIIQSPSSTGLLKSG
685	9		TOTAL STREET TO TOTAL STREET S
1	1		
1		l	GCDCDUGDDUGDLDTMFIEESRUKUGAIFKSALGK
			1 CONODVILTAT TO WINNSHMINSTELL VIDE 44 DIG 44
1			
1	İ	1	
1			SQAPKIVRCSTHGTPGPEGMITCH VAPVTFASIVEEELQQEAALIRSREKPLALIQIEEHAIQDLLVI
1			
-			YEAFGNPEEFVIVERTPOGPLAVPMWNKHGC YEAFGNPEEFVIVERTPOGPLAVPMWNKHGC
	3000	1515	YEAFGNPEERVIVERIPGGFIMAWLFQHLTHPYPSEEQKKQLA
68	60 1889		mrt OURDIWETNADDTTV()PMIDQSNRAVSQSSCIO
1			
	61 1889	1515	DTGLTILQVNNWFINARRIIVQPMIDQSNRAVSQGAAYSPEGQ
68			

	I D 21 - 5 - 3	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
		to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first	residue of	S=Serine, T=Threonine, V=Valine,
	amino acid	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	1	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence	<u> </u>	MGSFVLDGOOHMGIRPAGPMSGMGMNMGMDGQWHYM
			EEIDREFHNKLKLKEDKLEKQEKPVNGEDKGDSGVDTQNSEGNA
6862	2	471	DEEDPLGPNCYYDKTKSFFDNISCDDNRERRPTWAEERRLNAET
			FGIPLRPNRGRGGYRGRGGLGFRGGRGGGGGGTFTAPRGFRG
			GFRGGRGGREFADFEYRKTTAFGP
6863	2216	487	POEPALKSEFSQVASNTIPLPLPQPNTCKDNGPCKQVCSTVGGS
		ļ	AICSCFPGYAIMADGVSCEDQDECLMGAHDCSRRQFCVNTLGSF
			YCVNHTVLCADGYILNAHRKCVDINECVTDLHTCSRGEHCVNTL
			GSFHCYKALTCEPGYALKDGECEDVDECAMGTHTCQPGFLCQNT
			KGSFYCQARQRCMDGFLQDPEGNCVDINECTSLSEPCRPGFSCI
			NTVGSYTCQRNPLICARGYHASDDGTKCVDVNECETGVHRCGEG
			QVCHNLPGSYRCDCKAGFQRDAFGRGCIDVNECWASPGRLCQHT
		1	CENTLGSYRCSCASGFLLAADGKRCEDVNECEAQRCSQECANIY
	·		GSYQCYCRQGYQLAEDGHTCTDIDECAQGAGILCTFRCLNVPGS
		i	YQCACPEQGYTMTANGRSCKDVDECALGTHNCSEAETCHNIQGS
			FRCLRFECPPNYVQVSKTKCERTTCHDFLECQNSPARITHYQLN
	1		FQTGLLVPAHIFRIGPAPAFTGDTIALNIIKGNEEGYFGTRRLN
	}		AYTGVVYLQRAVLEPRDFALDVEMKLWRQGSVTTFLAKMHIFFT
			TFAL
6864	1 2	2933	LADSSPSNLQIIIKELLSMHHQPDPALTKEFDYLPPVDSRSSSG
0004			FVGLRNGGATCYMNAVFQQLYMQPGLPESLLSVDDDTDNPDDSV
			FYQVQSLFGHLMESKLQYYVPENFWKIFKMWNKELYVREQQDAY
			EFFTSLIDQMDEYLKKMGRDQIFKNTFQGIYSDQKICKDCPHRY
		}	ERBEAFMALNLGVTSCQSLEISLDQFVRGEVLEGSNAYYCEKCK
			EKRITVKRTCIKSLPSVLVIHLMRFGFDWESGRSIKYDEQIRFP
			WMLNMEPYTVSGMARQDSSSEVGENGRSVDQGGGGSPRKKVALT
			ENYELVGVIVHSGQAHAGHYYSFIKDRRGCGKGKWYKFNDTVIE
			EFDLNDETLEYECFGGEYRPKVYDQTNPYTDVRRRYWNAYMLFY
			QRVSDQNSPVLPKKSRVSVVRQEAEDLSLSAPSSPEISPQSSPR
			PHRPNNDRLSILTKLVKKGEKKGLFVEKMPARIYQMVRDENLKF
		İ	MKNRDVYSSDYFSFVLSLASLNATKLKHPYYPCMAKVSLQLAIQ
		f	FLFQTYLRTKKKLRVDTEEWIATIEALLSKSFDACQWLVEYFIS
			SEGRELIKIFLLECNVREVRVAVATILEKTLDSALFYQDKLKSL
		· I	HQLLEVLLALLDKDVPENCKNCAQYFFLFNTFVQKQGIRAGDLL
			LRHSALRHMISFLLGASRQNNQIRRWSSAQAREFGNLHNTVALL
			VLHSDVSSQRNVAPGIFKQRPPISIAPSSPLLPLHEEVEALLFM
•			SEGKPYLLEVMFALRELTGSLLALIEMVVYCCFCNEHFSFTMLH
			FIKNQLETAPPHELKNTFQLLHEILVIEDPIQVERVKFVFBTEN
1			GLLALMHHSNHVDSSRCYQCVKFLVTLAQKCPAAKEYFKENSHH
			WSWAVQWLQKKMSEHYWTLQSNVSNETSTGKTFQRTISAQDTLA
			YATALLNEKEQSGSSNGSESSPANENGDRHLQQGSESPMMIGEL
L			RSDLDDVDP
6865	1820	1242	DPERWKHLSKVTPPGSSVSTTPVQVVRLQSPQSQGSMMPSCNRS
			CSCSRGPSVEDGKWYGVRSYLHLFYEGYAVPPKLEGIGEGEFLV
			LDQRAADYNQALGTCRLAGTALCVAAGVLLAICLFWAMIGWLSQ
1		(DTKAEPLDPEADSHVEVFGDEPEQQLSPIFRNASGQSWFSPPAS
			PFGQSSVQTIQPKRDS
6866	1571	495	DCPRPRYTLYGLRATCMRDLDWAWINAVSAFKALEQDLPVNIKF
1			IIEGMEEAGSVALEELVEKEKDRFFSGVDYIVISDNLWISQRKP
			AITYGTRGNSYFMVEVKCRDQDFHSGTFGGILHEPMADLVALLG
1			SLVDSSGHILVPGIYDEVVPLTEEEINTYKAIHLDLEEYRNSSR
	(VEKFLFDTKEEILMHLWRYPSLSIHGIEGAFDEPGTKTVIPGRV
,	1]	IGKFSIRLVPHMNVSAVEKQVTRHLEDVFSKRNSSNKMVVSMTL
1			
			GLHPWIANIDDTOYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF
			GLHPWIANIDDTQYLAAKRAIRTVFGTEPDMIRDGSTIPIAKMF QEIVHKSVVLIPLGAVDDGEHSQNEKINRWNYIEGTKLFAAFFL

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine C=Cvateine, D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	H-Wistidine, I=Isoleucine, K=Lysine,
	location	Corresponding	L=Leucine, M=Methionine, N=Asparagine,
Ì	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
ì	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	Codon, /=possible nucleotide delection)
	sequence		\=possible nucleotide insertion) GTRIMSQPKQKELAGFVRQKMLLDYSVYMGRCVPQESRSPQRSP
6867	2833	1704	GTRIMSQPKQKELAGYVKQKMLLDISVIPGKCVPQLSKSFQKOF
			LQSAESSPTAGKKLPEVPPSEEEEQEAWVNALLGRIFWDFLGEK
			YWSDLVSKKIQMKLSKIKLPYFMNELTLTELDMGVAVPKILQAF
	1		KPYVDHQGLWIDLEMSYNGSFLMTLETKMNLTKLGKEPLVEALK
			VGEIGKEGCRPRAFCLADSDEESSSAGSSEEDDAPEPSGGDKQL
	ì		LPGAEGYVGGHRTSKIMRFVDKITKSKYFQKATETEFIKKKIEE
			VSNTPLLLTVEVQECRGTLAVNIPPPPTDRVWYGFRKPPHVELK
			ARPKLGEREVTLVHVTDWIEKKLEQEFQKVFVMPNMDDVYITIM
			HSAMDPRSTSCLLKDPPVEAADQP
	<u> </u>	346	POTEDDTROERIKNLILPYISDMNFVODLCEDFYELFKTDKGFD
6868	1	240	KATFESQMSVMRGQILNLTQALRDGKSPFQLVQIPCVIVERSQG
		Į.	GSQGRIVHLSNSFTQTVNCRKPFFSSW
_			MYMERMDKRALISFWESVEHLKNANKNEIPQLVGEIYQNFFVES
6869	3	1619	KEISVEKSLYKEIQQCLVGNKGIEVFYKIQEDVYETLKDRYYPS
	1		FIVSDLYEKLLIKEEEKHASQMISNKDEMGPRDEAGEEAVDDGT
			NQINEQASFAVNKLRELNEKLEYKRQALNSIQNAPKPDKKIVSK
	ļ		LKDEIILIEKERTDLQLHMARTDWWCENLGMWKASITSGEVTEE
			NGEQLPCYFVMVSLQEVGGVETKNWTVPKRLSEFHNLHRKLSEC
			NGEQLPCYFVMVSLQEVGGVEINWIVPRRUSEINLINGEDED
			VPSLKKDQLPSLSKLPFKSIDHTFMEKFENQLNKFLQNLLSDER
			LCQSEALYAFLSPSPDYLKVIDVQGKKNSFSLSSFLERLPRDFF
			SHQEEETEEDSDLSDYGDDVDGRKDALAEPCFMLIGEIFELRGM
			FKWVRRTLIALVQVTFGRTINKQIRDTVSWIFSEQMLVYYINIF
	İ		RDAFWPNGKLAPPTTIRSKEQSQETKQRAQQKLLENIPDMLQSL
	Ì		VGQQNARHGIIKIFNALQETRANKHLLYALMELLLIELCPELRV
			ULDOLKAGOV
	1	1566	MAAVVAATRWWQLLLVLSAAGMGASGAPQPPNILLLLMDDMGWG
6870	1	1550	DICUVGEPSRETPNIDRMAAEGLLFPNFYSANPLCSPSRAALLT
ĺ			GDI.DIPNGFYTTNAHARNAYTPOEIVGGIPDSEQLLPELLKKAG
1			VVSKIVGKWHI.GHRPOFHPLKHGFDEWFGSPNCHFGPYDNKARP
1			NIDVYRDWEMVGRYYEEFPINLKTGEANLTQIYLQEALDFIKRQ
1			ARHHPFFLYWAVDATHAPVYASKPFLGTSQRGRYGDAVREIDDS
			IGKILELLQDLHVADNTFVFFTSDNGAALISAPEQGGSNGPFLC
			GKQTTFEGGMREPALAWWPGHVTAGQVSHQLGSIMDLFTTSLAL
			AGLTPPSDRAIDGLNLLPTLLQGRLMDRPIFYYRGDTLMAATLG
			QHKAHFWTWTNSWENFRQGIDFCPGQNVSGVTTHNLEDHTKLPI
			QHKAHFWTWINSWERFRQGIDFCFGGRV5GVITTALBBMITTALBERITSVVQQHQEALVPAQE
		1	IFHLGRDPGERPPLSFASAEIQEALSKIISVVQORQHALIVIIQU QLNVCNWAVMNWAPPGCEKLGKCLTPPESIPKKCLWSH
			QLNVCNWAVMNWAPPGCERLGACLIFPESTFARCHHOIT
6871	209	1126	RMSLNPPIFLKRSEENSSKFVETKQSQTTSIASEDPLQNLCLAS
1			QEVLQKAQQSGRSKCLKCGGSRMFYCYTCYVPVENVPIEQIPLY
1			KLPLKIDI IKHPNETDGKSTAIHAKLLAPEFVNIYTYPCIPEY
1		1	EKDHEVALIFPGPQSISIKDISFHLQKRIQNNVRGKNDDPDKP
			FKRKRTEEOEFCDLNDSKCKGTTLKKIIFIDSTWNQTNKIFTD
1			PLOGLLOVELKTRKTCFWRHQKGKPDTFLSTIEAIYYFLVDYH
}			DILKEKYRGOYDNLLFFYSFMYQLIKNAKCSGDKETGKLTH
		459	FGLIMVVLSLIEMKGNCVREDLIENFLFKLGLDVRETNGLFGN
6872	880	1 200	VKI.TTEVFVPOKYLEYRRIPYTEPAEYEFLWGPRAFLETSKML
			LRFLAKLHKKDPQSWPFHYLEALAECBWEDTDEDEPDTGDSAH
1		ļ	PTSRPPPR
1			DEQAVLCSKDKTYDLKIADTSNMLLFIPGCKTPDQLKKEDSHC
6873	1929	955	I I HTE I FGFSNNYWELRRRRPKLKKLKKLLMENPYEGPDSQKE
1		1	TINTETIGESNATABLEARCAPADACAMENTE TOOLOGICA
1			DSNSSKYTTEDLLDQIQASEERIMTQLQVLNACKIGGYWRILE
			DYEMKLLNHVTQLVDSESWSFGKVPLNTCLQELGPLEPEEMIE
			CLKCYGKKYVDEGEVYFELDADKICRAAARMLLQNAVKFNLAE
1			QEVWQQSVPEGMVTSLDQLKGLALVDRHSRPEIIFLLKVDDLP
			DNQERFNSLFSLREKWTEEDIAPYIQDLCGEKQTIGALLTKYS
			SSMQNGVKVYNSRRPIS

		1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 - 1 -	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	/A-Alanine, C=Cvsteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, k=olkhown,
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
6874	1	307	DSIADHVNSAAVNVEEGTKNLGKAAKYKLAALPVAGALIGGMVG
00/4	_		GPIGLLAGFKVAGIAAALGGGVLGFTGGKLIQRKKQKMMEKLTS
			SCROLPSOTOKKCS
	1.500	349	VIGTGERGNSASEKWEIMFNEELGDPFIIIHSISLLNAEEHSIA
6875	1688	345	TILLD IEKRELDMKGSGFYVSLEWVTISKKNQDNKKYBIIKRDI
		ì	LRGKSVPHYAAIEPDGNGLMIVSYKSLTFVQAGQDLEENMDEDI
		i	SEKIKEPLYYWQQTEDDLTVTIRLPEDNTKEDIQIQFLPDHINI
	ì	1	VLKDHQFLEGKLYSSIDHESSTWIIKESNSLEISLIKKNEGLTW
	1	į.	VLKDHOFLEGKLYSSIDHESSIWIIKESHSBBIOHIKEKPD
		•	PELVIGDKOGELIRDSAQCAAIAERLMHLTSEELNPNPDKEKPP
	1	l .	CNAQELEECDIFFEESSSLCRFDGNTLKTTHVVNLGSNQYLFSV
	1		IVDPKEMPCFCLRHDVDALLWQPHSSKQDDMWEHIATFNALGYV
	1		QASKRDKKFFACAPNYSYAALCECLRRVFIYRQPAPMSTVLYNR
		i	KEGRQVGQVAKQQVASLETNDPILGFQATNERLFVLTTKNLFLI
		}	WINTEN
		1285	VCEMTLIMENIA RPLCLVTSAPRILEMHPFLSLGTSRTSVTKLS
6876	41	1205	TUTY DDMDDCDFMDERYOVIFLVNSGSEANELAMLMARAHSNNI
			DIISFRGAYHGCSPYTLGLTNVGIYKMELPGGTGCQPTMCPDVF
		ì	RGPWGGSHCRDSPVQTIRKCSCAPDCCQAKDQYIEQFKDTLSTS
			VAKSIAGFFAEPIQGVNGVVQYPKGFLKEAFELVRARGGVCIAN
			EVQTGFGRLGSHFWGFQTHDVLPDIVTMAKGIGNGFPMAAVITT
	ļ		EVQTGFGRLGSHFWGFQTHDVLFDTVTFRGTGNGTTFLLTTT
		1	PEIAKSLAKCLQHFNTFGGNPMACAIGSAVLEVIKEENLQENSQ
		1	EVGTYMLLKFAKLRDEFEIVGDVRGKGLMIGIEMVQDKISCRPL
		1	PREEVNQIHEDCKHMGLLVGRGSIFSQTFRIAPSMCITKPEVDF
			AVEVFRSALTQHMERRAK
	1	778	GTSPSPARAYAPPTERKRFYQNVSITQGEGGFEINLDHRKLKTP
6877	_		OAKLETUDSEALAIAVATEWDSOODTIKYYTMHLTTLCNTSLDN
			PTOPNKDOLIRAAVKFLDTDTICYRVEEPETLVELQRNEWDPII
		ļ	FWARKRYGURISSSTSIMGPSIPAKTREVLVSHLASYNTWALQG
		l .	IEFVAAQLKSMVLTLGLIDLRLTVEQAVLLSRLEEEYQIQKWGN
		1	IEWAHDYELQELRARTAAGTLFIHLCSESTTVKHKLLKE
	_		QTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQN
6878	931	263	LEEDTVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAL
			EYTWFKDGIRLLENPRLGSQSTNSSYTMNTKTGTLQFNTVSKLL
			EYTWFKDGIRLLENPRLGSQSINSSIIMITRIGIDQITTIO
		İ	TGEYSCEARNSVGYRRCPGKRMQVDDLNISGIIAAVVVVALVIS
		l	VCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENDFKHTKSI
			II
6879	- 3	845	IRVIGESDIMQEFLSESDENYNGVSDVELRVALPDGTTVTVRVI
6879	1		KNSTTDOVYOAIAAKVGMDSTTVNYFALFEVISHSFVRKLAPNI
			FDUKLYIONYTSAVPGTCLTIRKWLFTTEEEILLNDNDLAVTY
			THE PROPERTY OF THE PROPERTY O
i.	•		MEITEPHCACDSRRKGHVITAISITHFKLHACTEEGQLBNQVI
ļ			FEWDEMQRWDTDEEGMAFCFEYARGEKKPRWVKIFTPYFNYMH
l			CFERVFCELKWRKEEY
1			RKDNCTAKEWTFPEAKWNTTARVFSHIRLGMGHVLIIVQCFIS
6880	2110	1437	MANIYNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQR
1			MANITYNEKILIKKUNQLIBSIFIQNSKBIFFGIBIRGIINMF
			NRDQIKNCGFFYGHRAFSVALIFVTAFQGLSVAFILKFLDNMF
1			VLMAQVTTVIITTVSVLVFDFRPSLEFFLEAPSVLLSIFIYNA
1	1		KPQVPEYAPRQERIRDLSGNLWERSSGDGEELERLTKPKSDES
1	1		FDTF
		2244	NDSKWEDIHVITGALKMFFRELPEPLFTFNHFNDFVNAIKQEP
688	2638	2277	OPUNAVKDI TROLPKPNODTMOILFRHLRRVIENGEKNRMTYQ
			TATUFGPTIJ.KPEKETGNIAVHTVYQNQIVELILLELSSIFGR
			GIPEAQLWIYPVKSCKGVPVSEAECTAMGLRSGNLRDRFWLVI
688	2 1	850	QEGNMVTARQEPRLVLISLTCDGDTLTLSAAYTKDLLLPIKTP
		}	QEGNMVTARQEPRLVETSETCOGDITETESATTROBLET TRAVERSET
)			
Ì		1	TNAVHKCRVHGLEIEGRDCGEAIAQUITSI MCQUITSI MRPRRPHQIADLFRPKDQIAYSDTSPFLILSEASLADLNSRLE

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
	i .	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, B=
ID	beginning	1	
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
ł	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ł	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	•		
ı	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence		\=possible nucleotide insertion)
			KVKATNFRPNIVISGCDVYAEDSWDELLIGDVELKRVMACSRCI
[1		LTTVDPDTGVMSRKEPLETLKSYRQCDPSERKLYGKSPLFGQYF
ĺ			VLENPGTIKVGDPVYLLGO
2000	1 2204	2256	NSKLKLNONLKLFITLTYOVLSLHGWGPGIHLOKEGAFPVTONR
6883	2794	2256	
1		ł	ALQLLYDLRYLNIVLTAKGDEVKSGRSKPDSRIEKVTDHLEALI
Į.		1	DPFDLDVFTPHLNSNLHRLVQRTSVLFGLVTGTENQLAPRSSTF
			NSQEPHNILPLASSQIRFGLLPLSMTSTRKAKSTRNIETKAQYD
ļ	ĺ	1	ANC
6884	2	99	BFERVTAEAVKPRETSEPRAAAQRFCEKFPFL
l		1	
6885	297	1554	STGQFWHVTDLHLDPTYHITDDHTKVCASSKGANASNPGPFGDV
1			LCDSPYQLILSAFDFIKNSGQEASFMIWTGDSPPHVPVPELSTD
Į.	1		TVINVITNMTTTIQSLFPNLQVFPALGNHDYWPQDQLSVVTSKV
1		1	YNAVANLWKPWLDEEAISTLRKGGFYSQKVTTNPNLRIISLNTN
Į.		1	LYYGPNIMTLNKTDPANQFEWLESTLNNSQQNKEKVYIIAHVPV
		1	GYLPSSONITAMREYYNEKLIDIFQKYSDVIAGQFYGHTHRDSI
1			1
			MVLSDKKGSPVNSLFVAPAVTPVKSVLEKQTNNPGIRLFQYDPR
1		}	DYKLLDMLQYYLNLTEANLKGESIWKLEYILTQTYDIEDLQPES
		i	LYGLAKOFTILDSKQFIKYYNYFFVSYDSSVTCDKTCKAFQICA
			IMNLDNISYADCLKQLYIKHNY
6886	2	1341	QCGGIPGREGGSSRPLEEGTGSSPACVRGAAPGSEDAFYPTRAK
0000	1		OARVSOELKKAAKRTVSISEGPDTLGDGMRERRETLALAPEPEP
		1	"
			LEKEACEKWKRPFRSASATSLTLSHCVDVVKGLLDFKKRRGHSI
i		1	GGAPEQRYQIIPVCVAARLPTRAQDVLDAHLSEVNAVRFGPNSS
	İ		LLATGGADRLIHLWNVVGSRLEANQTLEGAGGSITSVDFDPSGY
1	1	!	QVLAATYNQAAQLWKVGEAQSKETLSGHKDKVTAAKFKLTRHQA
1		1	VTGSRDRTVKEWDLGRAYCSRTINVLSYCNDVVCGDHIIISGHN
1	Í		DOKIRFWDSRGPHCTQVIPVQGRVTSLSLSHDQLHLLSCSRDNT
ļ			LKVIDLRVSNIRQVFRADGFKCGSDWTKAVFSPDRSYALAGSCD
1 .	1		
		1	GALYIWDVDTGKLESRLQGPHCAAVNAVAWCYSGSHMVSVDQGR
}	1	1	KVVLWQ
6887	1047	116	WTARPSQKPFWEAGAVPGDPLSTGCSQAQLGGCCPRGPWGPQHG
1		i	GQQRAAGPTLPRGERGGPQQSGPGLAAQTPPTSKQVAWRAFLTG
1		1	TYRSQSPRSPAGPFRGGTGWWPEPAVCLCVAVGPQRLSSPGLVY
i		1	NASGSEHCYDIYRLYHSCADPTGCGTGPDARAWDYQACTEINLT
1			_
1		l	FASNNVTDMFPDLPFTDELRQRYCLDTWGVWPRPDWLLTSFWGG
Į.			DLRAASNIIFSNGNLDPWAGGGIRRNLSASVIAVTIQGGAHHLD
1		1	LRASHPEDPASVVEARKLEATIIGEWVKAARREQQPALRGGPRL
1		1	SL
6888	1	992	FVAYVKKEIPHIVVTHCLLNPHALVIKTLPTKLRDALFTVVRVI
""	1		NFIKGRAPNHRLFQAFFEEIGIEYSVLLFHTEMRWLSRGQILTH
1		1	
1			IFEMYBEINQFLHHKSSNLVDGFENKEFKIHLAYLADLFKHLNE
1			LSASMORTGMNTVSAREKLSAFVRKFPFWQKRIEKRNFTNFPFL
1			EEIIVSDNEGIFIAAEITLHLQQLSNFFHGYFSIGDLNEASKWI
1			LDPFLFNIDFVDDSYLMKNDLAELRASGQILMEFETMKLEDFWC
			AOFTAFPNLAKTALEILMPFATTYLCELGFSITFTFQNKVPEAA
			LILSDDIRVAISKKVPSFLGHH
		+	
6889	1	1534	LTLENQIKEEREQDNSESPNGRTSPLVSQNNEQGSTLRDLLTTT
1		1	AGKLRVGSTDAGIAFAPVYSMGAPSSKSGRTMPNILDDIIASVV
			ENKIPPSKTSKINVKPELKEEPEESIISAVDENNKLYSDIPHSW
1			ICEKHILWLKDYKNSSNWKLFKECWKQGQPAVVSGVHKKMNISL
}	1		WKAESISLDFGDHOADLLNCKDSIISNANVKEFWDGFEEVSKRQ
1			
1			KNKSGETVVLKLKDWPSGEDFKTMMPARYBDLLKSLPLPEYCNP
1			EGKFNLASHLPGFFVRPDLGPRLCSAYGVVAAKDHDIGTTNLHI
1	1		EVSDVVNILVYVGIAKGNGILSKAGILKKFEEEDLDDILRKRLK
1	ľ		DSSEIPGALWHIYAGKDVDKIREFLQKISKEQGLEVLPEHDPIR
l .			DOSWYVNKKLRORLLEEYGVRTWTLIQFLGDAIVLPAGALHQVQ

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		Bedacuec	\=possible nucleotide insertion)
	sequence		NFHSCIQVTEDFVSPEHLVESFHLTQBLRLLKEEINYDDKLQVK
		l .	NILYHAVKEMVRALKIHEDEVDDMEEN
6890	3	667	THACGMWIPLYLHRALVVHKTAETCNSPPCGAKDSL1FGAITCF
			TGFLGVDTGAGATRWCRLKTQRADPLVCAVGMLGSAIFICLIFV
	į	1	AAKSSIVGAYICIFVGETLLFSNWAITADILMYVVIPTRRATAV
		1	ALQSFTSHLLGDAGSPYLIGFISDLIRQSTKDSPLWEFLSLGYA
			LMLCPFVVVLGGMFFLATALFFVSDRARAEQQVNQLAMPPASVK
	İ	1	v
6001	1,000	1262	LRIHQELLSKELKLLRGITIESIIHIGLAAGKEQFMQDASNVMQ
6891	1980	1202	LLLKTQSHLYNMEDNNPEVRQAAAYGLGVMAQFGGDDYRSLCSE
	1		AVPLLVKVIKRAHSKTKKNVIATENCISAIGKILKPKPNCVNVD
	\		MALITHA OR DI REDREES TOWN OF CONTROL DESIGNATION OF SERVICE AND THE WASHINGTON OF SERVICE AND T
			EVLPHWLSWLPLHEDKEEAIQTLSFLCDLIESNHPVVIGPNNSN
	Į.		LPKIISIIAEGKINETINYEDPCAKRLANVVRQVQTSEDLWLEC
		1	VSQLDDEQQEALQELLNFA
6892	3	876	RSVAAASGPGAWGTDHYCLELLRKRDYEGYLCSLLLPAESRSSV
	-	ł	FALRAFNVBLAQVKDSVSEKTIGLMRMQFWKKTVEDIYCDNPPH
		i	QPVAIELWKAVKRHNLTKRWLMKIVDEREKNLDDKAYRNIKELE
		l l	NYAENTQSSLLYLTLEILGIKDLHADHAASHIGKAQGIVTCLRA
		l.	TPYHGSRRKVFLPMDICMLHGVSQEDFLRRNQDKNVRDVIYDIA
	İ		SQAHLHLKHARSFHKTVPVKAFPAFLQTVSLEDFLKKIQRVDFD
			IFHPSLQQKNTLLPLYLYIQSWRKTY
6893	1	842	DGERKSMSVERTFSEINKAEEQYSLCQELCSELAQDLQKERLKG
			RTVTIKLKNVNFEVKTRASTVSSVVSTAEEIFAIAKELLKTEID
		1	ADFPHPLRLRLMGVRISSFPNEEDRKHQQRSIIGFLQAGNQALS
		l l	ATECTLEKTOKOKFVKPLEMSHKKSFFOKKRSERKWSHQDTFKC
			EAVNKQSFQTSQPFQVLKKKMNENLEISENSDDCQILTCPVCFR
ļ			AQGCISLEALNKHVDECLDGPSISENFKMFSCSHVSATKVNKKE
		ļ	NVPASSLCEKQDYEAH
	1	1463	TTLCKPLVPREHQFYETLPAEMRKFTPQYKGKSQLLEGLPHWRG
6894	1742	1463	DVRDRGHGRPWQPSLEPSLPPTLCFPSLSSFSSSWPSAQHLTPS
İ	1		
			VFNPW
6895	2379	478	VTYVELCOLASPTALLIMRTVLDLIVEDLQSTSEDKEQQYTSQT
}	1		TRLLALLYALASHKACKLAILHLINGTIKGDERYAEIFQDLLAL
1	[VRSPGDSVIRQQCVEYVTSILQSLCDQDIALILPSSSEGSISEL
			EQLSNSLPNKELMTSICDCLLATLANSESSYNCLLTCVRTMMFL
	1	1	AEHDYGLFHLKSSLRKNSSALHSLLKRVVSTFSKDTGELASSFL
		1	EFMROILNSDTIGCCGDDNGLMEVEGAHTSRTMSINAAELKQLL
	1		QSKEESPENLFLELEKLVLEHSKDDDNLDSLLDSVVGLKQMLES
1			SGDPLPLSDQDVEPVLSAPESLQNLFNNRTAYVLADVMDDQLKS
1			MWFTPFQAEEIDTDLDLVKVDLIELSBKCCSDFDLHSELERSFL
[SEPSSPGRTKTTKGFKLGKHKHETFITSSGKSEYIEPAKRAHVV
I			
1			PPPRGRGGGGGGGIRPHDIFRQRKQNTSRPPSMHVDDFVAAES
1			KEVVPQDGIPPPKRPLKVSQKISSRGGFSGNRGGRGAFHSQNRF
			FTPPASKGNYSRREGTRGSSWSAQNTPRGNYNESRGGQSNFNRG
		1	PLPPLRPLSSTGYRPSPRDRASRGRGGLGPSWASANSGSGGSRG
1	1		KFVSGGSGRGRHVRSFTR
6896	1 1	555	GNIVIQKKKYNKQHIIPLENVTIDSIKDEGDLRNGWLIKTFTKS
0000	,	1.	FAVYAATATEKSEWMNHINKCVTDLLSKSGKTPSNEHAAVWVPD
1	İ		SEATVCMRCQKAKPTPVNRRHHCRKCGFVVCGPCSEKRFLLPSQ
1	1		SSKPVRICDFCYDLLSAGDMATCQPARSDSYSQSLKSPLNDMSD
1	i	[
Į.	. 1		DDDDDDSSD
6897	3	920	GDGLMHEVVNGLMERPDWETAIQKPLCSLPAGSGNALAASLNHY
		1	AGYEQVTNEDLLTNCTLLLCRRLLSPMNLLSLHTASGLRLFSVL
1			SLAWGFIADVDLESEKYRRLGEMRFTLGTFLRLAALRTYRGRLA
1			
			YLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDE
			YLPVGRVGSKTPASPVVVQQGPVDAHLVPLEEPVPSHWTVVPDB DFVLVLALLHSHLGSEMFAAPMGRCAAGVMHLFYVRAGVSRAML

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	p=proline, Q=Glutamine, k=Alginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1	\=possible nucleotide insertion)
	Bequest		LRLFLAMEKGRHMEYECPYLVYVPVVAFRLEPKDGKGVFAVDGE
	Ì	· ·	LMVSEAVOGOVHPNYFWMVSGCVEPPPSWKPQQMPPPEEPL
	919	346	OKTVTAVASLLKGROGIYTENERRMGAVIKIRFFKIMLVLIICW
6898	913	1	LSNIINESLLFYLEMQTDINGGSLKPVRTAAKTTWFIMGILNPA
		Į	QGFLLSLAFYGWTGCSLGFQSPRKEIQWESLTTSAAEGAHPSPL
			MPHENPASGKVSQVGGQTSDEALSMLSEGSDASTIEIHTASESC
			NKNEGDPALPTHGDL
			MKVRKNNDAYLLDKNKINMDCFISCFFKKMLTTLMFSHSGILSL
6899	120	827	MKVRKNNDAYLLDKNAINFIDCF ISCFF KRAILITIDAT STOGILES
		1	LEHGEEYTFSLPCAYARSILTVPWVELGGKVSVNCAKTGYSASI
	Ì		TFHTKPFYGGKLHRVTAEVKHNITNTVVCRVQGEWNSVLEFTYS
			NGETKYVDLTKLAVTKKRVRPLEKQDPFESRRLWKNVTDSLRES
		1	EIDKATEHKHTLEERORTEERHRTETGTPWKTKYFIKEGDGWVY
		1	HKPLWKIIPTTQPAE
6900	3	451	TEVLGSKGIHELRSSTSALHHALEESASLLTMFWRAALPSTHIP
6900	1	1	VI.PGKVGESTERELLELRTKVSQQEQLLQSTTEHLKNANQQKES
		Į.	MEQFIVSQLTRTHDVLKKARTNLEVRKLLHQSEAPSLSPTHHHP
			LADLVGDSWPALRFQEK
		201	DDNMVQRLETDFKMTLQQQSTLEQWAAWLDNVMMQALKPYEGRP
6901	1	201	SFPKAARQFLLKWSFYRYHLGFS
			GAPPPPPSQPPRQPPQAAPSSHPHSDLTFNPSSALEGQAGAQGA
6902	2	267	SDMPEPSLDLLPELTNPDELLSYLDPPDLPSNSNDDLLSLFENN
			SDMPEPSLDLLPELTNPDELDS 1 DDPPDDPSNSNDDHESD1 ENN
6903	1	149	RINQVYRQGPTGIHILVIDQMVQNFQDESCFLFSTVKAESSDGI
		1	HIILK
6904	464	2092	MEASLPVSLSCVLACGDVEGKFDILFNRVQAIQKKSGNFDLLLC
0304	1	4	VGNFFGSTQDAEWEEYKTGIKKAPIQTYVLGANNQETVKYFQDA
		\	DGCELAENITYLGRKGIFTGSSGLQIVYLSGTESLNEPVPGYSF
		l,	SPKDVSSLRMMLCTTSOFKGVDILLTSPWPKCVGNFGNSSGEVD
			TKKCGSALVSSLATGLKPRYHFAALEKTYYERLPYRNHIILQEN
		1	AQHATRFIALANVGNPEKKKYLYAFSIVPMKLMDAAELVKQPPD
			VTENPYRKSGQEASIGKQILAPVEESACQFFFDLNEKQGRKRSS
		1	TGRDSKSSPHPKQPRKPPQPPGPCWFCLASPEVEKHLVVNIGTH
		:	CYLALAKGGLSDDHVLILPIGHYQSVVELSAEVVEEVEKYKATL
			RRFFKSRGKWCVVFERNYKSHHLQLQVIPVPISCSTTDDIKDAF
			ITQAQEQQIELLEIPEHSDIKQIAQPGAAYFYVELDTGEKLFHR
			ITQAQEQQIELLEIPEHSDIKQIAQPGAAIFIVEDDIGERLIM
	Ļ		IKKNFPLQFGREVLASEAILNVPDKSDWRQCQISKEDEETLARR
	(FRKDFEPYDFTLDD
6905	1	226	VSKTGEAETITSHYLFALGVYRTLYLFNWIWRYHFEGFFDLIAI
0,00	· · · · ·	}	VAGLVQTVLYCDFFYLYITKVLKGKKLSLPA
		611	CYDDHNGHIDFITAASNIRAKMYSIEPADRFKTKRIAGKIIPAI
6906	3		ATTTATVSGLVALEMIKVTGGYPFEAYKNWFLNLAIPIVVFTET
	1	1	TEVRKTKIRNGISFTIWDRWTVHGKEDFTLLDFINAVKEKYGI
		i	PTMVVQGVKMLYVPVMPGHAKRLKLTMHKLVKPTTEKKYVDLTV
	1	İ	SFAPDIDGDEDLPGPPVRYYFSHDTD
			LRGVPVWAAGAFRFSSGEESTSHLIMSRRSQRLTRYSQGDDDGS
6907	2	2228	LRGVPVWAAGAFRFSSGEESTSMEINSKRSQREITRISQGDDDG
1		1	SSSGSSVAGSQSTLFKDSPLRTLKRKSSNMKRLSPAPQLGPS
		1	DAHTSYYSESLVHESWFPPRSSLEELHGDANWGEDLRVRRRRG
			GGSESSRASGLVGRKATEDFLGSSSGYSSEDDYVGYSDVDQQSS
1			SSRLRSAVSRAGSLLWMVATSPGRLFRLLYWWAGTTWYRLTTA
Ì			SULDVEVLTRRFSSLKTFLWFLLPLLLLTCLTYGAWYFYPYGL(
I			TFHPALVSWWAAKDSRRADEGWEARDSSPHFQAEQRVMSRVHS
			ERRLEALAAEFSSNWQKEAMRLERLELRQGAPGQGGGGGLSHE
			TLALLEGLVSRREAALKEDFRRETAARIQEELSALRAEHQQDS
1	{		DLFKKIVRASQESEARIQQLKSEWQSMTQESFQESSVKELRRL
1	i	1	DPLVVTALWOODDDWTTAANVORMANII ATTA SEED ATTACHMENT
			DOLD OF THE PARTY OF STATE OF
			DQLAGLQQELAALALKQSSVABEVGLLPQQIQAVRDDVESQFP: WISQFLARGGGGRVGLLQREEMQAQLRELESKILTHVAEMQGK

000	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ		nucleotide	/a-alanine C=Cvsteine D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid. F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	H-Highidine, I=Isoleucine, K=Lysine,
	location	to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding		P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Walrypcopnan, illycoathe, kaonatown, and
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	ł	\=possible nucleotide insertion)
	201	·	AREAAASLSLTLQKEGVIGVTEEQVHHIVKQALQRYSEDRIGLA
		1	DYALESGGASVISTRCSETYETKTALLSLFGIPLWYHSQSPRVI
]	1	LOPDVHPGNCWAFOGPOGFAVVRLSARIRPTAVTLEHVPKALSP
	1		NSTISSAPKDFAIFGFDEDLQQEGTLLGKFTYDQDGBPIQTFHF
		1	QAPTMATYQVVELRILTNWGHPEYTCIYRFRVHGEPAH
			QVPSAAWLMAVCGLGSRLGLGSRLGLQGCFGAARLLYPRFQSRG
6908	3	780	POGVEDGDRPQPSSKTPRIPKIYTKTGDKGFSSTFTGERRPKDD
		Ī	PQGVEDGDRPQPSSKTPRIPKITTKIGDKGFSSIFIGEKKFKDD
	1		QVFEAVGTTDELSSAIGFALELVTEKGHTFAEELQKIQCTLQDV
		Ì	GSALATPCSSAREAHLKYTTFKAGPILELEQWIDKYTSQLPPLT
			AFILPSGGKISSALHFCRAVCRRAERRVVPLVQMGETDANVAKF
		\	LNRLSDYLFTLARYAAMKEGNOEKIYKKNDPSAESEGL
		409	GRILLAVGTDLYGORSSAPEOELLVQDATPVSNSLLPEKAFSDIF
6909	3	1 409	SPYLRGTIKMMQAVRQAFQDQDDRRTWDGRPLTMAATFDDCLYF
	ļ	ì	LCVVDTIKRSSQTGEWQNIAIMTEEPELSPAYLISEAMRRSRMS
		Į.	
			LYC
6910	1	1068	LVPVVVIDSYYYGKLVIAPLNIVLYNIFTPHGPDLYGTEPWYFY
••	1		LINGFLNFNVAFALALLVLPLTSLMEYLLQRFHVQNLGHPYWLT
			LAPMYIWFIIFFIQPHKEERFLFPVYPLICLCGAVALSALQHSI
		l	LYFQKCYHFVFQRYRLEHYTVTSNWLALGTVFLFGLLSFSRSVA
	· ·	1	LERGYHGPLDLYPEFYRIATDPTIHTVPEGRPVNVCVGKEWYRI
		ł	PSSFLLPDNWQLQFIPSEFRGQLPKPFAEGPLATRIVPTDMNDQ
		i	NLEEPSRYIDISKCHYLVDLDTMRETPREPKYSSNKEEWISLA
			RPFLDASRSSKLLRAFYVPFLSDQYTVYVNYTILKPRKAKQIRI
		!	
			KSGG
6911	1184	966	GEDAEEMETGNVANLISIFGSSFSGLLRKSPGGGREEEEGEES
		ĺ	PEAAEPGQICCDKPVLRDMNPWSTAIVAF
6912	1	844	AMKPVETHSFOMLFTILSTGSALKAQSYEDAYRCIKSSILLGS
0712	· -		SGGTDIISCFMGHNFSLPVYKGEIQARNLGMAVEAWNEEGKAV
	1	1	GESGELVCTKPIPCQPTHFWNDENGNKYRKAYFSKFPGIWAHG
			VCBINDKTGGIVMLGRSDGTLNPNGVRFGSSEIYNIVESFEEV
			DSLCVPQYNKYREERVILFLKMASGHAFQPDLVKRIRDAIRMG
	1	1	SARHVPSLILETKGIPYTLNGKKVEVAVKQIIAGKAVEQGGAF
		l	NPBTLDLYRDIPELQGF
			NPETEDEREDIPEDOS
6913	1643	1558	KKSHEESHKEELSYGAQASLPLPCSDFR
6914	1251	615	ELAAECKSAGYPGTLIPYRCDLSNEEDILSMFSAIRSQHSGVD
			CINNAGLARPDTLLSGSTSGWKDMFNVNVLALSICTREAYQSM
			ERNVDDGHIININSMSGHRVLPLSVTHFYSATKYAVTALTEGL
		1	OELREAOTHIRATCISPGVVETQFAFKLHDKDPEKAAATYEQM
	1	1	CLEPEDVAEAVIYVLSTPAHIOIGDIQMRPTEQVT
		652	CDCLCERTELIWYLTSTYOGGILMYGALVLFESEFVHVVAISF
6915	254	652	ALILTELLMVALTVRTWHWLMVVABFLSLGCYVSSLAFLNEYF
	1		VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLA
			VAFITTVTFLWKVSAITVVSCLPLIVDKIBARRUSPPSTCKIM
6916	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISF
			ALILTELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYF
		1	VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLA
C 0 2 7	254	652	GRSLSFKTFLIWVLISIYQGGILMYGALVLFESEFVHVVAISF
6917	254	332	ALTITELLMVALTVRTWHWLMVVAEFLSLGCYVSSLAFLNEYF
1			VAFITTVTFLWKVSAITVVSCLPLYVLKYLRRKLSPPSYCKLA
			PEAGTRSWREPDPEDLRRFLLSAACRSFPQWLPGGGGGQVSSC
6918	28	921	PEAGIKSWEDPEDERREDDAMERSET 200000 TOTALELIA
}			DTDVPYLLLAVKSEPGRFAERQAVRETWGSPAPGIRLLFLLGS
		i i	VGEAGPDLDSLVAWESRRYSDLLLWDFLDVPFNQTLKDLLLLD
1			LGRHCPTVSFVLRAQDDAFVHTPALLAHLRALPPASARSLYLG
1]	1	VFTOAMPLRKPGGPFYVPESFFEGGYPAYASGGGYVIAGRLAI
	1		LLRAAARVAPFPFEDVYTGLCIRALGLVPQAHPGFLTAWPADE
i		1	
	Ì	ı	ADHCAFRNLLLVRPLGPQASIRLWKQLQDPRLQC

PCT/US00/34263

WO 01/53312	Amino acid segment containing signal peptide Amino acid segment containing signal peptide D=Aspartic Acid, E= G=Glycine, D=Aspartic, G=Glycine, D=Peptinglalanine, G=Glycine, D=Peptinglalanine, G=Glycine, D=Peptinglalanine, G=Glycine, D=Peptinglalanine, G=Glycine, D=Aspartic Acid, E=
	Amino acid segment containing signal peptide. Amino acid segment containing signal peptide. (A-Alanine, C=Cysteine, D=Aspartic Acid, E= (A-Alanine, C=Cysteine, F=Phenylalanine, G=Glycine, (A-Alanine, Acid, F=Phenylalanine, K=Lysine,
Jand	Amino acid segment containing Dacid, Landon Acid, Landon Acid, Capataline, Cap
Predicted end nucleotide	(A=A=A=A=A=A=A=A=A=A=A=A=A=A=A=A=A=A=A=
SEQ -inning location sing	Amino acid C=cysteine, (A=Alanine, C=cysteine, K=Lysine, (A=Alanic Acid, F=phenylalanine, K=Lysine, Glutamic Acid, F=soleucine, K=Lysine, H=Histidine, M=Methionine, N=Asparagine, L=Leucine, M=Methionine, R=Arginine, L=Leucine, Q=Glutamine, R=Arginine, L=Leucine, Q=Glutamine, V=Valine, L=Leucine, Q=Glutamine, V=Valine, L=Leucine, Q=Glutamine, V=Valine, L=Leucine, Q=Glutamine, V=Valine, L=Leucine, Q=Glutamine, V=Valine, V=Stop
ID nucleotide correspond	
No: location sing to 12 acid	H=HISTIE M=METRITOR R=ARGINE N=LEGATE N
sirst regione	p=proline, T=Threonine, X=Unknown, S=Serine, T=Threonine, X=Unknown, S=Serine, T=Threonine, X=Unknown, W=Tryptophan, y=Tryrosine, X=Unknown, W=Tryptophan, y=Tryrosine, X=Unknown, Codon, /=possible nucleotide insertion) Codon, /=possible nucleotide insertion Codon
amino acro	- POSSYFCPF LOUDINAVLVFORDING TOTVILE PROTECTION
-ino acid	W=Tryptop- Codon, /=possible Nucleotide insertion Codon, /=possible nucleotide insertion -po
sequence 41	ASIDLOXTSHDYADARA ASIDLOXTSHDYADARA ASIDLOXTSHDYADARA ASIDLOXTSHDYADARA ASIDLOXTSHDYADARA ASIDLOXTSHDARA ASIDLO
6919	NCWALLSFFTHOST
	RDFT
	ACCULATION OF DEMENY LINE OF THE STATE OF TH
591	EAGOT EAGOT TO THE
1418 1711	PARKET OLKEDIID
6920 6921	QIA CEGDAGGC THALMON MEAMKYHUD
692-	NET PRODUCAL AND
	YIRD
	HIGH THREE CONGVALINATION OF THE STRICE
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	FDFILL
	EGROWNYVASMSTPRS. 1. EGROWNYVASMSTPRS. 1. EGROWNYVASMSTPRS. 1. FOPHTNKWSLCAPMSKKRGGVQVATYRNFU. FOPHTNKWSLCAPMSKKRGGVAFLAVPRACVVVVKLP FOPHTNLNTVESYDAQRNEWKEEYPVNIGRAGACVVVVKLP SRLSDCVBRYDPKGDSWSTVAPLSTGSELKONIHSIT YDGHTYLNTVESYDAQRNEWKEEYPVLGSTGSELKONIHSIT YDGHTYLNTVESYDAQRNEWKEYPVLGSTKVTSGAKIMGGSTINDVLA TOTOLOGIERHEVRORERERERERERERERERERERERERERERERERERE
	BGROWNY WELCAPMSKRIED SVPEDAVA FDPHTNKWSLCAPMSKRIED SVPEDAVA SRLSDCVBRYDPKGDSWSTVAPLSVPINIGRAGACVVVVKLF SRLSDCVBRYDPKGDRENEREREREREFELDSTGSELKONIHSIT YDCHTYLNTVBSYDAQRNEWKBEVPLNSTGSELKONIHSIT YDCHTYLNTVBSYDAQRNEWKBEVPLNSTGSELKONIHSIT 169 LITPFAGIRHEVRDREREREREREREREFELDSTGSELKONIHSIT LITPFAGIRHEVRDRERERERERERERERERERERERERERERERERERE
1075	VNTPKDAAQQDAKAELINKSGGKVRIITU
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	1660 LEVTFONKOKVLGKALSLIKTVCLKGKECCIMMIQIIEYEKR LEVTFONKOKVLGKALSLIKTVCLKGKECCIMMIQIIEYEKR LEVTFONKOKVLGKALSLIKTVCLKGKECCIMMIQIIEYEKR
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	LRDKSIALING TVRVMDVNTGEVLNTLIHHRNAN TVRVMDVNTGEVLNTLIHHRNAN TVRVMDVNTGEVLNTLIHHRNAN WIMASATDITLRRVLVGRRANVNVDFDDK:ILLWDLLEC WIMASATDITLRRVLVGRRANVNVUSGASSDNTIRLWDLLEC WIMASATDITLRRVLVGRRANVNUSGASYDGKIKVWDLQAALDF STCEFVRTLNGHKRGLACLQVRDVSGAYDGKIKVWDLQAALDF GACLRVLEGHEELVRCIRFDNKTLVSGAYDGKIKVWDLQAALDF GACLRVLEGHEELVRCIRFDNKTLVSGAYDGKIKVWDLGAALDF RAPASTLCLRTLVEHSGRVFRLQFDEFQISSSHDDTLLIWDFL RAPASTLCLRTLVEHSGRVFRLYTYISR WINDSSAQNETRSPSRTYTYISR
	GACLRVLBOOKPTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCLRTLVEHSGRVTADA RAPASTLCRTLVEHSGRVTA
	SGRVAMDGLGLQFF3Q
	133
6926	571
632-1	

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	ma Pantila
	mino acid segment containing signal Peptite A=Alanine, C=Cysteine, D=Aspartic Acid, E: A=Alanine, C=Cysteine, D=Aspartic Acid, E: A=Alanine, C=Cysteine, C=Cysteine, X=Lysine.
predicted end A	mino acid segment D=Aspartic Acid, La Alanine, C=Cysteine, D=Aspartic Acid, E=Aspartic Acid, F=Phenylalanine, G=Clycine, Silvamic Acid, F=Phenylalanine, K=Lysine.
SEO Predicted nucleotide	A=Alanine, Key-Malanine, Gety-Malanine, Glutamic Acid, F=Phenylalanine, K=Lysine, Glutamic Acid, F=Shenylalanine, N=Asparagine, M=Memethionine, N=Argi
SEQ prediction location location	W=Histidine, I=Isoudder, N=Asparagine,
ID beginning location nucleotide corresponding	- 101107mc, 1100 K=P-3-
	p-profile, veven t-stop
-crresponded amino	S=Serion, Y=Tyrosino,
to first residue of amino acid	
l ladue OL lanence	
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sequence	DGYPLFTAGPMHPRLGPEPAGFOF YAGPPEPPAGPMHPRLGPEPAGFOF PGAGGGGGGGGMQPQHQHQHQHQHHPVCKPEMGLPYQGHDSGVNLPD DPSQPAELLGEVDRTEFEQYLHFVCKPEMGLPYQGHDSGVNLPD DPSQPAELLGEVDRTEFEQYLHFVCKPEMGLPYQGTKEDQEILHSLHRESS
	PGAGGGROT GEVERTEFEQYLAFVC.
	PORGGGROUDTEFEROYLH VON DESQPAELLGEVORTEFEROYLH VON DESQPAELLGEVORTEFEROYLH VON DESQPAELLGEVORTEFEROYCH VON DESQPAELLGEVORTEFEROYCH VON DESQPAELLGEVORTEFEROYCH VON DESQUARE COGFANATOLSTOLESQLSVSCKCYEAANBILOFROLKSVSAAEQQLW CQGFANATOLSTOLESQLSVSCKCYEAANBILOFROLKSVSAAEQQLW CQGFANATOLSTOLESQUARGAALQSERLVSKSVSAAEQQLW CQGFANATOLSTOLEGOVET CON ADLILCTIGRIMRICAQAHGAA
	SHGAISSVUMLAQNANNRAAHLEELTI LTLCGDIQLMLAQNANNRAAHLEELTI CQGFAWATDLSTDLESQLSVSCKCYEAANBILQFRDLKSGNFUL CQGFAWATDLSTDLESQLSVSCKCYEAANBILQCAA YVQVLKRMGNIRNEIGVFYMNQAAALQSERLVSKSVSAAEQQAHCGA YVQVLKRMGNIRNEIGVFYMNQAALLLCNTGRLMRICAQAHCGA YVQVLKALRSLGTRDIHPAVWDSVN
1484	LTLCGDIQLIMATOLESQLSVSCKCISM CQGFAWATDLSTDLESQLSVSCKCISM CQGFAWATDLSTDLESQLSVSCKCISM CQGFAWATDLSTDLESQLSVSCKCISM CQGFAWATDLSTDLESQLSVSCKCISM CQGFAWATDLSTDLESQLSVSCKCISM CQGFAWATDLSTDLESQLSVSCAMATICAQAHCGA YQQVLKRMGNIRNEIGVFAMALLLCNTGRLMRICAQAHCGA YQQVLKRMGNIRNEIGVFAMALLLCNTGRLMRICAQAHCGA KKSFSCFEKGIHNFESIEDATNAALLLCNTGRLMGTRAMAKSLKYCD KNEFSPEEGLYYNKAIDYYLKALRSLGTRDHPAWMKSLKYCD
2	CQGFAMATIDAD COMPANDA CANADA C
6927	KKSFSCFEGLYYNKAIDTVAOEOIEKEVSEAMMASTATO
	GDELARDITATLOQDYAPLSACATOR
	KKSFSCFERGTHYNKAIDYTHKAIMSERSEAMMKSLKYCD GDELKREFSPEEGLYYNKAIDYTHKAIMSERSEAMMKSLKYCD GDELKREFSPEEGLYYNKAIDYTHKAIMSERSEAMMKSLKYCD WELSTTYFTMATLQQDYAPLSRKAPHSCLKNQVGDEHLKKQHR WELSTTYFTMATLQQDYAPLHRIASMYHSCLKNQVGDEHLKKQHR VDSVSRRQPLCQYRAATIHHRIASMYHSCLKNQVGDEHLKQSIKON VUSUKAIKTLSGALDIMVRTEHAFQLIQKELIEFGQPKSGDAAAA NVGKLKTLSGALDIMVRTEHAFQLIQKELIEFGQPKSGDAAAA NVGKLKTLSGALDIMVRTEHAFQLIQKELIEFINVIVHLLGQLAA
	VLADLHYSKAAKLEQLIDATEHAFQLIQKELIBETGGTAKKKTSNN
	NVGREAT TO THE TOTAL TOTA
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	EAIDLINNLLQVKMRKRIS VEGLQYPTHLINPSAGING
777	IEDDTILKINGURGER GSAASSNAVQ GSAASSNAVQ EAIDLINKILQVKMRKRYSVDKTLSHPWLQDYQTWLDLRELBCK EAIDLINKILQVKMRKRYSVDKTLSHPWLQDYQTWLDLRETETE IGRYITHESDDLRWEKYAGEQGLQYPTHLINPSASHSDTPETE IGRYITHESDDLRWEKYAGEQGLQYPTHLINPSASHSDTPETE ETBMKALGERVSIL ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGGRSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGGGGSATTAMPPPVPNG ETBMKALGERVSIL ROQRGYRDDRSPAREPGDVSARTRSGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
6928 1086	ETEMAADOGRAREPGDVSART
607	ETEMKALGEN VOJARTROGGOVARTROGGOVARDEN EN
1749	NLHQHDPQDDLCLQPPDGGTCVPEEPPVFFIATSC RGPAAGGLCLQPPDGGTCVPEEPSTRQKLALGSFFDDGPGTYTSC QEVRNQGQARTNSTSAQKNERESIRQKLALGSFFDDGPGTYTSCD QEVRNQGQARTNSTSAQKNERESIRQKLALGSFFDDGSGTSLD SKSKPSLSSRLQSGMNLQICFVNDSGSDKDSDADDSKTETSLD SKSKPSLSSRLQSGMNLQICFVNDSGSDKDSTRQKKLQAEAKM SKSKPSLSSRLQSGMNLQICFVNDSGSLDADDFLTRQKKLQAEAKM
6929	OEVRNOGOARTNST SAUTOLICE VNDSGSDRUSDRUSDRUSDRUSDRUSDRUSDRUSDRUSDRUSDRU
	RGPAAGGLCLVITSTSAQKNERESIKQASOKOSDADDSKTETSID QEVRNOGQARTNSTSAQKNERESIKOKOSGSDKOSDADDSKTETSID SKSGKPSLSSRLQSGMNLQICFVNDSGSDKDSDADDSKTETSID SKSGKPSLSSRLQSGMNLQICFVNDSGSDKDSDADADKTRQKKLQAEAKM TPLSPMSKQSSSYSDRDTTEEESESLDDMDFLTRQKKLQAEAKM TPLSPMSKQSSSYSDRDTTEEESESLDDMDFLTRQKKLQAEAKM ALAMAKPMAKMQVEVEKQNRKKSPVADLLDLIRDBLHTE ALAMAKPMAKMQVEVEKQNRKKSPAK
	TPLSPHISTONOVEVEKQNRRRRD
	ALAMAATIGOLOVIVNDLING
	ODAMLVDIEDLIRHAESQUARYFIEPSQLKLFYDVIIWA
	FKDTANVFVSLFOMRIVATIONSWYYCLHILGIDVIDLO
54	KPTDLRDMITOUT AND
6930 131	RKNTHENTE
(6933	HSSLRV PACILIVASGAAEGVAYASPAKLESIDGARILGC
6	FVERLPNKFYDVTESNARWVQDFKLINA PGGKAMEFVDVTESNARWVQDFKLINA PGGKAMEFVDVTESNARWVQDFKLINA LIPSCPGALTDLASSGSLARILOHFHSESKPICAVGHGVAALCG LIPSCPGALTDLASSGSLARILOHFHSESKPICAVGHGVASSK ATNEDRSWVFDSYSLTGFSVCELVRAPGFARLFLVVEDFVKDSG ATNEDRSWVFDSYSLTGFSVCELVRAPGASVESSSFGFKK
2	PGGKAMET VALASSGSLARTION TO THE PSCPGALIDIAN SINCE TO THE PSCPGALIDIAS SINCE LVRAPGFARLPLVVELF VALUE ATNEDRS NVFDS YSLTGES VCELVRAPGFARLPLVVELF VALUE ATNEDRS NVFDS VENT SINCE THE PSC S
6931	ATNEDRSNVFDSTVLDRHLVTGONASSTVESSSPGPKK
	ACFSASETEGGIQMNSRITETKYVSHQHPSHPQLFST
	ACFSASECTION ACTION OF THE PROPERTY OF THE PRO
2	SDMCEGCRSLAND STATE OF STATE O
6932	QACVRSUSCEVEN YLINSWPFILGANTALTSLTSDDNLWACH QRWYSIITIMMDRIYLINSWPFILGANTARSLTSLTSDDNLWACH EQFGCPQRAQRMNTAFTPFLHQRNGNAARSLTSLTSDDNLWACH EQFGCPQRAQRMNTAFTPFLHQRNGNAARSLTSLTSDDNLWACH HTSFANLLKACGSRLTEKLLEGAPTEDTLVQMEKLADLEEESS HTSFANLLKACGSRLTEKLLEGAPTEDTLVQMEKLADLEESS HTSFANLLKACGSRLTEKLLEGAPTEDTLVQMEKLANGLCLETTLASGPSTL
	EQFGCPQRAQRITEKLLEGAPTEDITUS
	HTSFARDULPESTRORDER PRANHGLCLPTRLASCE
	SLNLHCTLPPPPHQTTT
1 21	KTLQEVTDSLLGGWLMAQ:VOGT. KTLQEVTDSLLGGWLMAQ:VOGT. KTLQEVTDSLLGGWLMAQ:VOGT. SLNLHCTLPPPPHQYPAGYPSDKEGKKYRGOSKKQPSGT. SLNLHCTLPPPPHQYPAGYPSDKEGKKYRGOSKKQPSGT. SDDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCQNOK.W SDDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCQNOK.W SDDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCQNOK.W DEVLSHLUGGWLMAQ:VOGT. SDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCQNOK.W SDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCQNOK.W SDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCQNOK.W SDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCQNOK.W SDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCQNOK.W SDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCQNOK.W SDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCQNOK.W SDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCQNOK.W SDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCQNOK.W SDDCPSASKVYKASDSAEAIEAFQLTPQQOHLIREDCQNOK.W
6933	DEVLORE KAOVESCPACEHOLGONIII
	DEVLSHING DELQRISKAQVFSCPACRHDLGQNIIIN DELQRISKAQVFSCPACRHDLGQNIIIN DELQRISKAKIRTVKMTFIIVLAFIV SKGR DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLAFIV SKGR DRDHSQCGGIRRVALARVSSVKLISKAKIRTVKMTFIIVLAFIV
	CWTPFFI
6934 3030	LFTGHLFHELVQAL 2 HRSSSQRSCSQPSTA
5/2"	HRSSSURGE
	572

		The Market and	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end nucleotide	/A-Alamine C=Cvsteine. D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	corresponding	u-wistidine T=Tsoleucine, K=Lysine,
	location		L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		NSALYVAGGNDGTSCLNSVERYSPKAGAWESVAPMNIRRSTHDL
6935	886	543	NSALYVAGGNUGTSCLINSVERISPRAGAWES VAPINITION IN SCHETTERS
			VAMDGWLYAVGGNDGSSSLNSIEKYNPRTNKWVAASCMFTRRSS
			VGVAVLELLNFPPPSSPTLSVSSTSL
6936	1347	567	RSHRRQFLSRALLEFFGKSHPPPHRLFRKSLNVGLHYSHIPFLT
0,,,,			TCLHFLRKRLQKGEVGLSVETSKPQVPVGGLSRKKVPQEPWATV
		İ	MEKRLQEAQLYKEEGNQRYREGKYRDAVSRYHRALLQLRGLDPS
			LPSPLPNLGPQGPALTPEQENILHTTQTDCYNNLAACLLQMEPV
		1	NYERVREYSOKVLEROPDNAKALYRAGVAFFHLQDYDQARHYLL
	1		AAVNROPKDANVRRYLOLTQSELSSYHRKEKQLYLGMFG
	<u> </u>	727	AVEERCOPGROPACEARGWRLDRVYGTCFCDQACRFTGDCCFDY
6937	1	1 '2'	DRACPARPCEVGEWSPWSGCADQCKPTTRVRRRSVQQEPQNGGA
		l	DCDDLEERAGCLEYSTPOGODCGHTYVPAFITTSAFNKERTRQA
		1	TSPHWSTHTEDAGYCMEFKTESLTPHCALENRPLTRWMQYLREG
	}	1	YTVCVDCQPPAMNSVSLRCSGDGLDSDGNQTLHWQAIGNPRCQG
		1	TWKKVRRVDQCSCPAVHSFIFI
			NSRKLELAERVDTDFMQLKKRRQSSEKENDSGTLDTVGAVVVDH
6938	3	719	EGNVAAAVSSGGLALKHPGRVGQAALYGCGCWAENTGAHNPYST
			EGNVAAAVSSGGLADKAPGKVGQAALITGCGCKALLKTG
	İ	•	PFLASEDGVLGGVIVLRSCRCSAEPDSSQNKQTLLVEFLWSHTT
			PFLASEDGVLGGVIVLRSCRCSAEPDSSQNRQILBVER INSHIT
	1		ESMCVGYMSAQDGKAKTHISRLPPGAVAGQSVAIEGGVCRLGEP
			SELTLQAECEASQRHFRT
6939	3	810	KVTAPRRPQRYSSGHGSDNSSVLSGELPPAMGRTALFHHSGGSS
0555			GYESLRRDSEATGSASSAPDSMSESGAASPGARTRSLKSPKKRA
	•		TGLQRRRLIPAPLPDTTALGRKPSLPGQWVDLPPPLAGSLKEPF
		1	EIKVYEIDDVERLQRPRPTPREAPTQGLACVSTRLRLAERRQQR
		1	LREVQAKHKHLCEELAETQGRLMLEPGRWLEQFEVDPELEPESA
	ļ	\	EYLAALERATAALEQCVNLCKAHVMMVTCFDISVAASAAIPGPQ
			RVDV
	1188	496	GKMAAQPLRHRSRCATPPRGDFCGGTERAIDQASFTTSMEWDTQ
6940	1100	.,,,	VVKGSSPLGPAGLGAEEPAAGPQLPSWLQPERCAVFQCAQCHAV
			LADSVHLAWDLSRSLGAVVFSRVTNNVVLEAPFLVGIEGSLKGS
		1	TYNLLFCGSCGIPVGFHLYSTHAALAALRGHFCLSSDKMVCYLL
	1	}	KTKAIVNASEMDIQNVPLSEKIAELKEKIVLTHNRLKSLMKILS
			EVTPDOSKPEN
			SLSRADSDPHGPHTCGHVLNVIIGSNVLALAEAQRQAEALGYQA
6941	1	713	VVLSAAMQGDVKSMAQFYGLLAHVARTRLTPSMAGASVEEDAQL
1	1		HELAAELQIPDLQLEEALETMAWGRGPVCLLAGGEPTVQLQGSG
1			RGGRNQELALRVGAELRRWPLGPIDVLFLSGGTDGQDGPTEAAG
ŀ		Ĭ	RGGRNQELALKVGAELKRWPHOFIDVHFESGGTDGGGTTLLTG AWYTPELASQAAAEGLDIATFLAHNDSHTFFCCLQGGAHLLHTG
]			
İ			MTGTNVMDTHLLFLRPR
6942	1	246	GDYVERYDPKTDTWTMGAPLSMPTNAVGGCLLGDRLYADGGYDG
	1		QTYLNTMESYDPQTNEWTQMASLNIGRAGACVVVIKQP
6943	1	739	DMATGDGAKTLAIHVKALTADSIRITWKATLPASSFRLSWLRLG
0343	· · ·		HSPAGGSITETLVOGDKTEYLLTALEPKPTYIICMVTMETTNAY
1	1		VADETPVCAKAETADSYGPTTTLNQEQNAGPMASLPLAGIIGGA
1			VALVELELVLGAICWYVHQAGELLTRERAYNRGSRKKDDYMESG
1			TKKDNSILBIRGPGLQMLPINPYRAKEEYVVHTIFPSNGSSLCK
			ATHTIGYGTTRGYRDGGIPDIDYSYT
		152	VANILINGVKYESELTGSSERAEOPLSVGRLCSTICNMPKALRT
6944	960	156	LCVNHFLGWLSFEGMLLFYTDFMGEVVFQGDPKAPHTSEAYQKY
1		1	NSGVTMGCWGMCIYAFSAAFYSAILEKLEEFLSVRTLYFIAYLA
1		Í	NSGVTMGCWGMCTYAFSAAFTSATDERCEET DSVRCDTYC
1		ĺ	SKKFAGSSADGTRRGMGVDISLLSCQYFLAQILVSLVLGPLTSA
1	'		SKKFAGSSANGTRRGMGVDISHDSCQIFHAQIDVSDVDGFDISH
1	1		VGSANGVMYFSSLVSFLGCLYSSLFVIYEIPPSDAADEEHRPLI
1	i	l l	LMV

PCT/US00/34263 WO 01/53312

	10000	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	Amino acid segment containing signature Acid, E= (A=Alanine, C=Cysteine, D=Aspartic Acid, E= (A=Alanine, C=Cys
ID	beginning	location	
NO:	nucleotide	corresponding	
	location	to first	H=Histiane, M=Methionine, N=Asparagine, L=Leucine, M=Methionine, N=Asparagine, P=Proline, Q=Glutamine, R=Arginine,
	corresponding	amino acid	P=proline, Q=Glutamine, N=Nginine, S=serine, T=Threonine, V=Valine, **Stop
	to first amino acid	residue of	V-Timegine X=UNKTOWIII
	residue of	amino acid	W=Tryptophan, 1-14tosine, Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	amino acid		
	sequence	179	EGEDRGLPRTMGAALGITTKLAPMPGKACGAL HSKPGPARPVPLKKRGYDVTRNPHLNKGMAFTLEERLOLGIHGL HSKPGPARPVPLKKRGYDVTRPOOEN DKYIILMTLODRNEKLFY
6945	2007	į	HSKPGPARPVPLKKRGYDVIKNPHLNKA*HI LMTLQDRNEKLFY IPPCFLSQDVQLLR IMRYYERQQSDLDKYII LMTLQDRNEKLFY IPPCFLSQDVQLLR IMRYYERQCSDLDKYILTERRPRGLFITIHDKG
	\	1	IPPCFLSQDVQLLRIMRYIBRQSDLDATTFRRPRGLFITIHDKG RVLTSDVEKFMPIVYTPTVGLACQHYGLTFRRPRGLFITIHDKG
	}		RVLTSDVEKFMPIVYTPTVGBACHTYGDLGCYGMGIPVGKLA HLATMLNSWPEDNIKAVVVTDGERILGLGDLGCYGMGIPVGKLA
			HLATMLNSWPEDNI KAVVVTTGEKITGELLRDPLYIGLKHQRVHGK LYTACGGVNPQQCLPVLLDVGTNNEELLRDPLYIGLKHQRVHGK
	l		LYTACGGVNPQQCLEVLLDVGTRNEBIRANANAFRLLNKYRNKY AYDDLLDEFMQAVTDKFGINCLIQFEDFANANAFRLLNKYRNKY AYDDLLDEFMQAVTDKFGINCLIQFEDFANANAFRLLNKYRNKY
		}	AYDDLLDEFMQAVTDKFGINCLIQFEDFALVING CMFNDDIQGTASVAVAGILAALRITKNKLSNHVFGFQGAGEAAM CMFNDDIQGTASVAVAGILAALRITKNKLSNHVFFKGLIVQGRDH
			CMFNDDIQGTASVAVAGILAALKITANASMI G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLIVQGRDH G\IAHLLVMALE\KEGVPKA\EATRKIW\MVDF\KGLIVQGRDH
		1	G\IAHLLVMALE\KEGVPKA\EAIRKIN INVOLVATAEA\FTE LNHEKEMFAQD\HPEVNSLEEVVRLVKPTAIIGVAAIAEA\FTE LNHEKEMFAQD\HPEVNSLEEVVRLVKPTAIIGVAAIAEA\FTE
			LNHEKEMFAQD\HPEVNSLEEVVKLV AF ALTO QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGPRGF QILRDMASFHERP\IIFALSNPTSKAECTA\EKCYRVTEGPRGF
1		1	QILRDMASFHERP\IIFALSNPTSRALE-TAYDRGWQLGVHSPG FAS\GSPF*GVLIWEMGKTFIPGGRGNNA*RVPRGWQLGVHSPG FAS\GSPF*GVLIWEMGKTFIPGGRGRLYP\PLST\IR
}	1		FAS\GSPF*GVLIWEMGKTFIPGGRGMUA*\VIP\PLST\IR GDPGHIP\DEIFLPDSRAKLPQEVSEQHLSQGRLYP\PLST\IR
{			AND DIVIKOLD & CIKHNDA (2115-7-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-
1		1	YDSFYT/VDSYIWAQGAAMAVQIV
1		2551	SCEYSGITVAPGDPCPGVAHLLAPSMASATT SCENARAC NLDGTLGYLLDKETLRLHPDIFLPSEI\CDRLVNEYVELVNAAC NLDGTLGYLLDKETLRLHPDIFLPSEI\CDRLVNEYVELVNAAC
6946	133	222-	NLDGTLGYLLDKETLRLHPDIFLPSSI (LDKUD)QD\LE NF\EPHE\SFFNPLFRDPRKQPASRIHL\RED\LVQD\QD\LE NF\EPHE\SFFNTLGVP*AFFG
1			NF\EPHE\SFFNPLFRDPRKQPASKXINI\\KBFSHTLGVP*AFFG AIRKQDL\VEL\YLIN\CEKLSAKSLQTLRSFSHTLGVP*AFFG AIRKQDL\VEL\YLIN\CEKLSAKSLQTLRSFSHTLGVP*AFFG
1	1		AIRKQDL\VEL\YLTN\CEKLSARSLQIMAN C\TNILLLRKENPGGL\CEEYLFNPTCQVLVKDFTFEGFSRLR
1	1		C\TNILLLRKENPGGL/CEDEYLFNPICQUETGDAA\FLTQ F\LKLGRMIDWVPVES\LLRPLNSLAALDLSGIQTSDAA\FLTQ F\LKLGRMIDWVPVES\LLRPLNSLAALDLSGIQTSDAA\FLTQ
Ì	1		F\LKLGRMIDWYPVES\LLKPLNSLAKHLDISRDRLSS WKDSL\VSLVL\YNMDLSDDHIR\VIVQLHKLRHLDISRDRLSS WKDSL\VSLVL\YNMDLSDHIR\VIVQLHKLRHLDISRDRLSS
1			WKDSL\VSLVL\YNMDLSDDHIR\VI\V\DHMILENCSISKIGKR YYKFKLTREVLSLFVQKLGNLMSLDISG\HMILENCSISKIGKR
1	1	1	YYKFKLTREVLSLFVQKLGANLMSDLTSG(MTVF*GIFCGRLTH EAGQTSI\EPSK\SSIIPFRGFEGGPLQF\LGVF*GIFCGRLTH
	1		EAGQTSI\EPSK\SSIIFFKGFEGGFAQ\\Circ\EPSK\SSIIFFKAQ\EPSK\SSIIFFKA
1		1	IPAYKVSGDKNEEQVLNAI EAI IERK PATTANEYRSE RCNQLLRALKLVITALKCHKYDRNIQVTGSAALFYLTNSEYRSE RCNQLLRALKLVITALKCHYDRVITVOPUCCLITLCNFSIPBELEF
1		}	RCNQLLRALKLVITALKCHKYDKNIVYORNCCLTLCNFSIPEELEF QSVKLRRQVIQVVLNGMESYQEVTVQRNCCLTLCNFSIPEELEF
1	Ì	1	QSVKLRRQVIQVVLNOMESYQEVIVQARCEDALVCQVDNDHKEA QYRRVNELLLSILNPTRQDESIQRIAVHLCNALVCQVDNDHKEA
1			QYRRVNELLLSILNPTROBESIONIVATESW\SALWNITDETPD VGKMGFVVTMLKLTOKKLLDKTCDQVMEFSW\SALWNITDETPD VGKMGFVVTMLKLTOKKLLDKTCDQVMEFSW\SALWNITDETPD
1		1	VGKMGFVVTMLKLTQKKLDKTLDKYVML NCEMFLNFNGMKLFLDCLDEFPEKQELHRNMLGLLGNVAEVKEL NCEMFLNFNGMKLFLDCLDEFPEKQELHRNMLGLLGNVAEVKEL
	1	1	NCEMFLNFNGMKLFLDCLNEFFERQEBIRGHT RPQLMTSQFISVFSNLLBERGERSKADGIEVSYNACGVLSHIMFDGPEA RPQLMTSQFISVFSNLLBERGERSKADGIEVSTRNLNYRSFEPILRLLPC
1	1	1	RPOLMTSQFISVFSNLLBSKADSTENSRRNINYRSFEPILRLLPC WGVCEPQREBVEERMWAAIQSWDINSRRNINYRSFEPILRLLPC
1			The second state of the second
			GISPVSOHWATWALLTHOOF ATTARQETKEMARKVIEHCSNFKEENMOTSR ATARQETKEMARKVIEHCSNFKEENMOTSR
		1682	ATARQETKEMARKVIEHCSNFAEENINIS TSVSTIPRGLASARPOSRSWRCCPVWRRSPGRAGGGLKMLNVI
69	47 2	1002	TSVSTIPRGLASARPQSRSWRCCFVWARDFGMTRLTKSGKDLTG SQSFPAPRSQQRVASGGRSKVPLKQGRSLMDWIRLTKSGKDLTG SQSFPAPRSQQRVASGGRSKVPLKQGRSLMDWIRLTKSGKDLTG
1		ì	LKGRLIEVTEEELKKHNAKDDCHTCIMLKECLVGRMAIKPAVL
	1		LKGRLIEVTEBELKKHNKKDLCWITTMLKECLVGRMAIKPAVLI DELMRAAGSDGTELFDQVHRWVNYESMLKECLVGRMAIKPAVLI DYREEEKKVLNGMLPKSQVTDTLAKEGPSYPSYDWFQTDSLVT
1			DYREEEKKVLNGMLPKSQYTDILARGFSITCH /EHIY*TEGYQFRLNNS*SSE*FLYSRNNY*GLLLISYTYW/R*.
1		}	/EHIY*TEGYQFRLNNS*SSE*FIISANNI MRFRKIFLCGL/CESVGKIEIVLQKKENTSWDFIGHPLKNHNS
-		1	MRFRKIFLCGL/CESVGKIELVLQARANISMISMISMISMISMISMISMISMISMISMISMISMISMI
1			IPRKDTGLYYRKCQLISKBDYTHDIRBIT LIPRKYTYFLI HVYLKLPITGTEIVKPYTPVSGSLLSEFKEPVLPNNKYTYFLI
			HVYLKLPITGTEIVKPYTPVSGSILLSENKISKFQELEDLFLL IYPTGLFTPELDRLQIGDFVSVSSPEGNFKISKFQELEDLFLL
1			IYPTGLFTPELDRLQIGDFVSVSSFBGM. THE THE THE SQL AGTGFTPMVKILNYALTDIPSLRKVKLMFFNKTEDDIIWRSQL AGTGFTPMVKILNYALTDIPSLRKVKLMGHISPALLSEFLKRNLD
1			
j			KLAPKDKRLDVEFVLSAPISCHULHDLNFSKNEIHSFTA SKVLVCICGPVPFTEQGVRLHDLNFSKNEIHSFTA
ţ			SKVLVCICGPVPFTEOGYRLHHJUVFSKITHERKEVPHEAKS PDGAHSFFPDEYFTCSSLLLSCGVGCKKSMNHGKEGVPHEAKS PDGAHSFFPDEYFTCSSLLLSCGVGCKKSMNHGKEGVPHEAKS
L	104	58	PDGAHSFFPDEYFTCSSLCLSCGVGCKRSHTSASTDSPWMGLAR CRYSHQYDNRVYTCKACYBRGEEVSVVPKTSASTDSPWMGLAR CRYSHQYDNRVYTCKACYBRGEOVDPVDTVVRTEIVHVPC
	5948 104		CRYSHQYDNRVYTCKACYBRGEEVSVVFMVTVRTEIVHVWPG AWSGYVIECPNCGVVYRSRQYWFGNQDPVDTVVRTEIVHVWPG AWSGYVIECPNCGVVYRSRQYWFGNQDPVDTVRTEIVHVTDC
1		1	AWSGYVIECPNCGVVYRSKQIWFOKQI DGFLKDNNNAAQRLLDGMNFMAQSVSBLSLGPTKAVTSWLTDC DGFLKDNNNAAQRLLDGMNFMAQSVSBLSLGPTKAVTSWLTDC
1	1		DGFLKDNNNAAQRILDGMNFMAQSVSILG APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGEGFCDSCSS APAYWRPNSQILSCNKCATSFKDNDTKHHCRACGEGFCDSCSS
1	1		APAYWRPNSQILSCNKCATSFRUNDITAMEST TRPVPERGWGPAPVRVCDNCYEAR/TRPVSCYRGTSGR*RRN
\)	}	TRPVPERGWGPAF
1		}	QETVE GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGKRTRRG GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGKRTRRG GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGGGGGKRTRRG GRANDEN GARAGA
L	15	46	GLRLCLSRPLTRPGDDSVGGSAMASGAGGVGVQ QGPIKPYQQGRQQHQGILSRVTESVKNIVPGWLQRYFNKNED
	6949		L ACDI KUTUKARUWAY

	Predicted	Predicted end	Amino acid segment containing signal peptide
SEQ		nucleotide	(A=Alanine, C=Cvsteine, D=Aspartic Acid, E=
ID	beginning	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide		H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Alginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
	Sequence	 	SCSTDTSEVPRWPENKEDHLVYADEESSNITDGRITPEPAVSNT
	ļ	ì	EEPSTTSTAST\YPDVLTRVSLYRSHLNFSMLESPALHCQPSTS
		1	SAFPIGSSGFSLVKBIKDSTSQHDDDNISTTSGFSSRASDKDIT
	1	· I	VSKNTSLPPLWSPEAERSHSLSQHTATSSKKPAFNLSAFGTLSP
		l.	SLGNSSILKTSQLGDSPFYPGKTTYGGAAAAVRQSKLRNTPYQA
		1	SLGNSS1LKTSQLGDSPF1PGKT11GGAAAAVKQSKLKUT11QA
]	1	PVRRQMKAKQLSAQSYGVTSSTARRILQSLEKMSSPLADAKRIP
			SIVSSPLNSPLDRSGIDITDFQAKREKVDSQYPPVQRLMTPKPV
			SIATNRSVYFKPSLTPSGEFRKTNQRIDKKCSTGYEKNMTPGQN
	1	1	REQRESGFSYPNFSLPAANGLSSGVGGGGGKMRRERHAFVASKP
	1	1	LEEEEMEGPVLPKISLPITSSSLPTFNFSSPEITTSSPSPINSS
			QALTNKVQMTSPSSTGSPMFKFSSPIVKSTEANVLPPSSIGFTF
			SVPVAKTABLSGSSSTLEPIISSSAHHVTTVNSTNCKKTPPEDC
			EGPFRPAEILKEGSVLDILKSPGFASPKIDSVAAQPTATSPVVY
		1	FOR KANTITURGS AND INVOCATION AND LINE AND
			TRPAISSFSSSGIGFGESLKAGSSWQCDTCLLQNKVTDNKCIAC
		1	QAAKLSPRDTAKQTGIETPNKSGKTTLSASGTGFGDKFKPVIGT
		1	WDCDTCLVQNKPEAIKCVACETPKPGTCVKRALTLTVVSESAET
	i		MTASSSSCTVTTGTLGFGDKFKRPIGSWECSVCCVSNNAEDNKC
	ļ		VSCMSEKPGSSVPTSSSSTVPVSLPSGGSLGLEKFKKPEGIWDC
			ELCLVONKADSTKCLACESAKPGTKSGFKGFDTSSSSSNSAASS
		1	SFKFGVSSSSGPSQTLTSTGNFKFGDQGGFKIGVSSDSGYINP
		1	MSEGF*FSKHIVGFKFGVSSESKPEEVKKDSKNDNFKFGLSFGL
		1	SNPVFLTPFQFGVSNLGQEEKKEELLKSSCAGFRFGTGVINSTR
		l .	VPANTIVTSENKSSFNLGTIETKSVSVAPLKCQTSEAKKEEMPA
		1	VPANTIVTSENKSSTNLGITEIKSVSVAFERCQISERIGEERI
		(TKGGFSFGNVEPASLPSASVFVLGRTEEKQQEPVTSTSLVFGEG
		l .	KLTMKEPKC\QPVFSFGEFQRQTKDENSSKSTFSFSMTKPSEKE
			SEQPAKATFAFGAQTNTTADQGAAKPDLSYLNNSSSSSSTPATS
	}	1	AGGG\IFGSSTSSSNPPVATFVFGQSSNPGSSS\AFGNTAESST
		Ì	SOSLLFSODSKLATTSSTGTAVTPFVFGPGASSNNTTTSGFGFG
		1	ATTTSSSAGSSFVFGTGPSAPSASPAFGANQTPTFGQSQGASQP
		· I	NPPGFGSISSSTALFPTGSQPAPPTFGTVSSSSQPPVFGQQPSQ
		ļ	SAFGSGTTPNSSSAFQFGSSTTNFNFTNNSPSGVFTFGANSSTP
		j	AASAQPSGSGGFPFNQSPAAFTVGSNGKNVFSSSGTSFSGRKIK
		1	
		1 _	TAVRRK
6950	2585	411	PRPGSRSGLCRRAGERGAVRAGGLSRRTRAE * IMDELHYQDTDS
	ļ	1	DVPEQRDSKCKVKWTHEEDEQLRALVRQFGQQDWKFLASHFPNR
			TDQQCQYRWLRVLNPDLVKGPWTKEEDQKVIELVKKYGTKQWTL
l	1		IAKHLKGRLGKQCRERWHNHLNPEVKKSCWTEEEDRIICEAHKV
1			LGNRWAEIAKMLPGRTDNAVKNHWNSTIKRKVDTGGFLSESKDC
			KPPVYLLLELEDKDGLQSAQPTEGQGSLLTNWPSVPPTIKEEEN
		1 .	SEEELAAATTSKEQEPIGTDLDAVRTPBPLEEFPKREDQEGSPP
ŀ			ETSLPYKWVVEAANLLIPAVGSSLSEALDLIESDPDAWCDLSKF
}	1		PIODE I UMA A CHUMAT TOT ON CACCOAT DEBOUGA / I ADGREGA
1			DLPEEPSAEDSINNSLVQLQASHQQQVLPPRQPSA\LVPSVTEY
1			RLDGHTISDLSRSSRGELIPISPSTEVGGSGIGTPPSVLKRQRK
1	1	1	RRVALSPVTENSTSLSFLDSCNSLTPKSTPVKTLPFSPSQFLNF
{	1	İ	WNKODTLELESPSLTSTPVCSQKVVVTTPLHRDKTPLHQKHAAF
	1		VTPDQKYSMDNTPHTPTPFKNALEKYGPLKPLPQTPHLEEDLKE
1			VLRSEAGIELIIEDDIRPEKQKRKPGLRRSPIKKVRKSLALDIV
	1	}	DEDMKLMMSTLPKSLSLPTTAPSNSSSLTLSGIKEDNSLLNQGF
	1		DEDINGHING I DEVOTOTE I TALONOSOTI DOCTIONA COMBOLI
			LQAKPEKAAVAQKPRSHFTTPAPMSSAWKTVACGGTRDQLFMQE
			KAROLLGRLKPSHTSRTLILS
6951	1940	239	KARQLLGRLKPSHTSRTLILS AGPDDTMKRSLOALYCOLLSFLLILALTEALAFAIQEPSPRESL
6951	. 1940	239	KARQLLGRLKPSHTSRTLILS AGPDDTMKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESL OVLPSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSQAAAPMA
6951	. 1940	239	KARQLLGRLKPSHTSRTLILS AGPDDTMKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESL QVLPSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSQAAAPMA TPTPRAEGHPPT\TPSPPSLRQ*PPPILKAP/SSTGPAPAAMAT
6951	. 1940	239	KARQLLGRLKPSHTSRTLILS AGPDDTMKRSLQALYCQLLSFILILALTEALAFATQEPSPRESL QVLPSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSQAAAPMA TPTPRAEGHPPT\TPSPPSLRQ*PPPILKAP/SSTGPAPAAMAT TSSKPEGRPRGOAAPTILLTKPPGATSRPTTAPPRTTTRRPPRP
6951	. 1940	239	KARQLLGRLKPSHTSRTLILS AGPDDTMKRSLQALYCQLLSFILILALTEALAFATQEPSPRESL QVLPSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSQAAAPMA TPTPRAEGHPPT\TPSPPSLRQ*PPPILKAP/SSTGPAPAAMAT TSSKPEGRPRGOAAPTILLTKPPGATSRPTTAPPRTTTRRPPRP
6951	. 1940	239	KARQLLGRLKPSHTSRTLILS AGPDDTMKRSLQALYCQLLSFLLILALTEALAFAIQEPSPRESL QVLPSGTPPGTMVTAPHSSTRHTSVVMLTPNPDGPPSQAAAPMA TPTPRAEGHPPT\TPSPPSLRQ*PPPILKAP/SSTGPAPAAMAT

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
ю:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	L=Leucine, M=Mechionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
)	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
i	sequence		\=possible nucleotide insertion)
		 	TVPSNTSWAPTTTSLGPAKDKPGLRRAAQGGGSTFTSQGGTPDA
		Į.	TAASGAPVSP/PSCPSAFSAPPPR*PTGWPQP**LLAYCYP\CT
			SRPLSTSSGVFTAATGPTPAAFDTSVSAPSQGIPQGASTTPQAP
	l	Ţ	THPSRVSESTISGAKEETVA\PSP*PTGCPVLSPQWYPQPQAIS
			STAWSPPGPGSLGQQGTSPMWPRGTNRSTEPPSA*ARWISPG*S
		1	WPSACPSPP\LCPADGVLHEBEEEDRQPGEQPEAYGNNTHHPGT
		1	TFQQAC\RGAAPGEIPVPLKPLRTQLSEPRSPANGDYRDTGMVP
			C C
			PESEGESGEMTDRYTIHSQLEHLQSKYIGT\ATPTPPSGSG\CE
6952	658	304	PTPRLVLLLHGPLRPSQLLRHCGE*EQSASPLQLDGKDASALWT
			P.T. P. C. E. S. D
			ASRQARGELRLCLTTAVRGTSPSVSPVCQSS
6953	1512	349	NWGKTRALASGKHVPFGKQTNPNKS/VHCDS*G**RRETTQDES
			FSPHFRGKMGGVV\KLEKELENTEQPVGGNEG*EHEVTGNLNSD
			PLLELCQCPLCQLDCGSREQLIAHVYQHTAAVVSAKSYM\CPVC
			GRALSSPGSLGRHLLIHSEDORSNCAVCGARFTSHATFNSEKLP
		ı	EVLNMESLPTVHNEGPSSAEGKDIAFSPPVYPAGILLVCNNCAA
		l .	YRKLLEAQTPSVRKWALRRQNEPLEVRLQRLERERTAKKSRRDN
	1		ETPEEREVRRMRDREAKRLQRMQETDEQRARRLQRDREAMRLKR
			AIETPEKRQARLIREREAKRLKRRLEKMDMMLRAQFGQDPSAMA
1		}	ALAAEMNFFQLPVSGVELDSQLLGKMAFEEQNSSSLH
	<u> </u>	 	PPPPFIIPSHPREAGT*AG*KRSGDSECSPPVEQ*A*TRAAAQN
6954	819	1 -	*PQR*RWTEGNSPQASAVATPGQGASPAAPRCTP*PSRRHRRLP
			PGARPPAG*AAPAPTKPWLAGPASAPQPGAAPLSPPAPPLIRTR
ł		i	*CAGAAARGRPRRDRSPRPRTPGGCSWSEPRTPPAVSASAQTPS
ĺ			*CAGAAARGKPKKDKSPKPKIPGGCSWSEFKIPFAVSASAQIID
i			DAG*AGGR*GQRQRPSTGR*PPGVGGAGRSHRREGTIPGNPHPR
ı			AS*RAGWQR*PGP/REWGL*EPQGBEMSGPGGPGGAPPNQVGSS
1			VMQAMSTGI
6955	1968	782	PPGRRQVRAQVAGAPVGHWGTRARQVKTGGRRRARRTMPFLGQD
1			WRSPGWSWIKTEDGWKRCESCSQKLERENNHCNISHSIILNSED
		1	GEIFNNEEHEYASKKRKKDHFRNDTNTQSFYREKWIYVHKESTK
 			ERHGYCTLGEAFNRLDFSSAIQDIRRFNYVVKLLQLIAKSQLTS
1	1	ì	LSGVAQKNYFNILDKIVQKVLDDHHNPRLIKDLLQDLSSTLCIL
	1		/N*RSREVCISGKHQYLDLPIRNYSRLATTATGSSDD*ASE\NG
		1	LTLSDLPLHMLNNILYRFSDGWDIITLGQVTPTLYMLSEDRQLW
}		1	KKLCQYHFAEKQFCRHLILSEKGHIEWKLMYFALQKHYPAKEQY
		j	GDTLHFCRHCSILFWKDSGHPCTAADPDSCFTPVSPQHFIDLFK
			F
		3030	QTSTSIFASPTSPPVLGESVLQDNSFDLNNGSDAEQEEMETQSS
6956	8605	3839	DFPPSLTQPAPDQSSTIQLHPATSPAVSPTTSPAVSLVVSPAAS
			PEISPEVCPAASTVVSPAVFSVVSPASSAVLPAVSLEVPLTASV
			TSPKASPVTSPAAAFPTASPANKDVSSFLETTADVEEITGEGLT
1			TSPKASPVTSPAAAFPTASPANKDVSSFDEI IADVEET IGEGII
İ			ASGSGDVMRRRIATPEEVRLPLQHGWRREVRIKKGSHRWQGETW
1		1	YYGPCGKRMKQFPEVIKYLSRNVVHSVRREHFSFSPRMPVGDFF
	1		EERDTPEGLQWVQLSAEEIPSRIQAITGKRGRPRNTEKARTKEV
			PKVKRGRGRPPKVKITELLNKTDNRPLKKLEAQETLNEEDKAKI
1			AKSKKKMRQKVQRGECQTTIQGQARNKRKQETKSLKQKEAKKKS
	1		KAEKEKGKTKQEKLKEKVKREKKEKVKMKEKEEVTKAKPACKAD
	1		KTLATORRLEEROROOMILEEMKKPTEDMCLTDHQPLPDFSRVP
1	1		GLTLPSGAFSDCLTIVEFLHSFGKVLGFDPAKDVPSLGVLQEGL
1			LCQGDSLGEVQDLLVRLLKAALHDPGFPSYCQSLKILGEKVSEI
1			PLTRDNVSEILRCFLMAYGVEPALCDRLRTQPFQAQPPQQKAAV
	t .	1	LD1KDMA9ETDKCLDkW1GABLWHCDKDKJK1AL1AGGLAGGKWA
1	ŀ		
			LAFLVHELNGSTLIINEIDKTLESMSSYRKNKWIVEGRLRRLKT
			VLAKRTGRSEVEMEGPEECLGRRRSSRIMEVTSGMEBEEEEESI
			VLAKRTGRSEVEMEGPEECLGRRRSSRIMEVTSGMEBEEEEESI AAVPGRRGRRDGEVDATASSIPELERQIEKLSKRQLFFRKKLLH
			VLAKRTGRSEVEMEGPEECLGRRRSSRIMEVTSGMEBEEEEESI

		Dardt and and	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	H=Histidine, i=isoleucine, k=hysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	4	\=possible nucleotide insertion)
	sequence		TKPGSMQPRHLKSPVRGQDSEQPQAQLQPEAQLHAPAQPQPQLQ
	l		LQLQSHKGFLEQEGSPLSLGQSQHDLSQSAFLSWLSQTQSHSSL
	1 .		LSSSVLTPDSSPGKLDPAPSQPPEEPEPDEAESSPDPQALWFNI
		Į.	SAQMPCNAAPTPPPAVSEDQPTPSPQQLASSKPMNRPSAANPCS
	ì	1	SAOMPCNAAPTPPPAVSEDOPTPSPOODMS CORPEDCEDOS
	}		PVQFSSTPLAGLAPKRRAGDPGEMPQSPTGLGQPKRRGRPPSKF
	1		FKQMEQRYLTQLTAQPVPPEMCSGWWWIRDPEMLDAMLKALHPR
		\	GIREKALHKHLNKHRDFLQEVCLRPSADPIFEPRQLPAFQEGIM
			SWSPKEKTYETDLAVLQWVEELEQRVIMSDLQIRGWTCPSPDST
	1	1	REDLAYCHLISDSQEDITWRGRGREGLAPQRKTTNPLDLAVMRL
		1	AALEQNVERRYLREPLWPTHEVVLEKALLSTPNGAPEGTTTEIS
		1	YEITPRIRVWRQTLERCRSAAQVCLCLGQLERSIAWEKSVNKVT
	ļ		CLVCRKGDNDEFLLLCDGCDRGCHIYCHRPKMEAVPEGDWFCTV
			CHACKERMORE HERCAGONACULI CUKI MIGHAL BARMICIA
			CLAQQVEGEFTQKPGFPKRGQKRKSGYSLNFSEGDGRRRRVLLR
			GRESPAAGPRYSEEGLSPSKRRRLSMRNHHSDLTFCEIILMEME
			SHDAAWPFLEPVNPRLVSGYRRIIKNPMDFSTMRERLLRGGYTS
	Į.		SEEFAADALLVFDNCQTFNEDDSEVGKAGHIMRRFFE\SRWEEF
	1	1	YQGKQGQSVRQGRWGVTLWHLPPTFQTKTCHFHLLMLPWVQTQV
		l	RYNPDF
	82	3514	HLIVAMPETTKKEENEVPAPAPPPEEPSKEKEAGTTPAKDWTLV
6957	02	3324	ETPPGEEQAKQNANSQLSILFIEKPQGGTVKVGEDITFIAKVKA
	· l	1	EDLSEKPTINGSRKWMDLASKAGKHLQLKBTFERHSRVYTFEMQ
		1	IIKAKDNFAGNYRCEVTYKDKFDSCSFDLBVHESTGTTPNIDIR
		<u> </u>	SAFKRSGEGQEDAGELDFSGLLKRREVKQQEEEPQVDVWELLKN
		}	SAFKRSGEGQEDAGEDDFSGLDKRKEVRQQEEEFQVDVWEDDAG
		1	TKPSEYEKIAFQYESPTCSGMLKRLKRSIREEKKSAAFAKILDP
	1		VYQVDKGGRVRFVVELADPKLEVKWNKNGQELRPSTKYIFEDTR
	1	\	CQSILNIDNCQMTDDSEYYVTAGDEKCSTELLVREPPIMVTKQL
	1	[EDTTDYCGERVELECEVSEDDAQVKWFKNGBEIILVQTRYRIRV
	i		EGKKHILIIEGATKADAADYSVMTTGGQSSAKLSVDLKPLKILT
			PLTDQTVNLGKEICLKCEISENIPGKWTKNGLPVQESDRLKVVH
	1		KGRIHKLVIDHALTEDEGDYVFAPDAYNVTLPAKVHVIDPPKII
	1		LDGLDADNTVTVIAGNKLRLEIPISGEPPPKAMWSRGDKAIMEG
	İ		SGRIRTESYPDSSTLVIDIAERDDSGVYHINLKNEAGEAHASIK
	1	1	VKVVDFPDPPVAPTVTEVGDDWCIMNWEPPAYDGGSPILGYFIE
	1	ļ	VKVVDFPDPPVAPTVTEVGDDWCIMNWEPPATDGGSFIBGITIE
			RKKKQSSRWMRLNFDLCKETTFEPKKMIEGVAYEVRIFAVNA\1
		Ì	GISKPSMPSRPFVPLAVTSPPTLLTVDSVTDTTVTMRWRPPDHI
	i	{	GAAGLDGYVLEYCFEGSTSAKQSDENGEAAYDLPAEDWIVANKD
1			LIDKTKFTITGLPTDAKIFVRVKAVNAAGASEPKYYSQPILVKE
			IIEPPKIHSPKHLKQTYIRRVGDRVILVIPFQGKPRPELTWKKD
1		1	GAEIDKNQINIRNSETDTIIFIRKAERSHSGKYDLQVKVDKFVE
		İ	TASIDIRIIDRPGPPQIVKIEDVWGRNVALTWTPPKDDGNAAIT
		i	GYTIQKADKKSMEWLRVIEHIIEPVPHTELVIGNEYYFRVFSEN
]			MCGLSEDATMTKESAVIARDGKIYKNPVYEDFDFSEAPMFTQPL
1		1	VNRLCHSGYMATLNCSVRGNPKPKITWMKNKVAIVDDPRYRMFS
1			VNKLCHSGIMATENCSVKGNPKPKT I WMKNKVAT VDDFKIKNT S
1		J	NQGVCTLEIRKPSPYDGGTYCCKAVNDLGTVEIECKLEVKVIAQ
6958	274	1663	PRTSRVKTEGSQGSSAMDFSVKVDIEKEVTCPICLELLTBPLSL
1			DCGHSFCQACITAKIKESVIISRGESSCPVCQTRFQPGNLRPNR
			HLANIVERVKEVKMSPOEGOKRDVCEHHGKKLQIFCKEDGKVIC
1	1		WVCELSQEHQGHQTFRINEVVKECQEKLQVALQRLIKENQEAEK
1			LEDDIRQERTAWKNYIQIBRQKILKGFNEMRVILDNEEQRELQK
1			LEEGEVNVLDNLAAATDQLVQQRQDASTLISDLQRRLRGSSVEM
			LQDVIDVMKRSESWTLKKPKSVSKKLKSVFRVPDLSGMLQVLKE
			IMPATRAMENTAL PROGRAMMENT TO TO DO CHAMBOLO DE CARACAD
1		}	LTDVQYYWVDVMLNPGSATSNVAISVDQRQVKTVRTCTFKNSNP
L .	1	1	CDFSAFGVFGCQYFSSGKYYWEVDVSGKIAWILGVHSKISSLNK
			RKSSGFAFDPSVNYSKVYSRYRPQYGYWVIGLQNTCEYNAFEDS
			RKSSGFAFDPSVNYSKVYSRYRPQYGYWVIGLQNTCEYNAFEDS SSSDPKVLTLFMAV\LPVVLGFS SLVHVVEFGRGIEDFPYLFFQLTHCQQRICSVTQAGVQWCDHSS

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	Amino acid segment containing signal pertide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		LOPOTPGLNQSSHLSLLSSRDYRMLSSFNEWFWQDRFWLPPNVT
			WTELEDROGRVYPHPQDLLAALPLALVLLAMRLAFERFIGLPLS
			RWLGVRDQTRRQVKPNATLEKHFLTEGHRPKEPQLSLLAAQCGL
	}		TLOQTQRWFRRRRNQDRPQLTKKFCEASWRFLFYLSSFVGGLSV
			LYHESWLWAPVMCWDRYPNQLTLSCPAADSEA\SLYWWYLLELG
			FYLSLLIRLPFDVKRKGGPSSIKPRPHYDPPSTA\DFKEQVIH
			HFVAVILMTFSYSANLLRIGSLVLLLHDSSDYLLEACKMVNYMQ
			YQQVCDALFLIFSFVFFYTRLVLFPTQILYTTYYESISNRGPFF
			GYYFFNGLLMLLQLLHVFWSCLILRMLYSFMKKGQMEKDIRSDV
			EESDSSEEAAAAQEPLQLKNGTAGGPRPAPTDGPRSRVAGRLTN
			RHTTAT
		2068	AKWAREKEMOEF\TRSFF\RGRPDLSTLTHSIVRRRYLAHSGRS
6960	387	2068	HLEPEEKOALKRLVEEEPLKMOVDEAASREDKLDLTKKGKRPPT
			PCSDPERKRFRFNSESESGSEASSPDYFGPPAKNGVASRSHTHP
	ľ	İ	KEENPRRA\SKAVEBSSDEERQRDLPAQRGEESSEBEEKGYKGK
			TRKKPVVKKOAPGKASVSRKQAREESEESEAEPVQRTAKKVEGN
	1		KGTKSLKESEOESEEEILAQKKEQREEEVEEEEKEEDEEKGDWK
			PRIRSNGRRKSAREERSCKOKSQAKRLLGDSDSEEEQKEAASSG
			DDSGRDREPPVORKSEDRTQLKGGKRLSGSSEDEEDSGKGEPTA
			KGSRKMARLGSTSGEESDLEREVSDSEAGGGPQGERKNRSSKKS
		}	SPKGRTRSSSSSSDGSPEAKGGKAGSGRRGEDHPAVMRLKRYIR
	1		ACGAHRNYKKLLGSCCSHKERLSILRAELEALGMKGTPSLGKCR
			ALKEOREEAAEVASLDVANIISGSGRPRRRTAWNPLGEAAPPGE
			LYRRTLDSDEERPRPAPPDWSHMRGIISSDGESN
6961	340	1646	RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL
0301	3*0		NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG
			LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
			SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK
			ADVVLLCGDLNMHPEDLGCCLLKEWTGLHDAYLETRDFKGSEEG
ļ			NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET
ļ			TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
ļ			PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
(LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG
ļ			LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ
6962	340	1646	RPWSSPTMKPNFSLRLRIFNLNCWGIPYLSKHRADRMRRLGDFL
)		NQESFDLALLEEVWSEQDFQYLRQKLSPTYPAAHHFRSGIIGSG
1			LCVFSKHPIQELTQHIYTLNGYPYMIHHGDWFSGKAVGLLVLHL
			SGMVLNAYVTHLHAEYNRQKDIYLAHRVAQAWELAQFIHHTSKK
l	1		ADVVLLCGDLMMHPEDLGCCLLKEWTGLHDAYLETRDPKGSEEG
1	1		NTMVPKNCYVSQQELKPFPFGVRIDYVLYKAVSGFYISCKSFET TTGFDPHRGTPLSDHEALMATLFVRHSPPQQNPSSTHGP\AERS
	1	1	TTGFDPHRGTPLSDHEALMATTFVRHSPPQQNPSSTAGF (AEAS PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SYVIGLGL\LL
			PL/MCVCLKEALDGSLGLGMA\QARWWA\TFA\SIVIGHGL\LDL LALLCVLAAGGGAGEAAILLWTPSVGLVLWAGAFYLFHVQEVNG
1	1		LALLCYLAAGGGAGEAAILLWTPSVGLVLWAGAFILFNVQLVNG
	ľ		LYRAQAELQHVLGRAREAQDLGPEPQLYALL\LGQQEGDRTKEQ
6963	374	2618	RVTPLILKLLKKPKTAENQKASEENEITQPGGSSAKPGLPCLNF
			EAVLSPDPALIHSTHSLTNSHAHTGSSDCDISCKGMTERIHSIN
	1		LHNFSNSVLETLNEQRNRGHFCDVTVRIHGSMLRAQRCVLAAGS
	İ		PFFQDKLLLGYSDIEIPSVVSVQSVQKLIDFMYSGVLRVSQSEA
1			LQILTAASILQIKTVIDECTRIVSQNVGDVFPGIQDSGQDTPRG
	1		TPESGTSGQSSDTESGYLQSHPQHSVDRIYSALYACSMQNGSGE
	j		RSFYSGAVVSHHETALGLPRDHHMEDPSWITRIHERSQQMERYL
1			STTPETTHCRKQPRPVRIQTLVGNIHIKQEMEDDYDYYGQQRVQ
			ILERNESEECTEDTDQAEGTESEPKGESFDSGVSSSIGTEPDSV
	1		EQQFGPGAARDSQAEPTQPEQAAEAPAEGGPQTNQLETGASSPE
	1		
		ŀ	RSNEVEMDSTVITVSNSSDKSVLQQPSVNTSIGQPLPSTQLYLR QTETLTSNLRMPLTLTSNTQVIGTAGNTYLPALFTTQPAGSGPK

		1 = 1 = 3 and	Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	1 /2 31 C-Custeine D=Aspartic Actu, D-
ID	beginning	nucleotide	Clutamic Acid. F=Phenylalanine, G=GlyCine,
NO:	nucleotide	location	n_uistidine T=Tsoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, ksonkhown,
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	1 -	\=possible nucleotide insertion)
	Bequence	+	PFLFSLPQPLAGQQTQFVTVSQPGLSTFTAQLPAPQPLASSAGH
		1	STASGQGEKKPYECTLCNKTFTAKQNYVKHMFVHTGEKPHQCSI
	1	1	OUDGEST VOVI.TK\ HMVTHTGVRAYOCSICNKRFIQKSSLINVAM
	1	1	DI UDGEVEVECTICKKKESHKTLLERHVALHSASNGTPPAGTPP
		l	CARACIDEGIALA CTECTTYVCSVCPAKFDOIEQFNDHMRMHVSDG
			SGRPFFFFFSNTDVYFIKKVTNRWTAGSSYKMTRMKSIGKILLL
6964	1	178	SGRPFFFFSRIDVITIAL INC.
	İ		QIFIG\NCSMFVLVI NVFIEPRIQGFMKTSAHPGQKHPDFSMGLLFPLLAALEVCSCGS
6965	757	208	NVFIEPRIQGFMKTSAHPGQKHPDFSMGLLFFLLAABBVCBCBF
6963	1	j	SGSLGYNLPONH\GLLGRNTLVLLGQMRRISPFLCLKDRSDFRF
		l	POEKVEVSQLQKA\QAMSFLYDVLQQVFNFSHKALL\CCMEHDL
	l .	1	PGPTPHFTSSAAGTPGDLLGAGDGRRRSWGQWVIEGSTLALRRY
	1	1	PORCICEER
	<u> </u>	1067	THE CURCURE CREEKING THE PROPERTY OF THE PROPE
6966	820	1867	(DEDCEOUTE CRIDNERSES WIGHLISGER LDTWICSLIGS LMVG
		1	T COMPRIE THE PROTECT OF THE PROTECT
		l l	HLLPEAWAYTCSASPGGEGQSLQQQQQLGLWVIAGILTFLALEK
		1	/HUPGQQGGDQPGPQQRPHCCCRRAQWRPLSGPAGCRARPRCR
			GP\DIKVSGYLNLLANTIDNFTHGLAVAASFLVSKKIGLLTTMA
		· ·	GP\DIKVSGYLNLLANTIDNFIRGHAVAADFBUOLGAGFA
		\	ILLHEIPHEVGDFAILLRAGFDRWSAAKLQLSTALGGLLGAGFA
		\	ICTQSPKGVEETAAWVLPFTSGGFLYIALVNVLPDLLEBEDPW
	1	633	CHI DEVUNITIBLE ASSEMET DENPMELS SMSGFEEGSELINGFEG
6967	162	(033	TOWN THE TAKEN T
			ERNRYCLELTEAGLKVVGYAFDQVDDHLQTPYHETVYSLLDTL\
	1	}	GRAVIER ECVÉ \ LLOPI.EALKRDGOS
			RGGGGGRGCPGARERERPGEPERTMEAAAGGRGCFQPHPGLQKT
696B	1	2265	RGGGGGRGGPGAREKERFGET EN AGEAYKKESAKEAGAAAVPAPV
		ļ	LEQFHLSSMSSIGGFAATSAKUAGUSTUURE PAATEPPPVLHLPAIQPPPPVLPGPFFMPSDRSTERCETVLEGE
	ì	•	PAATEPPPVLHLPATOPPPPVLFGFTFMFDMCXCDFLHTYCSR
	Ì	(TISCFVVGGEKRLCLPQILNSVLRDFSLQQINAVCDELHIYCSR
		į	CTADQLEILKVMGILPFSAPSCGLITKTDAERLCNALLYGGAYP
	1		PPCKKELAASLALGLELSERSVRVYHE\CFGKCKGL\LVPELYS
		Į.	SPSAACIQCLD\CRLMYPPHKFVVHSHKALBNRTCHWGF\DSA\
	1	1	ATTITUTE OF THE PROPERTY OF TH
	\	ļ	PROCEDDACIDERTDDTSSOSPAPSEKDKPSSWLKTLAGSSNAS
		l	TOWNDOOD, SAFDDWSDAVSASEKELSPHLPALIRDSF1S1KS
		1	DEMANDATION OF THE PROPERTY OF
			DAY TOTAL A DETINDUA PEEDKD SEAEVEVESKEEFTS SUS
		1	LSSPSFTSSSSAKDLGSPGARALPSAVPDAAAPADAPSGLEAEI
			LSSPSFTSSSSAKDLGSPGARADFOATTE
			EHLROALEGGLUTKEAKEKE DHEVVKIKVKODDICESTEDEN AFKEKKKE
	1		LHQELEFLRVAKKEKLREATEAKRNLRKEIERLRAENEKKMKE
	İ		NESRLRLKRELEQARQARVCDKGCEAGRLRAKYSAQIEDLQVKI
1		1	QHAEADREQLRADLLREREAREHLEK\VVK\ELQEQLWPRARP
l		1	ARCODO ARTIPO
L		118	PORTUGEL KUNTSEFODEAKRI EREOKLKLYOSATQAVFQKRQ
696	9 1855	1 110	L COLUMN THE MEATING TO AND TATION CREVIOUS TO A SPEC
1		1	A PARTY NET CET ECCLEUNDKSYGTWHRCWLLGRLPEPNWIKE
1			THE GARDY BUDGENEUCHDVRRFVATOAAVPPAKELAFTDSLLL
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1			NFSNYSSWHYRSCLLPQLHPQFDSGFQSKHI
1			AFFTDPNDQSAWFYHKWILLGKADPQDALKCLITTOKOBIAGDITCOL
1	-		SRPLLVGSRMEILLLMVDDSPLIVEWRTPDGRNRPSHVWLCDL
1			Language Pour Edutablitation (NECAPTRON DE 175
Į.			or proper compressor OSELESCKELOELEPENANCU(LITTLE
ļ			Lear DRIT VENERAL OVECTINA AMIDENCATA (PDD DROVE DECA
1		İ	TO THE PARTY OF TH
1			VILLED BODD BOT VILLED BY TRUPK DE LA COLLEGA DE LA CO
			PPALAALRCLEDPPPRI (VII) DE PRALACIA DE LA PRALACIA DEL PRALACIA DE LA PRALACIA DE LA PRALACIA DEL PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DEL PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DE LA PRALACIA DEL PRALACIA DE LA ACIA DEL PRALACIA DEL PRACIONA DEL PRALACIA DEL PRALACIA DEL PRALACIA DEL PRALACIA DEL PR
1		i	PSVSSVLT

			Amino acid segment containing signal peptide
SEQ	Predicted	Predicted end	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	H=Histidine, I=Isoleucine, K=Lysine,
	location	corresponding	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	to first	P=Proline, Q=Glutamine, R=Arginine,
	to first	amino acid	S=Serine, T=Threonine, V=Valine,
	amino acid	residue of	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of	amino acid	Codon, /=possible nucleotide deletion,
	amino acid	sequence	\=possible nucleotide insertion)
	sequence		SFPPLLSSPSAVGEGKVAVAAPCPGRSECARAKMAYIQLEPLNE
6970	3	1528	GFLSRISGLLLCRWTCRHCCQKCYESSCCQSSEDEVEILGPFPA
			QTPPWLMASRSSDKDGDSVHTASEVPLTPRTNSPDGRRSSSDTS
			KSTYSLTRRISSLESRRPSSPLIDIKPIBFGVLSAKKEPIQPSV
		i	LRRTYNPDDYFRKFEPHLYSLDSNSDDVDSLTDEEILSKYQLGM
	}		LHFSTQYDLLHNHLTVRVIEARDLPPPISHDGSRQDMAHSNPYV
			KICLLPDQKNSKQTGVKRKTQKPVFEERYTFEIPFLEAQRRTLL
			LTVVDFDKFSRHCVIGKVSVPLCEVDLVKGGHWWKALIPSSQNE
			VELGELLLSLNYLPSAGRLNVDVIRAKQLLQTDVSQGSDPFVKI
	1		QLVHGLKLVKTKKTSFLRGTIDPFYNESFSFKVPQEELENASLV
			FTVFGHNMKSSNDFIGRIVIG\QYSSGP\SEPNHWRRMLNTHRT
	l		AVEQWHSLRSRAECDRVSPASLEVT
		1	ACFYVPGSRSFKLIPRHGLVNMGRSGKLPSGVSAKLKRWKKGHS
6971	37	3702	SDSNPAICRHRQAARSRFFSRPSGRSDLTVDAVKLHNELQSGSL
			RLGKSEAPETPMEEEAELVLTEKSSGTFLSGLSDCTNVTFSKVQ
			RFWESNSAAHKEICAVLAAVTEVIRSQGGKETETEYFAALIRKA
			AQHGVCSVLKGSEFMFEKAPAHHPAAISTAKFCIQEIEKSGGSK
			EATTTLHMLTLLKDLLPCFPEGLVKSCSETLLRVMTLSHVLVTA
			CAMQAFHSLFHARPGLSTLSAELNAQIITALYDYVPSENDLQPL
		}	LAWLKVMEKAHINLVRLQWDLGLGHLPRFFGTAVTCLLSPHSQV
	1		LTAATQSLKEILKECVAPHMADIGSVTSSASGPAQSVAKMFRAV
1	İ		EEGLTYKFHAAWSSVLQLLCVFFEACGRQAHPVMRKCLQSLCDL
			RLSPHFPHTAALDQAVGAAVTSMGPEVVLQAVPLEIDGSEETLD
		1	FPRSWLLPVIRDHVQETRLGFFTTYFLPLANTLKSKAMDLAQAG
ł			STVESKIYDTLQWQMWTLLPGFCTRPTDVAISFKGLARTLGMAI
}			SERPDLRVTVCQALRTLITKGCQAEADRAEVSRFAKNFLPILFN
1			LYGQPVAAGDTPAPRRAVLETIRTYLTITDTQLVNSLLEKASEK
1			VLDPASSDFTRLSVLDLVVALAPCADEAAISKLYSTIRPYLESK
ļ			AHGVQKKAYRVLEEVCASPQGPGALFVQSHLEDLKKTLLDSLRS
			TSSPAKRPRLKCLLHIVRKLSAEHKEFITALIPEVILCTKEVSV
1		Į	GARKNAFALLVEMGHAFLRFGSNQBEALQCYLVLIYPGLVGAVT
1			MVSCSILALTHLLFEFKGLMGTSTVEQLLENVCLLLASRTRDVV
		ļ	KSALGFIKVAVTVMDVAHLAKHVQLVMEAIGKLSDDMRRHFRMK
			LRNLFT\KFIPK\FGILTWGKKAVGPKEYHRVLVNIRKAEARAK
	\		RHRALSQAAVEEEEEEEEEEPAQGKGDSIEEILADSEDEEDNE
			FEERSRGKEORKLARORSRAWLKEGGGDEPLNFLDPKVAQRVLA
			TOPGPGRGRKKDHSFKVSADGRLIIREEADGNKMBEEEGAKGED
			FEMADPMEDVIIRNKKHOKLKHOKEAEEEELEIPPOYQAGGSGI
			HRPVAKKAMPGAEYKAKKAKGDVKKKGRPDPYAYIPLNRSKLNR
1			PKKMKLOGOFKGLVKAAORGSQVGHKNRRKDRRP
(0.00	3370	973	PCGATLLPLWRRTRPREATVPRGAAQRGRARSAEGRIPSSQSPS
6972	2179	1	DAEAGGATRSPPPRPPRPPRPARPPGPSAPPLLRSDAGPGATVSAAA
	1	1	AAATRRARRGATMGAOLSTLGHMVLPPVWFLYSLLMKLFQRSTP
			ATTLESPOTKYPLELIDREIISHDTERFRFALPSPQHILGLPVG
			OHIVLSARIDGNLVVRPYTPISSDDDKGFVDLVIKVYFKDTHPK
			FPAGGKMSOYLESMOIGDTIEFRGPSGLLVYQGKGKFAIRPDKK
			SNDITETVKSVGMIAGGTGITPMLQVIRAIMKDPDDHTVCHLLF
		1	ANOTEYDILLEPELEELRNKHSARFKLWYTLDRAPEAWDYGQG\
1			FVNEEMIRDHLPPPE\EEPLVLMCGPPPMIQYACLPNL\DHVGH
Į.		Ì	DTERCEVE
		1964	LOPECAHEGLEAOKCGRPAPGVDAMVLCPVIGKLLHKRVVLASA
6973	1	1304	CDPPORTISNAGIR FEVVPSKFKEKLDKASFATPYGYAMETAKO
1		ĺ	VALEVANDI.YOKDI.RAPDVVIGADTIVTVGGLILEKPVDKQDAY
1	1	i	THE PROPERTY OF THE PROPERTY O
	1		RMLSRFE/SGREHSVFTGVAIVHCSSKDHQLDIRVSEFTEETKV
	}		RMLSRFE/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFYEETKV KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFI
			RMLSRFE/SGREHSVFTGVAIVHCSSKDHQLDTRVSEFFEETRV KFSELSEELLWEYVHSGEPMDKAGGYGIQALGGMLVESVHGDFI NVVGFPLNHFCKQLVKLYYPPRPEDLRRSVKHDSIPAADTFBDI

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1.0.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
. [to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	boqueou	\=possible nucleotide insertion)
	bequeinee		SDVEGGGSEPTORDAGSRDEKAEAGEAGQATAEAECHRTRETLP
Ì			PFPTRLLELIEGFMLSKGLLTACKLKVFDLLKDEAPOKAADIAS
1			KVDASACGMERLLDICAAMGLLEKTEQGYSNTETANVYLASDGE
			YSLHGFIMHNNDLTWNLFTYLEFAIREGTNOHHRALGKKAEDLF
1			QDAYYQSPETRLRFMRAMHGMTKLTACQVATAFNLSRFSSACDV
			GGCTGALARELAREYPRMOVTVFDLPDIIELAAHFOPPGPOAVO
			IHFAAGDFFRDPLPSAELYVLCRILHDWPDDKVHKLLSRVAESC
			KPGAGLLLVETLLDEEKRVAQRALMQSLNMLVQTEGKERSLGEY
ł	-		QCLLELHGFHQVQVVHLGGVLDAIL\PPKWPPEAQAACSL
6974	3082	2172	RSCAAFASFASRPPLELFAPPGSHRSPPGRGVATSAQCALSVRK
03/4	3002	21,2	LLAARPGLGTKYQATMVYKTLFALCILTAGWRVQSLPTSAPLSV
			SLPTNIVPPTTIWTSSPONTDADTASPSNGTHNNSVLPVTASAP
			TSLLPKNISIESREEEITSPGSNWEGTNTDPSPSGFSSTSGGVH
			LTTTLEEHSLGTPEAGVAATLSQSAAEPPTLISPQAPASSPSSL
1			STSPPEVFSASVITNHSSTVTSTQPTGAPTAPESPTEESSSDHT
		ļ	PTSHATAEPVPQEKTPPTTVSGKVMCELIDMET\PPPFPG
6975	2	500	RPRPTVHCCKWALKLETAMETLINVFHAHSGKEGDKYKLSKKEL
05/3	-		KELLOTELSGFLDVKELML*ATEALKTFREA*KSPIIOCSSSRS
1			SLPPAPOPPPYL+LSAVPFPIHLPLPLLPPOAOKDVDAVDKVMK
			BLDENGDGEVDFQBYVVLVAALTVACNNFFWENS
6976	1216	970	GCOL*VAYGTTENSPVTFAHFPEDTVEOKAESVGRIMPHTEARI
03/0	1210	1	MNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPOKTEEAVDQDKW
			YWTGDVATMNEQGFCKIVGRSKDMIIRGGENIYPAELEDFFHTH
			PKVQEVQVVGVKDDRMGEEICACIRLKDGBETTVEEIKAFCKGK
			ISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL*IKQQ
		ŀ	ACPGRLA
6977	1298	588	SLFINTNLLSNQIRKTSFGMCSEPISDNTEDQKGKLKTPDFA*R
			ANKKSKHHVNGNRTVEPFPEGTQMAVFGMGCFWGAERKFWVLKG
1			VYSTQVGFAGGYTSNPTYKEVCSEKTGHAEVVRVVYQPEHMSFE
			ELLKVFWENHDPTQGMRQGNDHGTQYRSAIYPTSAKQMEAALSS
			KENYQKVLSEHGFGPITTDIREGQTFYYAEDYHQQYLSKNPNGY
ļ	}	}	CGLGGTGVSCPVGIKK
6978	3	242	SFPFRDSRRCGCCKGSSLRHTAVAMVKLSKEAKQRLQQLFKGSQ
		1	FAIRWGFIPLVIYLGFKRGADPGMPEPTVLSLLWG
6979	3917	1146	DEARVRGEAVAAAILSRCRHWSGPPPFPPSPPDRKGLRGTEPWE
			AGPGSGATPGARAMDVRRLKVNBLREELQRRGLDTRGLKTELAE
			RLQAALEAEEPDDERELDADDEPGRPGHINEEVETEGGSELEGT
}			AQPPPPGLQPHAEPGGYSGPDGHYAMDNITRQNQFYDTQVIKQE
	1		NESGYERRPLEMEQQQAYRPEMKTEMKQGAPTSFLPPEASQLKP
			DRQQFQSRKRPYEENRGRGYFEHREDRRGRSPQPPAEEDEDDFD
	1		DTLVAIDTYNCDLHFKVARDRSSGYPLTIEGFAYLWSGARASYG
	Ī		VRRGRVCFEMKINEEISVKHLPSTEPDPHVVRIGWSLDSCSTQL
į			GEEPFSYGYGGTGKKSTNSRFENYGDKFAENDVIGCFADFECGN
1	1		DVELSFTKNGKWMGIAFRIQKEALGGQALYPHVLVKNCAVEFNF
			GQRAEPYCSVLPGFTFIQHLPLSERIRGTVGPKSKAECEILMMV
			GLPAAGKTTWAIKHAASNPSKKYNILGTNAIMDKMRVMGLRRQR
			NYAGRWDVLIQQATQCLNRLIQIAARKKRNYILDQTNVYGSAQR
			RKMRPFEGFQRKAIVICPTDEDLKDRTIKRTDEEGKDVPDHAVL
			EMKANFTLPDVGDFLDEVLFIELQREEADKLVRQYNEEGRKAGP
1			PPEKRFDNRGGGGFRGRGGGGGGFQRYENRGPPGGNRGGFQNRGG
-			GSGGGGNYRGGFNRSGGGGYSQNRWGNNNRDNNNSNNRGSYNRA
			PQQQPPPQQPPPPQQPPPPQQPPPPSYSPARNPPGASTYNKNSNI
		1	PGSSANTSTPTVSSYSPPQSFGFFPSTFQPSYSQPPYNQGGYSQ
			GYTAPPPPPPPPPAYNYGSYGGYNPAPYTPPPPPTAQTYPQPSY
			NQYQQYAQQWNQYYQNQGQWPPYYGNYDYGSYSGNTQGGTSTQ
6980	1	420	GTRGRKTGRVAAPSTRRRTGNMQKLQTRSPAMSLSDPGLGYHPT
			· · · · · · · · · · · · · · · · · · ·

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1 1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1 1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1 1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1 1	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	•	\=possible nucleotide insertion)
<u> </u>			CWTLRWPPLCSLHALHVFHCLFSSRLGTPVSPRLAMDPNCSCEA
1 1			GGSCACAGSCKCKKCKCTSCKKSCCSCCPLGCAKCAQGCICKGA
1 1			SEKCSCCA
6981	10	1054	PGRGFRRASLRPAFAARGVFQGGLGQAKQARTRACAALPTPHPS
1		-	APRLLEPQGVFSLFPPPPGPWPNMILTKAQYDEIAQCLVSVPPT
1			RQSLRKLKQRFPSQSQATLLSIFSQEYQKHIKRTHAKHHTSEAI
1			ESYYORYLNGVVKNGAAPVLLDLANEVDYAPSLMARLILERFLO
1			EHEETPPSKSIINSMLRDPSQIPDGVLANQVYQCIVNDCCYGPL
1			VDCIKHAIGHEHEVLLRDLLLEKNLSFLDEDQLRAKGYDKTPDF
1 1			ILQVPVAVEGHIIHWIESKASFGDECSHHAYLHDQFWSYWNRFG
1			PGLVIYWYGFIQELDCNRERGILLKACFPTNIVTLCHSIA
6982	153	1285	FPQQDCSAPAAPGLAGSEPRRLRAYRRRQRARGLKRVAWLAPP
			PSLLQGLQGWAQAPVDGTLGPEDSRASSPMIQNSRPSLLQPQDV
]			GDTVETLMLHPVIKAFLCGSISGTCSTLLFQPLDLLKTRLQTLQ
1			PSDHGSRRVGMLAVLLKVVRTESLLGLWKGMSPSIVRCVPGVGI
1 1			YFGTLYSLKQYFLRGHPPTALESVMLGVGSRSVAGVCMSPITVI
1 1			KTRYESGKYGYESIYAALRSIYHSEGHRGLFSGLTATLLRDAPF
1			SGIYLMFYNQTKNIVPHDQVDATLIPITNFSCGIFAGILASLVT
1 1			QPADVIKTHMQLYPLKFQWIGQAVTLIFKDYGLRGFFQGGIPRA
		,	LRRTLMAAMAWTVYEEMMAKMGLKS
6983	82	773	EMSFLQDPSFFTMGMWSIGAGALGAAALALLLANTDVFLSKPQK
****	0.2	,,,,	AALEYLEDIDLKTLEKEPRTFKAKELWEKNGAVIMAVRRPGCFL
1			CREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDFQPYFKGE
1			IFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLE
			GEGFILGGVFVVGSGKQGILLEHREKEFGDKVNLLSVLEAAKMI
1			KPOTLASEKK
6984	1845	1282	GGRSAYSLPAGSLPRVPATAAAKMASGVQVADEVCRIFYDMKVR
}	20.0	1002	KCSTPEEIKKRKKAVIFCLSADKKCIIVEEGKEILVGDVGVTIT
			DPFKHFVGMLPEKDCRYALYDASFETKESRKEELMFFLWAPELA
1			PLKSKMIYASSKDAIKKKFQGIKHECQANGPEDLNRACIAEKLG
1			GSLIVAFEGCPV
6985	1887	1324	RRTAGIYPCFPKPGRTRHALCSVVLLLLTGQLAFDDFQESCAMM
1	200.	1301	WQKYAGSRRSMPLGARILFHGVFYAGGFAIVYYLIQKFHSRALY
1			YKLAVEQLQSHPEAQEALGPPLNIHYLKLIDRENFVDIVDAKLK
			IPVSGSKSEGLLYVHSSRGGPFQRWHLDEVFLELKDGQQIPVFK
1	ı		LSGENGDEVKKE
6986	642	1350	YHLYFKMGDPNSRKKQALNRLRAQLRKKKESLADQFDFKMYIAF
	~ . 	100	VFKEKKKKSALFEVSEVIPVMTNNYEENILKGVRDSSYSLESSL
1 1			ELLQKDVVQLHAPRYQSMRRDVIGCTQEMDFILWPRNDIEKIVC
			LLFSRWKESDEPFRPVQAKFEFHHGDYEKQFLHVLSRKDKTGIV
1			VNNPNQSVFLFIDRQHLQTPKNKATIFKLCSICLYLPQEQLTHW
			AVGTIEDHLRPYMPE
6987	1623	341	LEAAEKASRAFKESQRQTDSKNYETENWSPQKSQRRYDMYNTAC
1		311	FLGE1EVGLYTIQILQLTPFFHKENELSKKHMVQFLSGKWTIPP
}			DDDNRCVIALCKETCHI KNI OCH KROERDEETRAATI 1 100 100
			DPRNECYLALSKFTSHLKNLQSDLKRCFDFFIDYMVLLKMRYTQ KEIABIMLSKKVSRCFRKYTELFCHLDPCLLQSKESQLLQBENC
1			
			RKKLEALRADRFAGLLEYLNPNYKDATTMESIVNEYAFLLQQNS
			KKPMTNEKQNSILANIILSCLKPNSKLIQPLTTLKKQLREVLQF
			VGLSHQYPGPYFLACLLFWPENQELDQDSKLIEKYVSSLNRSFR
			GQYKRMCRSKQASTLFYLGKRKGLNSIVHKAKIEQYFDKAQNTN
			SLWHSGDVWKKNEVKDLLRRLTGQAEGKLISVEYGTEEKIKIPV ISVYSGPLRSGRNIERVSFYLGFSIEGPPGL
6000			
6988	3	689	TQLLRRPAVFVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR
6988	3	689	TQLLRRPAVFVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR LVRGLGAASTAAPQDAQTGPQPMPRADCIMRHLPYFCRGQVVRG
6988	3	689	TQLLRRPAVFVGSAASGIRSGLWSASSGHWCAPAAGRAHAPVPR

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
			RPEKNFDSLESLISAIQGDIBEAKKRLELPEHLKIKEDNFFQVS KSKIMNGH
6000		1110	LMPSDRPLSPSTHASAGSHCHAPPTTARRAFPIPFGSKSNMATL
6989	_ 2	1118	KDQLIYNLLKEEQTPQNKITVVGVGAVGMACAISILMKDLADEL
			ALVDVIEDKLKGEMMDLOHGSLFLRTPKIVSGKDYNVTANSKLV
	1		IITAGARQOEGESRLNLVORNVNIFKFIIPNVVKYSPNCKLLIV
	Í		SNPVDILTYVAWKISGFPKNRVIGSGCNLDSARFRYLMGERLGV
	}		HPLSCHGWVLGEHGDSSVPVWSGMNVAGVSLKTLHPDLGTDKDK
			EQWKEVHKQVVESAYEVIKLKGYTSWAIGLSVADLAESIMKNLR
]		RVHPVSTMIKGLYGIKDDVFLSVPCILGQNGISDLVKVTLTSEE
	1		EARLKKSADTLWGIQKELQF
6990	719	258	THASGMASVVLALRTRTAVTSLLSPTPATALAVRYASKKSGGSS
			KNLGGKSSGRRQGIKKMEGHYVHAGNIIATQRHFRWHPGAHVGV
	İ		GKNKCLYALEEGIVRYTKEVYVPHPRNTEAVDLITRLPKGAVLY
			KTFVHVVPAKPEGTFKLVAML
6991	169	451	RRSSDFHNPGFLSRPVSLRENIHHQVICSTKNKRRNPKKIAYLL
			SSLLMTNLNPNESTENQPVDAYWAFTLDQEFLTYACVEGTGCLF
			CGRHVH
6992	944	510	ROAPGCSSLALROVROVYCGLVRAPOVOTRPLSSRFVERRGALY
			RSPMNQENPPPYPGPGPTAPYPPYPPQPMGPGPMGGPYPPPQGY PYQGYPQYGWQGGPQEPPKTTVYVVEDQRRDELGPSTCLTACWT
			ALCCCCLWDMLT
6993	1	374	OWCVTCPQHNARQGPAVPPGIQAYGAAPFEDLQVDFTEMSKCRG
درره	1	5/4	DRVWIKNWNVASLCPLWKGPQTVVLSPPTAVKVEGIPAWIHHSH
			VKPAARETWEARPSPDNPFRVTLKKTTSPAPVTPGS
6994	346	1100	QWPEKDPVMAASSISSPWGKHVFKAILMVLVALILLHSALAQSR
			RDFAPPGQQKREAPVDVLTQIGRSVRGTLDAWIGPETMHLVSES
			SSQVLWAISSAISVAFFALSGIAAQLLNALGLAGDYLAQGLKLS
			PGQVQTFLLWGAGALVVYWLLSLLLGLVLALLGRILWGLKLVIF
		Ì	LAGFVALMRSVPDPSTRALLLLALLILYALLSRLTGSRASGAQL
			EAKVRGLERQVEELRWRQRRAAKGARSVEEE
6995	144	1346	GSVAVGLSGIMAAQKDLWDAIVIGAGIQGCFTAYHLAKHRKRIL
			LLEQFFLPHSRGSSHGQSRIIRKAYLEDFYTRMMHECYQIWAQL
		i	EHEAGTQLHRQTGLLLLGMKENQELKTIQANLSRQRVEHQCLSS EELKORFPNIRLPRGEVGLLDNSGGVIYAYKALRALQDAIROLG
			GIVRDGEKVVEINPGLLVTVKTTSRSYQAKSLVITAGPWTNQLL
	1.		RPLGIEMPLOTLRINVCYWREMVPGSYGVSQAFPCFLWLGLCPH
			HIYGLPTGEYPGLMKVSYHHGNHADPEERDCPTARTDIGDVQIL
			SSFVRDHLPDLKPEPAVIESCMYTNTPDEQFILDRHPKYDNIVI
			GAGFSGHGFKLAPVVGKILYELSMKLTPSYDLAPFRISRFPSLG
1			KAHL
6996	543	1942	ETANAEAAARKSAMDWKEVLRRRLATPNTCPNKKKSEQELKDEE
[MDLFTKYYSEWKGGRKNTNEFYKTIPRFYYRLPAENEVLLQKLR
			EESRAVFLQRKSRELLDNEELQNLWFLLDKHQTPPMIGEEAMIN
{			YENFLKVGEKAGAKCKQFFTAKVFAKLLHTDSYGRISIMQFFNY
			VMRKVWLHQTRIGLSLYDVAGQGYLRESDLENYILELIPTLPQL
			DGLEKSFYSFYVCTAVRKFFFFLDPLRTGKIKIQDILACSFLDD
1		1	LLELRDEELSKESQETNWFSAPSALRVYGQYLNLDKDHNGMLSK
1		1	EELSRYGTATMTNVFLDRVFQECLTYDGEMDYKTYLDFVLALEN
1		1	RKEPAALQYIFKLLDIENKGYLNVFSLNYFFRAIQELMKIHGQD
1			PVSFQDVKDEIFDMVKPKDPLKISLQDLINSNQGDTVTTILIDL
		ļ	NGFWTYENREALVANDSENSADLDDT
6997	370	1104	AMBLTIFILRLAIYILTFPLYLINFLGLWSWICKKWFPYFLVRF
1	1		TVIYNEQMASKKRELFSNLQEFAGPSGKLSLLEVGCGTGANFKF YPPGCRVTCIDPNPNFEKFLIKSIAENRHLOFERFVVAAGENMH
i		1	TELOCKALCIDEMENTEREDITYSTWENKUDALEKE AAAGENMU

Predicted Predicted en Incleation In				nontide
NO: muclaotide corresponding to first anino acid residue of anino acid residue of anino acid residue of anino acid acquence complete the first anino acid acquence anino acid residue of anino acid acquence complete the first anino acid acquence complete the first acquence complete the first anino acid acquence complete the first acquence complete th	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first amino acid	ID	beginning		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
Lefeucine, Membrihonine, N-Asparagine, amino acid residue of residue of amino acid residue of amino acid sequence solvent in the state e state of the state o	NO:	nucleotide	location	Glutamic Acid, F-Phenylalanine, G-Glycine,
amino acid amino acid			corresponding	H=Histidine, I=Isoleucine, K=Lysine,
to first amino acid residue of residue of amino acid RARORPEDAPTECPGAINCPEPLMC SHLPVPAPPTMESRCKABERAGPELMC SHLPVPAPPTMESRCKASASSVRDTKVPQVTTEARVPPAADCK APLTRYSKKALRAPAGKOPTALRVSKALRAPAGKALR		corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence				P=Proline, Q=Glutamine, R=Arginine,
amino acid sequence Codon, /-possible nucleotide insertion		amino acid	residue of	S=Serine, T=Threonine, V=Valine,
amino acid sequence Codon, /-possible nucleotide insection	j		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
A-possible nuclectide insection				Codon, /=possible nucleotide deletion,
QVADOSUDVIVOTUVLOSVINOERILAEVORVILEPROGETYPENG VARACCITRINTPOQULDPANHLIPGOCINITESNIKALERASPSK LIKLOHIOAPLSMELVRPHIVOYAVK 8HLPVPNAPPTMESRCKSASSPRPDTVENDVIVTEAKVPPAADGE 8HLPVPNAPPTMESRCKSASSPRPDTVENDVIVTEAKVPPAADGE APLITVESKREAPRAGOOPAAPTHAPAKKTSKAKDAPALINHEN LIKPAPTVPSSPDATPEPKOPDGAGEDERASOGPOGROPHSCEN PUPLLINAGGVVANALALILGVALIVEKK PUPLLINAGGVVANALALILGVALIVEKK 6999 14 1591 GRAGACSREDTAMSIEIESSDVIRLIMOYIKENSLIBPALATICAL LIKPAPTVUSSIESPVADINSCHIDVIKANSLIBPALATICAL LIKPAPTVUSSIESPVADINSCHIDVIKANSLIBPALATICAL LIKPAPTVUSSIESPVADINSCHIDVIKANSLIBPALATICAL LIKPAPTVUSSIESPVADINSCHIDVIKANSLIBPALATICAL LIKPAPTVUSSIESPVADINSCHIDVIKANSLIBPALATICAL LIKPAPTVUSSIESPVADINSCHIDVIKANSLIBPALATICAL LIKPAPTVUSSIESPVADINSCHIDVIKANSCHIPPATICALISP PUPLLAMOKOGOLIPPATILLIREKARAVETUSERSHALAL LIKPAKAMOKOGOLIPPATILLIREKARAVETUSERSKIPTOLISH IKPOKSHVECARFSPROGYLVATGSVOGFIEWANTTIKKINGL KYOKONNENGANICANSTERITALATAORAVETVALISMENICAL KYOKONNENGANICANSTERITALATAORAVETVALISMENICAL KYOKONNENGANICANSTERITALATAORAVETVALISMENICANS QCILKRFERAISKAVTICLSFSKOSSOLISASFOQTIRIHGLISKO KYOKONNENGANICANSTERITALISPASILANDATICASSOLILAANSTERITALISASSOTIVANINMETTECS NTYKSLISSTAGTOLITVASVILLERDERIPVACURSATVAVINNE QCILKRFERAISKAVTICLSFSKOSSOLISASFOQTIRIHGLISCHITVASKATILASSASTIVATIMMETTECS NTYKSLISSTAGTOLITVASVILLERDERIPVACURSATVAVINNETCESS NTYKSLISSTAGTOLITVASVILLERDERIPVACURSATVAVINNETCESS NTYKSLISSTAGTOLITVASVILLERDERIPVACURSATVAVINNETCESS NTYKSLISSTAGTOLITVASVILLERDERIPVACURSATVAVINNETCESS NTYKSLISSTAGTOLITVASVILLERDERIPVACURSATVAVINNETCESS NTYKSLISSTAGTOLITVASKATULISASSOCIALEANTIVILLERAAVETOLITVASKAT LIKAPAMAGOSPOTISTAATAORAVALUSATICANSTAGTARAVANA LIKLKYLIAVASAATAORAVALUSATAATAORAVALUSATAATAORAVALUSATAATAORAVALUSATAATAORAVALUSATAATAATAORAVALUSATAATAATAATAATAATAATAATAATAATAATAATAATA		1	1	\=possible nucleotide insertion)
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### BTTYSINTYDSIESPYADINGGHDYLQAIGSLKIDRTCHILDRICAL YEQVULELIERIEGAARSLIGRTDPHMIAGOPSPHYIHLENL LARSYPDPREAYPDGSSKEKRRAAIAQALAGEWSVYPSRIMAL LGQALKWQCHQGLLPPGMTLDLFRGKAAVKUVEPSRIMAL LGQALKWQCHQGLLPPGMTLDLFRGKAAVKUVEPSRIMAL LGQALKWQCHQGLLPPGMTLDLFRGKAAVKUVEPSRIMAL LGQALKWQCHQGLLPPGMTLDLFRGKAAVKUVEPSKIPFOLSHR IKPGQKSHVPCAFSPBOQYLVTGSVUDFIEVWNFTTGKIRKDL KYQAQNIPMMDDAVLCKCFSRTIEMLATGAQDGKIKWKLIGG QCURRFERSHSGWTLGSFGSSGLISASPDQTIRIHGLKSGK TLKEFRGHSSFVMBAFFTODGHYIISASSDGTVKLWNKKTECS NTFKSLGSTAGTDITVNSVILLPKPDEHFUKRSNTVLIMNQ QGIVRSFSSGKREGOFVCCALSFRGENIYCVCGDFVLYCFSTV TGKLERILTVHEKDVIGIAHPHQNLLATVGRSTVTVLIMNQ QGIVRSFSSGKREGOFVCCALSFRGENIYCVCGDFVLYCFSTV TGKLERILTVHEKDVIGIAHPHQNLLATKRSNTVLIMNGV QGIVRSFSSGKREGOFVCCALSFRGENIYCVCGDFVLYCFSTV TGKLERLTVHUKENVIGIAHPHQNLATKRSNTVLIMNGV QGIVRSFSSGKREGOFVCCALSFRGENIYCVCGDFVLYCFSTV TGKLERLTVHUKENVIGIAHPHQNLATKRSTTLLHCAARMGL ETLKALVELDVILEALMPHQNLATKRSTVLLHCAARMGL ETLKALVELDVILEALMPHQNLATTGYTLLHCAARMGL ETLKALVELDVILEALMPHGNLATKRSTLLHCAARMGL ETLKALVELDVILEALMFVGVANTSVGTGCVELDWAA RITLKKY LAKVSLAVTUTEKSGSCKLLKEKNTILSACRAKMENL ETHTEAS INELFEGRQLEDTVTFIFTKMTFPCQVKSAKSVTSH DOKKSQDDTSN 7001 2056 844 RRCGITAFLKGCFIFIYPJFJFFEFLSCCPGWSAVAQSRLIAN FASQVQAIPILPKDSQVGPDVKSEAAPKRALYSEVYGSGEICGF TSPKRLCIRFSEPVDAVVVVSVKUDPLPLLPEANGGRSTMSPJT VSPALVSPTODSRTNMSRELLTKSPSSLIAGEDGTEPIVLDSLKQ HYFIDRGGMFSYLLHFLETSKLLIPDDFKDYTLLYEBAKFQLL TSPKRLCIRFSEPVDAVVVVSVKUDPLPLLPEANGGRSTMSPJT VSPALVSPTODSRTNMSRELLTKSPSSLIGELDGTEPIVLDSLKQ HYFIDRGGMFSYLLHFLETSKLLIPDDFKDYTLLYEBAKFQL PRALVERSKRYCTSRSPCCLVVVAPDLGGRTTLSGDK SLIEEVFPELGDVMCNSVANGWNINGSTHVIRFPLNGVCHLNSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRELERRTPRVFSVI TCSRHQSKRRIPTMSSPCCLVVAPDLGGRTTLSGDK SLIEEVFPELGDVMCNSVANGWNINGSTHVIRFYLKKDA FROGKVQVVIRGRMNVVVGGINTHYSYLGKTMDFSGABS SKTSAGTSRPAGRRTGTATSGTAATTTSVAPGCGGTRMSTQMSSV PRSSRCCGSRATTPPSKFQAPHAPCASSRHLAHALAPSSPGLP RGGSVADKKNPPHIRRRFVVVEFISDEDMYLPCGDTVELIEGKDA GKQGKVQVIRGRMNVVVGGINTHYSYLGKTMDFSGABA LHRGVKLUVPDPKKPTETEIMFFTGAGEGLLVNTTTVCLKTLQEEVMEAM GKNGLPTTVGVTGSGKTHTMTSSPGGGLUPCLANDIVNTLLHLE GKNGLLPTVGVTGSKTHTMTSSGCGLUPCLAN	1			FNPDDVAGGVAVAATADTEGCOVTDT.IMOVI.KENGLHRALATI.OE
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LARSYEDPREAYPDGSSKEKRRAJAGALAGEVSVYPFSRLMAL LGQALKUQCGGLLPPGMTIDLFRGKAAVGWEEKEFTDLSHH IKPGQKSHVECARFSPDGQYLVTGSVDGFIEWMNTTGKIRKDL KYQAQDNFMMMDDAVLGMCFSRDTEMLATGAQDGKIKVUKIQSG QCLRRFERAHSKGYTCLSFSKDSSGILSASFPQTIRHGLKSGK TLKEFRGHSSFVNERTFTDDGHYIISASSGTVKMMKKTTECS NTFKSLGSSTAGDTITWSVILLPKNEPHFVVCNRSNTVYLMMKQ GQIVRSFSSGKEEGDPVCCALSFRGENIVCVGEDFVLYCFSTV TGKLERTLTVHEKDVILLAHPHQNLLATYSBGLLKLWRP PROFILOPALTGHVEGLGKIFEDPENPHHEQAMGLLLEEDIVGRN LLYAACMAGGSDVIRALAKYGVINLENTGTTLLHCAAMGGL ETLKALVELDVDIBALMFREERARDVAARYSOTECVEFLDWADA RLIKAKYIAKAGSSDVIRALAKYGVINLENTGTTLLHCAAMGGL ETLKALVELDVDIBALMFREERARDVAARYSOTECVEFLDWADA RLIKKYIAKAGSSDVIRALAKYGVINLENTGTTLLHCAAMGGL ETHKALSINELFEGRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH DOKKSQDDTSN RGCLILAFLKGGFFIYPFIFFETEFLSCCPGWSAVAQSRLIAN FASGVQAIFTLEKDSQVGFDVKSEAAPKRALVESVGSGEICGF TSPKRLCIRFSEPVDAVVVVSVKHDPLLIPERANGHESTNSPTI VSPAIVSPTQDSRFMMSRPLITRSPASPHNNQGIPTPAQLTKSN APVHIDVGGHMYTSSLATLIKYPESRIGRLFFGTEFIVLDSKQ HYFIDRDGMFFILIHRIRSKLLIPDKYTHLYBEAKYFGL QPMLLEMERNKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK SLIEVFPETGDVMCNSVANGNHNETVIRFFLNSVCHLINSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKGEPLD 7002 1043 498 PPESTKHTIS*TYTDTSSAWACRFTTGTCT*TAAPGPTVRWP TPCSRHGSRRRITCCCSTSRPCGR-GGLCVRTAPTEPTTSSASS SNTSAGTSMFDAGRRTGTTTSGTATTTVRFFLNSVCHLINSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKGEPLD 7003 618 61 0GRFFAPCHQRDFLQPFGMRLSALLALASKYTLPPHYYGMSPP GSVADKRNIPPHYRRPVVPETISDEDMYLFCGDTVETLLGKDA GKOGKVQVJTRGRNWVGGLNTHVTSPCATKTDMYSSTP TPCSRHGSRFRITCCCSTSRPCGR-GGLCVRTAPTEPTTSASSS SNTSAGTSMFDAGRRTGTTTSGTATTTSTYTTDTSASSS SNTSAGTSMFDAGRTGTTTSGTATTTSTYTTTSTYTDTSASSS SNTSAGTSMFDAGRTGTTTSGTATTTSTTTTTSTATSTYPDYSSCY PRSSCCSRPATTPPSKFGABLERTYVPCLKTLQEEVWAP GGYGKTVVGVVTRGNWVVGGLNTHVTSCELDVVANDFLVNNLTHFSEAP LLHRQVKLVDPMDRKPTEIBMFTEAGERVRNETRSGRIIPKPE FPRADGIVPETWIDDFNUTSVEDABLERTYVPCLKTLQEEVWAP GKYLTKNTRSIGIEPGABOLLPRCLEDVNANDHANDLIH GRNGLLPTYGVTGSKKTHTMTGSPGGCGLVRTANTVQLHTPE GYRLNRNGDYKETQYSKYGHTTQGEEDVXCTEBSFTE GYRLNRNGDYKETQYSKYGHTTTQGELDVAUMPLNNDLIH GRNGLLPTYGVTGSKKTHTMTGSPGGCGLLPRCLDMIPNSIGSF QAKTVYFSNDRNSMDICCEVDAKS				ETTVSLNTVDS1ESFVADINSGAWDIVLQAIQSDADFDXIDIDD
LGOALKWQCHGGLLPFGMTDLFRGKAAVKDVEEKFFTQLSRH IKPGQKSHVCARFSPDGGYLVTGSVDETWMTTTGKIKTRDL KYQAQDNFMMDDAVLCMCFSRDTEMLATGAQDGKIKVWKIQSG QCLRRFERAHSKGVTCLSFSKDSG1LSASFDGTTRINGLKSGK TLKEFFGRHSSYVNRATFTQOGHYILSASSDGTVKIMMKTTECS NTFKSLGSTAGTDTVWSVILLDFNPEHFVCARSTVVIMMQ GQIVRSFSSGKREGGDFVCCALSPREMIYCVGEDFVLVCFSTV TGKLERTLTVHEKDVIGIAHPHQNLLATYSBDGLLKLWKP TGKLERTLTVHEKDVIGIAHPHQNLLATYSBDGLLKLWKP TGKLERTLTVHEKDVIGIAHPHQNLLATYSBDGLLKLWKP KNPLLQPALTGDVSGLGK, FEDPREMPHEQAMQLLLEEDIVGRN LLYAACMAGQSDVTRALAXYGUNIMENTTRGYTLLHCAAWGRL ETLKALVELDVDIELALAXYGUNIMENTTRGYTLLHCAAWGRL ETLKALVELDVDIELALAXYGUNIMENTTRGYTLHCAAWGRL ETLKALVELDVDIELALAXYGUNIMENTTRGYTLHCAAWGRL ETLKALVELDVDIELALAXYGUNIMENTTRGYTLHCAAWGRL ETHTEAS INELFEGRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH DQKRSQDDTSN RRCLLIAFLKGCFIFIVFIFIFTEFLSCCFGWSAVAGSRLIAN ETHTEAS INELFEGRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH DQKRSQDDTSN RRCLLIAFLKGGFFIFIVFIFIFTEFLSCCFGWSAVAGSRLIAN FASQVQAIFTLAKDSQVGPPVKSEAAPKRALVESVFGSGEICGF TSPKRLCIRPSPPVDAVVVSVKLDPPLLPBANGHRSTNSFTI VSPAIVSPTODSRPMMSRPLITTSFSASELMNGGIFPAQLTKSN APVHIDVGGHMTTSSLATLTLKYPESRIGRLFFGTBPTULDSLKQ HYFIDRGQMFFYILMTLRTSKLLIPDDFKDYTLLYBEAXYFQL QPMLLEMENKQDRETTGFSRPCCLLVVVARPDLGERTILGGDK SLIEEVFPEIGDVMCNSVNAGNNHDSTHVTRFPLKGYCHLNSVQ VLEELQQQRFETVGSCQGGDSSQFSETVLRRELRRTPRVPSVI RIKOEPLD TTSRHGSRRITICNCSTSRPCGR*GGLCVTAPPTPTTSASS SMTSAGTSRPAGRRTGTATSGTATTTTSWPGCGTRMWSTQSV PRSSCCSRPATTPPSKFGAPHAPCASSRHARGLAPSSPCLPA GGVADKKNIPPMYRRFVVVVPCLKTLQEEVMEAM GKQGKVQVVIVQRNNVVVGCINTHVYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMRRYPTTSLERTVPCTLTSGERUMEAM GKQGKVQVIVQTRGRNNVVGGLNTHYTJGKTMDYRGTMIPSEAP LLHRQVKLVDPMRRYPTTVCLKTLQEEVMEAM GKYGKVQVITQRTMRVVVGGLNTHYTJGCTMDYRGTMIPSEAP FPRADGIVPFTTHTGRGFTAMKSARARTPRKPTVK GYRLRRNGDYRFTGSRTTTTGCETGARQLLPRCCLDEVXAPPLVNDLIH GRNGLLFTVYGSCKTTMTTGCGERQRALAPPRKTSSKRQ VJPEPADMITVQSFCKABEVDEDSVYGVFVSTLEINNNTIVOLLT GYRLRRNGDYRFTYSDRINGTYGGRCTTTTTVQLKTEQEEVMEAM GRNGLLFTVYGFCKABEDDFCLDMIPNSIGSF GARRYPTKSDRINGTYGGRCTTTTTTTTVALLTDGCCTEVANTTVOLLTTPE GYRLRRNGDYRFTYSDRIN	1	1		AEÖAAPETEPKETENETENETENETENETENETENETENETENETENETE
TKPQQKSHVECARPSPDGYTLVTGDFTEWNFTTGKTRKDL KYQAQDNFMMDDAVLGMCFSRDTBATADQGKIKWANIGS QCURRFERAHSKGVTCLSFSKDSQILSASFDOTTRIHGLKSGK TLKSFRGHSSFVMEATFTDDGHYIISASSIGTVKIMMKTTECS NTFKSLGSTAGDTITVKSVILLPKNPBFFVVCKRSNTVVIMMNQ GQIVRSFSSGKREGDFVCCALSFRGBNIVCVGEDFVLYCFSTV TGKLERFLTVHEKDVIGLAHHHONLTSBGGLLKLKMRP TGKLERFLTVHEKDVIGLAHHHONLTSBGGLLKLKMRP GPGVVFLEIMESEGPFSERSEFFSQREEENEEERAGEPEETGF KNPLLQPALTGDVBGLQKIFEDPENPHHEQANQLLLEEDIVGRN LLYARACMAGQSDVIRALAKTGVINLBKTTRGVTLLHCAAMGRL ETLKALVELDVDIBALMFREERARDVAARNSGTECVFFLDWADA RLTLKKYLKIAKVSLAVTDTEKGSGKLLKDNTILSACRAKNENL ETHTEASINELFEQRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH DOKRSQDDTSN RRCLIIFAKGGFFIYFFIFFETEFLSCCPGWSAVAQSRLIAN FASQVQAIFILFKDSQVGPDVKSEAAPKRALVESVGSGEICGF TSPKRLGFRSEPVDAVVVSVKHDPJELIPEANGHRSTNSPTI VSFAIVSPTODSRPMMSRPLITRSPASPLNNQGIPPPAQLTKSN APVHIDVGGHMTTSLATLKYPESRIGRLFDGTEPILDGLKG HYFIDRDGQMFRYILMFLRTSKLLIPDDFKDYTLLYEEAKYPQL QPMLLEMERNKQDRETGRFSRPCECLVVRVAPDLGRTTLSGOK SLIEEVPPEIGDVMCNSVANGNHNEDTHVIRFPLNNYCVLINSVQ VLERLQORGFEIVGSCGGVDSSQFSEYVLRRELRRTPRVPSVI RIKGEPLD 7002 1043 498 FPMSSTKRTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWP TPCSRHGSRRRITCNCSTSRPCGR-CGLCVWTAPDLGRTTLSGOK SMTSAGTSPWSAGRRTGTTSTGTATTSVPCCTRTMSTQWSV PRSSCCSRPATTPPSKFGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFFAPCMQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRNIPPHTRRPDVVEPISDEDMYLFCGDTVEILBCKDT GKGKGKVQVJTRQRMWVGGLNTHVTPSLAGEVENAM GKGKGTVQVJTRQRMWVGGLNTHVTPSLAGE LLHRQVKLVPPMDRPTTIBMFTEAGERVRNDSTRSGRIIFKPE FPRADGIVPFTWIDGPKDTSUEDALERTYVPCLKTLQEEVWAAM GIKETT, MTRRSIGIEPGABCLLDVFCSLEG GYGKRVQVJTRGRMWVGGLNTHVTPCLEBLURAMA GKKETK,NTRRSIGIEPGABCLLDVFCSLEG GYLFTKNTGGFGTGFSPGGGCLEVINNTTVQLHTPE GYRLRNGDYKETQYSFKQVFGTHTTQCELDVNAMPLVNDLIH GRNGLLFTYVGVCIGSKTTHTTGSPEGGLLPRCLDMIFNSIGSF QAKRYPFSNDRNSMOLICGEVDALLERGKRAMPNNTNSSSKRQ VDPEPADMITVQSFCKAEEVDEDSVYGVFVSYTEAFE				LARSYFDPREAYPDGSSKEKRRAATAQALAGEVSVVPPSKLIMAL
RYQAQDNEMMIDANLCMCESRDTEMLATGADGKIKVMKIOSG QCLRRFERAHSKGYTCL9FSKDSSOLISASPDQTIRIHGLKSGK TLKEFRGHSSFVMEATFTQDGHYIISASSDGTVKIWMMKTTECS NTFKSLGSTAGTDITVMSVILLPKMPEHFVVLVERBSTVVLWIMMQ QGIVRSFSSKREGDFVCCALSFRGEWIYCVGEDFVLYCFSTV TGKLERTLTVHEKDUIGIAHPHQNLLATYSBGLLKLMKP TGKLERTLTVHEKDUIGIAHPHQNLLATYSBGLLKLMKP GPGVVFLELMESGPPESERSEFFSQREEENBEEEAGEPEETGP KNPLLQPALTGDVEGLGKIFEDPENPHEQAMQLLLEEDIVGRN LLYAACMAGGSDVIRALAKYGVNLNKKTTRGYTLLHCAAAWGKL ETLKALVELDVDIEALNREERRAAAYSGTECVEFLDWADA RLTLKKYIAKVSLAVTTEKGSGKLLKEDKNTILSACRAKNEHL ETHTEASINELFEQRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH DOKKSQDDTSN RCGLIAFLKGGFIFTYPIFIFTEFLSCCPGWSAVAQSRLIAN FASQVQAIPTLEVRGSGKLLKEDKNTILSACRAKNEHL ETHTEASINELFEQRQQLEDIVTPIFTKMTPCQVKSAKSVTSH DOKKSQDDTSN RRCGLIAFLKGGFIFTYPIFFTESCCPGWSAVAQSRLIAN FASQVQAIPTLEVRGSGVGPDVKSEAAPKRALYESYFGSGEICOP TSPKRLCIRPSEPVDAVVVVSVKHDPLPPLAPANGHRSTNSPTI VSPALVSPTODSRPMNSRPLITRSPASPLNNOGIPTPAQLTKSN APVHIDVGGHMYTSSLATLTXYPESRIGRLFDGTEPIVLDSLKG HYFIDROGMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFOL QPMLLEMERNKODRETGRSPR DECLVVRNAPDLGERTILSGDK HYFIDROGMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFOL QPMLLEMERNKODRETGRSPR DECLVVRNAPDLGERTILSGDK SLIEEVPFEIGDVMCNSVNAGNNHDSTHVIRFPLNGYCHLNSVQ VLERLQQRGFEIVGSCGGVDSSGFSEYVLRREERRTPRVSVI RIKGPLD 7002 1043 498 PPESSTRMTTS*TYTDTSSAWACRPTTGTCT*TAAPGFTVRWP TPCSRHQSRRICTCSTSRPCGR*CGLCVTRTAPTPTTSASSS SNTSAGTSWPAGRRTGTATSTATTSVWPGCGTRMWSTQWSSV PRSSCCSRPATTPPSKGGAPHAPCASSRHLAHGLAPSSPGLPA GGAGCV QGRFRAFCWQRDFLQPPGMRLSALLALASKYLIPPHYRYGMSP GSVADKKRNPPHIRRRPVVVEPISDEDMYLFCGDTVEILIGKDA GKGGKVVQVIRGNWVVVGGINTHYRYIGKTMDYRGMTIPSEAP LLHRQVKLVUPMDRKFTEIBWFTFAGERWYSTRSGRIIPKDE FPRADGIVPETWIGFKDTSVEDALERTYYPCLKTIQEEVMEAM GIKETR\NTRSIGIEPGABQLLPNFCPSLEG GYBLKRNGDYKETQYSFKQVFGTHTTGKELFDVVANPLVNDLIH GKNGLLFTYGVTGSKFTHTMTGSPGEGLLPRCLOMINSIGSF QKPLKRNGDYKETQYSFKQVFGTHTTGKELFDVVANPLVNDLIH GKNGLLFTYGVTGSKFTHTMTGSPGEGLLPRCLOMINSINSIGSF QKRYVFKSNDRNSMDIQCBVDALLERQKREAMPNPKTSSSKRQ VDPEPADMITVQBFCKAEEVDEDSVYCVYSTEITNNYIVDLL EEUPPPDINDRIHALNGCYKIKINNTYVAGCTTEVEKYSTESERF				LGQALKWQQHQGLLPPGMTIDLFRGKAAVKDVEEEKFPTQLSKH
OCLRRFERAHSKOVICLSFSKDSSOLIASASPOTIRINGKSK TIKKEFRGHSSFVHENTPYOGGHT/15ASDGTVKINMIKTTEGS NTFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVVIMNO GQIVRSFSSKREGGDFVCCALSFRGEHIYCVGDFVLYCFSTV TGKLERFLTVHEKDVIGIAHHPHONILATYSEDGLLKLMKP TGKLERFLTVHEKDVIGIAHHPHONILATYSEDGLLKLMKP TGKLERFLTVHEKDVIGIAHHPHONILATYSEDGLLKLMKP REPROBLEM SEGPPESERSEFFSGREENBEERAGPEBTOP KNPLLQPALTGDVEGLKKIFEDPENPHEQAMQLLLEEDIVGRN LLYARCMAGGSDVIRALAKYGVHLMSKTTRGYTLLHCARAWGKL ETHKALVELDVDIEALNREERARDVAARYSTECVEPLDWADA RLTLKKYIAKVSLAVTDTEKSGSKLEKKNILISAGCRANNEHL ETHKTEASINELFEGRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH DQKRSQDDTSN RCGLIIAFLKGGFIFIYFIFIFETEFLSCCPGWSAVAQSRLIAN FASQVQAIFILPKDSQVGPDVKSERAPKRALYESVFGGGEICGP TSPKRLCIRRSEPVDAVVVVSKHDPLPLLPBANGHRSTNSPTI SPKRLCIRRSEPVDAVVVVSKHDPLPLPBANGHRSTNSPTI SPKRLCIRRSEPVDAVVVVSKHDPLPLPBANGHRSTNSPTI SPKRLCIRRSEPVDAVVVVSKHDPLPLPBANGHRSTNSPTI SPKRLCIRRSEPVDAVVVVSKHDPLPLPBANGHRSTNSPTI SPKRLCIRRSEPVDAVVVVSKHDPLPLPBANGHRSTNSPTI SPKRLCIRRSEPVDAVVVVSKHDPLPLPBANGHRSTNSPTI SPKRLCIRRSEPVDAVVVSKHDPLPLPBANGHRSTNSPTI SPKRLCIRRSEPVDAVVVSKHDPLPKPSTNSLDKG HYFIDRDGQMFRYILNFLRSTKLIDPKSDYLTRELKFTNSVQ VLERLQORGEFIVGSCGGGVDSSQFSVYLRRELKFTNSVQ VLERLQORGEFIVGSCGGGVDSSQFSVYLRRELKFTRVPSVI RIKQEPLD 7002 1043 498 PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVKWP TCSSRLGSRRRILCMCSTSRPCG*GGLCURTAPTRPTTSASS SMTSAGTSWPAGRRTCTATSGTATTTSVMPGCGTMMSTQMSSV PRSSCCSRPATTPPSKPGAPHAPCASSRTLHBHANGSVP PRABGEVC 7003 618 61 QGRFRAFCMGDFILQPFGMLSALLALASKVTLPPHYRYGMSPP GSVADKRNDPWIRRRPVVVSFISDEDWYLFCGDTVEILBGKDA GKGGKVVQVIRQRNWVVVGGINTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIBERFFAGGERRRVSTRSGTIPKPE FPRADGIVPETWINGFKDTSVGTMTTTCGLHTPE GYRLNRIGNKETQYSFKQUFGTHTTYCLKTLQEEVMEAM GIKETT,NTRSIGIEPGARGLLPRTCTURITTVCLHTPE GYRLNRIGNKETQYSFKQUFGTHTTTCSPEGGGLLPRCLDMITNSIGSF QARRYVFKSDRRISMDIQCEVDALLERTVYPCLKTLQEEVMEAM GKRILLFTYGVTGSKTTHTTGSPEGGGLLPRCLDMITNSIGSF QARRYVFKSDRRISMDIQCEVDALLERGKREAMPNPKTSSSKRQ VDPEPADMITVQEFCKAEEVDEDSVYCVYVSTEITNNYITVDLI EEUPPPINPINHILANLOFYKIKINNMYVAGCTTEVEVKSTEERFE	1		İ	IKFGQKSHVECARFSPDGQYLVTGSVDGFIEVWNFTIGKIRKDL
TIKEFRGHSSFWBATFTODGHYIISASSGTVKINNMKTTECS NTFKSLGSTAGTDITVNSVILIPKNPEHFVUCNSSTVVIMMO GQIVRSFSSKREGGDFVCALSFRGEWIYCVGEDFVLYCFSTV TGKLERTLTVHEKDVIGIAHHPHONLIATYBBOCLKLKRP TOKOO 2 827 GPGVVFLEIMESBEPESERSEFFSQREEENEEERAQFPEETGP KNPLLQPALTGDVGLGKIFEDPENPHHEQAMGLLLEEDIVGRN LLYRACCHAGGSDVIRALAKYGVUNLNEKTTRGYTLLHCAAAWGRL ETIKKKYIAKVSLAVTDTEKGSGKLLKEDKNTILISACRAKNEML ETHTHEASINELFERQQLEDIVTPIFKMTTPCQVKSAKSVTSH DQKRSQDDTSN RCCLIIAFLKGCFFFIYPFIFFETEFLSCCFGWSAVAQSRLIAN FASQVQAIFFILPKGSQVGPUVKSEAPKRALYESVFGSGEIGGP TSPKRLCIRSEPYDAVVVVSVKHDPLPLJERAMGHSTMSPFI VSPAIVSPTODSRPMSFRLITTSFSARSLINNGGIPTPAGUTKSN APVHIDVGGMWYTSLATLTKYPESRIGRLFDGTEPIVLDSLKQ HYFIDRDGMFYTLMFLATSKLLIPDPKDYTLLYEBAYFQL QPMLLMSRWKDDRETMFSFPTCECLVVVNAPDLGERITLSGKK SLIEEVFPEIGDVMCMSVAGMNHDSTHVIRFLMGKCHINNSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRTPRVPSVI RIKGSFLD 7002 1043 498 PMPSSTRWTTS*TYTDISSAWACRFTTGTCT*TAAPGPTVWWP TPCSRHQSRRFILTCWCTSTSP.CGR*GGLCVATAPTRPTTSASS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMSTOWSSV PRESSCCSRPATTPPSKGAPHAPCASSRHLAHGLAPSSPGLPA RGGEVC 7003 818 61 QGRFRAFCQRGFLQPFGMRLSALLALASKVTLPPHYRYGMSP RGGEVC 7004 121 2285 FLLPVLTSRSLKQPAVPHARLGGVEFAAMKSARAKTPRKPTVKK G\PKKTL\NTRRSIGIEPCABOLLPNPCPSLG GYKLNENGYKETYDGYCHALAGEVVENAM GIKETR\NTRRSIGIEPCABOLLPNPCPSLG GYKLNENGYKETYGVFTGKETTVVCLHTQEEVMEAM GIKETR\NTRRSIGIEPCABOLLPNPCPSLG GYKLNENGYKETYGVFTGKETTVVCLHTQEEVMEAM GIKETR\NTRRSIGIEPCABOLLPNPCPSLG GYKLNENGGYKETYGVFTGKETTVVCLHTQEEVMEAM GIKETR\NTRRSIGIEPCABOLLPNPCPSLG GYKLNENGGYKETYGVFTGKETTUVCLHTPE GYKLNENGGYKETYGFTGKETTUVCHTTPLTTSSKRQ QAKRYYFKSNORNSMDICCEVDALLERQVERSAMPNPKTSSSKRQ VDPEPADMITVQEFCKAEEVDEDSVGVFSVIEITVNNTYDLHTPE GYKLNENGGYKETYGFTGKETTDWTSSKRQ VDPEPADMITVQEFCKAEEVDEDSVGVFSVIEITVNNTYDLHTE EKUPPPD INPRIJENLOPCVIKKHNMYVAGGCTEVEVKSTEETXP				KYQAQDNFMMMDDAVLCMCFSRDTEMLATGAQDGKIKVWKIQSG
NTFKSLGSTAGTDITWSVILLPKNPERFYCVRRSNTVVIMMOG GQIVRSPSSGKREGGDFVCALSPRGBWIYCVGEDFVLYCFSTV TGKLERTLTVHEKDVIGIAHPHONLIATYSEDGLIKLMKP 7000 2 827 GFGVVFLELMESGOPPGSERSEFFSQREEENEEEEAQDPFETGP KNPLLQPALTGDVGGLQKIFEDPNPHHEQAMQLLLEEDIVGRN LLYAACMAGQSDVIRALAKYGVNLNEKTTRGYTLLHCAAAWGRL ETLKALVELDVDIEALNFREERARDVAARSQTECVEFLDWADA RLTLIKKYIAKVSLAVTDTKKGSGKLLKEDKNTILSACRAKNEKL ETHTEASINELFEQRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH DQKRSQDDTSN 7001 2056 844 RRCLIIAFLKGCFIFTYPIFIFETEFLSCCFGWSAVAQSRLIAN FASGQVAFILIPKDSQVGPDVKSEAPKRALYESVGSGEICGP TSPKRLCIRPSEPVDAVVVVSVKHDPLPLJPEAMGHRSTNSFTI VSFALVSFTODSRPNMSRPLITRSPASPLNNQGIPTPAQLTKSN APVHIDVGGMYTSLATLTKYPESRICHEDGTEPIVDSLKQ HYFIDRQGMPTYSLATLTKYPESRICHEDGTEPIVLDSLKQ QPMLLEMERWKQDRETGRFSRPCECLVVRAPDLGERITLGGK SLIEEVFPEIGDVMCSVAGMNHDSTHVIRPLINSYCHLNSVQ VLERLQQRGFEIVGSCGGGUSSQFSETVLRRELRRTPRVPSVI RIKGEPLD 7002 1043 498 PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWP TPCSRHOGSRRILTCWCSTSRPCGCCGUVTAPTRPTTSASSS SMTSAGTSWPAGRRIGTGATGTTSTYWPGCGTRMMSTQWSSV PRSRSCCSRPATTPPSKFGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLFPHYRYGSPP RGAECC 7004 121 2285 FLLPVLTSRSLGIEECABQLLPNTCFGDTVSILBGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDVRGTMIPSEAP LLHRQVKLVDPMDKRPTEIBWRFTEAGERVRYSTRSGRIIPKPE FPRADGIVPETWIGOPKDTSVEDALERTTVPCLKTLQEEVMEAM GIKETR\NTRSIGIEECABQLLPNTCFDLEG TLLHRQVKLVDPMDRKPTEIBWRFTVSGRIIPKPE GYRLNRNGDYKSTQSSYKQVFGTHTTQKKELFDVVANPLVNDLIH GKNGLLFTTGVTGSGKTHTMTGGGGGGLUPKTDWINDLTPLE GYRLNRNGDYKSTQSSYKQVFGTHTTQKKELFDVVANPLVNDLIH GKNGLLFTTGVTGSGKTHTMTGGGGGGLUPKCLDMIFNSIGSF QAKRYVFKSNDRNNMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEPADMITVQBCCTSCBCFGGGLUPKCLDMIFNSIGSF QAKRYVFKSNDRNNMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEPADMITVQBCCTSCBCDDESVGVVSVISIBIYNTYNDLL LEEUPPPD INPRIJNLINGPVKIKHNNYVAGGTEVEVKSTEELYFE				QCLRRFERAHSKGVTCLSFSKDSSQILSASFDQTIRIHGLKSGK
GQIVESESSCKREGGDFVCCALSPREGBITCVCEDEVLYCFSTV TGKLERTLTVHEKDVIGIAHHPHQNLIATYSBUGLKLMKF TGKLERTLTVHEKDVIGIAHHPHQNLIATYSBUGLKLMKF TGKLERTLTVHEKDVIGIAHHPHQNLIATYSBUGLKLMKF APPHLQPALIGDVEGLQKIFEDPENPHHEQMQLLLEEDIVGRN LLYAACMAGQSDVIRALAKYGVINDEKTRGYTLHCAAMGKL ETHEASINELFEQRQQLEDIVTPIFKMTTPCQVKSAKSVTSH DQKRSQDDTSN 7001 2056 844 RECLIIAFLKGCFIFTYFIFFETEFLSCCFGWSAVAQSRLIAN FASQVQAFFILNESQVGPDVKSEAPKRALYESVFGSGEICGP TSPKRLCIRPSEPVDAVVVVSVKHDPLPLLPEAMGHRSTMSPTI VSPALVSPTODSRPNMSRFLITTSFASFLNNQGIPTPAQLITKSN APVHDVQGMMYTSLATLTKYPESRIGRLEDGTEPIVLDSLKQ HYFIDRDQQMFRYILMFLSTSKLL1PDDFKOYTLLYEEAKYFGL QPMLLEMERWQDRETGFRSRCECLVVVRAPDLGERITLSGDK SLIEBVFFEIGDVMCMSVAAGNHDSTHVIFFPLMGVCHLMSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQEPLD 7002 1043 498 PMPSSTRWTTS*TTTDTSSAWACRPTTGTCT*TAAPGPTVWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVNTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTSVWPGCGTRWMSTOWSSV PRESSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QRFFRAFCWQRDFLQPPGWRLSALLALASKVTLPPHYRYGMSPP GSVADKRNNPPWIRRREVVVEPISDEDWYLFCGDTVEILBGKDA GKGGKVVQVIRQRMWVVVGGLNTHYRYIGKTMDVRGTMISSAP LLHRQVKLVDPMDRKPTEIE MERTFEAGERVRVSTYRSGRIIPKPE FPRADGIVPETWIGSPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETT\NTRRSIGIEFGABQLLPNNCTSLEG GYRLNRNGDYKETQSSKTHTTSGPGEGGLLPRCLDMIFNSIGSF QKRYVVKSNDRNSMDIQCEVDALLERQKREMMPMPKTSSSKRQ VAPRENDRYKTYGSKTHTMTSGFGEGGLLPRCLDMIFNSIGSF QKRYVFKSNDRNSMDIQCEVDALLERQKREMMPMPKTSSSKRQ VAPRENDRYMTYGSCKTHTMTSGFGEGGLLDWINTTYSSKRQ VAPRENDRYMTYGSCKTHTMTSGFGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREMMPMPKTSSSKRQ VAPRENDRYMTYGSCKTHTMTSGFGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREMMPMPKTSSSKRQ VAPRENDRINGNINGLOCEVDENSUGVVSYIEIYNNYIYDLL EEUPPDPINFININGNINGLOCEVDENSUGVVSYIEIYNNYIYDLL EEUPPDPINFININGNINGLOCEVDENSUGVVSYIEIYNNYIYDLL EEUPPPDINFININGNINGNINGNINGNINGTEVEVKSTEERSFE				TLKEFRGHSSFVNEATFTQDGHYIISASSDGTVKIWNMKTTECS
TGKLERTLTVHEKDVIGIAHHPHQNILATYSBUGLKKUMEP 7000 2 827 GPGVVFLEMESEGPPESERSEFSQREENEEEAQPEETOP KNPLLQPALTODVEGLQKI FEDPENPHEQAMQLLLEEDIVGNN LLYAACMAGQSDVIRALAKYGVNINKEKTTGTTLLHCAAAWGRL ETLKALVELDVDI EALMPREBRARDVAARYGOTECVEFLDWADA RLITLKKYIAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEWL ETHTEASINELFEGRQOLEDIVTPIFTKMTTPCQVKSAKSVTSH DOKKSQDDTSN 7001 2056 844 RRCLIIAFLKGCFIFIYFIFIFETELSCCFGWSAVAQSRLIAN FASQVQAIFILPKDSQVGPDVKSEAAPKRALYESVFGSGEICGP TSPKKLCIRSEPVDAVVVVVXKHDPLLPEANGHRSTNSFTI VSPALVSPTODSRPNMSRPLITRSPASPLMNGGIPTPAQLIKSN APVHIDVGGMMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ HYFIDRDGMFRYILNFLRTSKLLIPDDFKDYTLLVEEAKYFQL QPMLLEMERWKQDRETGFSSPCECLVVRVAPDLGERITLSGDK SLIEEVFPEIGDVMCNSVANAGWHIDSTHVITFPLNGYCHINSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQEPLD 7002 1043 498 PMFSSTRWTTS*TYDTSSAWACRPTTGTCT*TAAPGPTVRWP TPCSRHQSRRITCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SMTSAGTSWPAGRRTGTATSGTATTTSVWFGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKFBAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGFKFRFCWQRDFLQPFGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPHIRRPVVVPPISDEDWYLFCGDTVELLEGKDA GKQGKVVQVIRQRNWVVGGLNTHYRIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETK\NTRRSIGIEPGAEQLLPNFCPSLES 7004 121 2285 FLLPVLTSRSLRGPAVPHARLGGVFPAMKSARAKTPRKPTVKK G\PKRTLKTQLG/YYCRVRPLGFPDRCCLEVINNTTVQLHTPE GYKLNRNGDYKETQYSFKQVGTHTTTTQKELFDVVADFLVNDLIH GKGGLFTTGVTGSKSTHTMTGSPGGGGLLBPRCLDMIFNSIGSF QARRYFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDDEFAMNINMQVKGTONSKTINMTYVAGGTTEVEKSTEAFF			}	NTFKSLGSTAGTDITVNSVILLPKNPEHFVVCNRSNTVVIMNMQ
7000 2 827 GPGVVFLELMESGOPESGESEFFSQREENEEEBAGFPEETGP KNPLLQPALTGDVEGLQKI FEDPENPHHEQAMQLLLEEDIVGRN LLYAACMAGGSDVIRALAKYGVMLNEKTTRGYTLLHCAAAWGRL ETLKALVELDUDI EALMFREERARDVAARYSOTECVEFLDWADA RLTLKKY IAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEKL ETHTFASINELFEGRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH DQKRSQDDTSN RRCLIIAFLKGCFIFIYFIFIFETELSCCFGWSAVAQSRLIAN FASQVQAIFILPKDSQVGPDVKSEAAPKRALYESVFGSGEICGP TSPKRLCIRPSEPVDAVVVVSVKHDPLPLLPEANGRRSTNSPTI VSFAIVSPTQDSRPNMSRPLITRSPASPLNNGGIPTPAQLTKSN APVHDDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ HYFIDRDGQMRFYILNFLRTSKLLIPDFKDYTLLISGDK SLIEBVFPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQ VLERLQQRGFEIVGSCGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQFPLD 7002 1043 498 PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWP TPCSRHQGRRFLTCNCSTSRPCGR*GGLCVRTAPTRPTTSASS SWTSAGTSWPAGRRTGTATTSUMPGCTGRMSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKGGKVVQVIRQRNWVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLUDPMDRYFTEIGRFTAGGERVRVSTRSGRIPKEE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETT\NTRRSIGIEPGABQLLDNFCPSLEG 7004 121 2285 FLLPVLTSSERDRPAVFHARFTEAGGERVRVSTRSGRIPKEE GYRLNRNGDYKETQYSFKQUTGTHTTYQELFDVANPLVKDLIH GKRGLLFTVGVGSKKTTHTMTGSPGGGGLLDRAFCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPBPKTSSSKRQ VDPEPADMITVQBFCKAEEUVDEDSVYGFVSYIBIYNNYIYDLL EEUPPPDIEMPLINLINCFVKK KINHMYVAGGTEVEVKSTEBAFF			1	GQIVRSFSSGKREGGDFVCCALSPRGEWIYCVGEDFVLYCFSTV
7000 2 827 GPGVVFLELMESGOPESGESEFFSQREENEEEBAGFPEETGP KNPLLQPALTGDVEGLQKI FEDPENPHHEQAMQLLLEEDIVGRN LLYAACMAGGSDVIRALAKYGVMLNEKTTRGYTLLHCAAAWGRL ETLKALVELDUDI EALMFREERARDVAARYSOTECVEFLDWADA RLTLKKY IAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEKL ETHTFASINELFEGRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH DQKRSQDDTSN RRCLIIAFLKGCFIFIYFIFIFETELSCCFGWSAVAQSRLIAN FASQVQAIFILPKDSQVGPDVKSEAAPKRALYESVFGSGEICGP TSPKRLCIRPSEPVDAVVVVSVKHDPLPLLPEANGRRSTNSPTI VSFAIVSPTQDSRPNMSRPLITRSPASPLNNGGIPTPAQLTKSN APVHDDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ HYFIDRDGQMRFYILNFLRTSKLLIPDFKDYTLLISGDK SLIEBVFPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQ VLERLQQRGFEIVGSCGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQFPLD 7002 1043 498 PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWP TPCSRHQGRRFLTCNCSTSRPCGR*GGLCVRTAPTRPTTSASS SWTSAGTSWPAGRRTGTATTSUMPGCTGRMSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKGGKVVQVIRQRNWVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLUDPMDRYFTEIGRFTAGGERVRVSTRSGRIPKEE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETT\NTRRSIGIEPGABQLLDNFCPSLEG 7004 121 2285 FLLPVLTSSERDRPAVFHARFTEAGGERVRVSTRSGRIPKEE GYRLNRNGDYKETQYSFKQUTGTHTTYQELFDVANPLVKDLIH GKRGLLFTVGVGSKKTTHTMTGSPGGGGLLDRAFCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPBPKTSSSKRQ VDPEPADMITVQBFCKAEEUVDEDSVYGFVSYIBIYNNYIYDLL EEUPPPDIEMPLINLINCFVKK KINHMYVAGGTEVEVKSTEBAFF				TGKLERTLTVHEKDVIGIAHHPHQNLIATYSEDGLLKLWKP
NPLLQPALTGOVEGLQKI FEDDENPHHEQAMQLLLEEDIVGRN LLYAACMAGQSDVIRALAKYGVNLNEKTTRGYTLLHCAAAMGRL ETHKALVELDVOI EALMFREERARDVAARYSOTECVEFLDWADA RLTLKKYIAKVSLAVTOTEKGSGKLLKEDNTT LLSACRAKNEKL ETHTEAS INBLFEQRQLEDIVTPI FKMTTPCQVKSAKSVTSH DOKKSQDDTSN 7001 2056 844 RRCLIIAFLKGCFIFIYFI FFETEFLSCCFGWSAVAQSRLIAN FASQVQAIFILPKDSQVGPDVKSEAAPKRALYESVFGSGEICGP TSPKRLCTRSEPUDAVVVVSVKHDPLPLLPEANGHRSTNSPTI VSFAIVSPTQDSRPNMSRPLITRSPASPLMNQGI PTPAGLTKSN APVHDVGGHWYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ HYFIDROGMRYTILNFLATSKLLIPDDFKDYTLLYEERAKYFGL QPMLLEMERWKQDRETGRFSR PCECLVVRVAPDLGERITLSGDK SLIEEVFEEIGDVMCNSVNAGWNIDSTHVIRFPLNSYCHLNSV VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQEPLD 7002 1043 498 PPMSSTRWTTS*TYTDTSSAWACRFTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRITCMCSTSRPCGR*GGLCVRTAPTPTTSASSS SMTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKFGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPMIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKMYDYGTMIPSEAP LLHRQVKLJOPMDRKPTEIBWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETMIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG GYKLNRNGDYKETQYSFKQVFGTHTTYGELFDVVANPLVNDLIH GKNGLLFTGVGTGSKKTHTMTGSPGGGLIPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERTYVPCLEDHTPSSSKRQ VDPEPADMITVQBFCKAEEUVEDSVYFVSYIBIYNNYIYDLL EKUPPDPINGNINGNYKINGNINMYVAGGTEVEVKSTEKAFF	7000	 	827	GPGVVFLELMESEGPPESERSEFFSQREEENBEEEAQEPEETGP
LLYAACMAGQSDVIRALAKYGVILMEKTTRGYTLHCAAAMGRL ETIKALVELDVDIEALNFREERARDVAARYSQTECUEPLDWADA RLITLKKYIAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEWL ETHTEASINELFEQRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH DQKRSQDDTSN PASQVQAIFILPKDSQVGPDVKSEAPKRALYESVFGSGEICGP TSPKRLCIRPSEPVDAVVVSVKHDPLPLLPBANGHRSTNSPTI VSPATVSPTODSRPMMSRPLITRSPASPLNNGGIPTPAQLTKSN APVHLDVGGHMYTSSLATLTKYPESRIGRLFPGTEIVLDSLKQ HYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQL QPMLLEMERWKQDRSTGRFSRPCECLVVRVAPDLGERITLSGDK SLIEEVFPEIGDVMCNSVNAGNNHDSTHVIRFPLNGYCHLNSVQ VLERLQQRGFEIVGSCGGGVSSGFSEYVLRRELRTPRVPSVVI RIKQEPLD 7002 1043 498 PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAFGPTVRWMP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSWPGGGTRWSTQWSSV PRSRSCCSRPATTPPSKFGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGFRRAFCWQRDFLQPFGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA GKQGKVQVVIRGRNWVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLUPPHDRKSTEIEWRTEAGERURVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTTYPCLKKLQEEVMEAM GIKETT\NTRRSIGIEPGABCLLPNFCPSLEG 7004 121 2285 FLLPVLTSRSLRGPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG/YYCRVRPLGFPDQBCCLEVINNTTVQLHTPE GYKLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTVAVTGSGKTHTTTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDEPFADMITVQSFCKAEEVDEDSVVGVFVSYIEIYNNYIYDLL EEUPPDBINNINNINGFVKIKHNHYVYAGCTEVEVKSTEEAFF	7000	2	1 ""	KNPLLOPALTGDVEGLQKIFEDPENPHHEQAMQLLLEEDIVGRN
### TIKALVELDUDIEALNPREERARDVARYSGTECVEFILDWADA RLITLKKYIAKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEWL ETHTEASINELFEQRQQLEDIVTPIFTKMTTPCQVKSAKSVTSH DQKRSQDDTSN 7001 2056				LIYAACMAGOSDVIRALAKYGVNLNEKTTRGYTLLHCAAAWGRL
RLTLKKY IAKVSLAVTDTEKGSCKLLKEDKNT ILSACRAKNEWL ETHTEAS INELFEQROQLED VTPI FTKMTTPCQVKSAKSVTSH DQKRSQDDTSN RRCLIIAFLKGCFIFIYFIFIFETEFLSCCPGWSAVAQSRLIAN FASQVQAIFILEKDSQVGEDVKSEAPKRALYSEVFGSGEIGGP TSPKRLCIRPSEPVDAVVVSVKIDPLPLIPEANGHRSTINSTI VSPATVSPTODSRPMNSRPLITRSPASPLNNQGIPTPAQLTKSN APVHIDVGGHMYTSSLATLTKYPPSRIGRLFDGTEPIVLDSLKQ QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK SLIEEVFPEIGDVMCNSVNAGWNHDSTHVIRFPLMGYCHILNSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQEPLD 7002 1043 498 PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRRQSRRRICTMCSTSRPCGCLCVWTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSVWPGCGTRWMSTQWSSV PRSRSCCSRPATTPPSKFGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIBWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GLKGTK,NTTRSIGIEPCABGLLPNFCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAMKSARAKTPRKPTVKK G\PKRTLKTOLG/YYCRVRPLGFPDQBCCIEVINNTTVCLHTPE GYRLNRNGDYKETQVSFKVOYGFHTNTGRELFDVANPLVNDL HI GKNGLLFTYGVTGSGKTHTMTGSFGGGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKERAMPPRKTSSSKRQ VDPEPADMITVQEFCKAEEVUDEDVYGVFVSYIEIYNNYIYDLL EEVPPPPINNLHHLNOPVKIKNHYVAGCTEVEVKSTEEAFF	1	1		ETLKALVELDVDIEALNFREERARDVAARYSQTECVEFLDWADA
TOOL 2056 844 RRCLILAFLKGCFIFYFIFIFETEFLSCCFGWSAVAQSRLIAN FASQVQAIFILPKUSCFIFYFIFIFETEFLSCCFGWSAVAQSRLIAN FASQVQAIFILPKUSCVGPDVKSEAAPKRALYESVFGSGEIGGP TSPKRLCIRPSEPVDAVVVVSVHDPLPLLPEANGHRSTNSPTI VSPAIVSPTODSRPMSRPLITRSPASPLNNOGIPTPAQLTKSN APVHLDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ HYFIDRDGGMFRYILMFLRTSKLLIPDDFKDYTLLYEEAKYPQL QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK SLIEEVFPEIGDVMCMSVNAGMNHDSTHVIRFPLMGYCHLNSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKGEPLD PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSACTSWPAGRATGTATTGTUMPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC QGRFRAFCWGDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPFWIRRRPVVVEPISDEDWYLFCGDTVEILBGNDA GKGGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRYSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GINETRYNTRSIGIEFGABGLLPNFCPSLEG GLETRINTTRSIGIEFGABGLLPNFCPSLEG GYRLTKTOLG/YYCRVRPLGFPDQBCCIEVINNTTVOLHTPE GYRLTKNTGLG/YYCRVRPLGFPDQBCCIEVINNTTVOLHTPE GYRLTRYNTGLEFDVANPLNNDLIH GKNGLLFTYGVTGSGKHTMTGSFGGGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERGKEAMPPRKTSSSKRQ VDPEPADMITVQFCKAEEVUPDEDVYGVSYSELYNNYIYDLL EEUPPPDINNLHNLOFVKIKNHYVAGCTEVEVKSTEEAFF		j		RITLKKY I AKVSLAVTDTEKGSGKLLKEDKNTILSACRAKNEWL
7001 2056 844 RRCLIIAFLKGCFIFIYFIFIETEFLSCCPGWSAVAQSRLIAN FASQVQAIFILPKDSQVQPDVKSEAPKRALYRSVFGSGEIGGP TSPKRLCIRPSEPVDAVVVVSVKHDPLPLLPEANGHRSTNSPTI VSPALVSPTODSRPNMSRPLTTRSPASPLNNQGIPTPAQLTKSN APVHIDVGGHMYTSLATLTKYPESRIGRLFDGTEPIVLDSLKQ HYFIDRDGGMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYPQL QPMLLEMERWKQDRETGRFSRPCECLVVRAPDLGERITLSGDK SLIEEVFPEIGDVMCNSVNAGWHDSTHVIRFPLNGYCHLNSVQ VLERLQQRGFEIGDVSGGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQELD PMPSSTRWTTS*TYTDTSSAWAGRPTTGTCT*TAAPGPTVRWWP TDCSRRQSRRRLTCWCSTSRPCGR*eGLCVWTAPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPSCGTRMSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC GSGAGVUNGVIRGRNWVVVGGLNTHYRYIGKTMDYRGTHIPSEAP LLHRQVKLVDPMDRKPTEIEBRFTEAGERRVSSTRGRIIPKF FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRSIGIEPGABQLLPNCPSLEG GYRLNRRGDYKETGJFODGCCIEVINNTYQLHT GGYRLNRRGDYKETQJFODGCCIEVINTYQLHT GGYRLNRRGDYKETQJFODGCCIEVINTYQLHT GGYRLNRRGDYKETQJSFKQVFGTHTTQKELFDVVANPLVNDLH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFSNDRNSMDIQCEVDALLERQKREAMPMPKTSSSKRQ VDPEPADMITVQSFKKAFTYNTYSIGIFPNDNCFYSIEIYNNYIYDLL EEVPPDED INPRILINDCFYKIKNHNMYVAGCTEVEVKSTEEAFF		1	}	FTHTEASINELFEOROOLEDIVTPIFTKMTTPCQVKSAKSVTSH
7001 2056 844 RRCLIIAFLKGCFIFIYPIFIFETEJSCCFGWSAVAQSRLIAN FASQVQAIFILPKDSQVQPDVKSEAAPKRALYESVFGSGEICGP TSPKRLCIRPSEPVDAVVVSVKHDPLPLLPEANGHRSTNSPTI VSPAIVSPTODSRPMSRPLITRSPASPLNNGGIPTPAQLTKSN APVHIDVGGHMYTSSLATLTKYPESRIGRLFFGTEPIVLDSLKQ HYFIDRDGQMFRYILNFLRTSKLLIPPDFKDYTLLYEAKYFQL QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK SLIEEVFPEIGDVMCNSVNAGMNHDSTHVIRFPLNGYCHLNSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQEPLD 7002 1043 498 PMPSSTRWITS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCMCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATTSTVWPGCGTRMMSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGFFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA GKCGKVVQVIRQRNWVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGFKDTSVEDALERTVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPKKPTVKK GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QARRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSKRQ VDPEFADMITVQEFCKAEEVUDEDSVYGVFVSYIBIYNNYIYDLL EEVPPDPINPNLINLNCFYKIKNHMYVAGCTEVEVKSTEBAFE	1			
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TSPKRLCIRPSEPVDAVVVVSVKHDPLLPEANGRISTNSPTI VSPAIVSPTODSRPMNSRPLITRSPASPLNNQGIPTPAQLTKSN APVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ HYFIDRDGQMFRYILMFLRTSKLLIPDDFKDYTLLYEEAKYFQL QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK SLIEEVPPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQEPLD 7002 1043 498 PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRWMSTQWSSV PRSRSCCSRPATTPPSKFGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBEKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPRPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPPFCPSLEG 7004 121 2285 FLDFVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\RTLKTQLG\YYCRVRPLGFPDQBCCIEVINNTTVOLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEPADMITVQEFFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPPDPINPNLHNLNCFYKIKHNMYVAGCTEVEVSSTEBAFE	7001	2056	044	PAGOVOATETI.PKDSOVGPDVKSEAAPKRALYESVFGSGEICGP
VSPAIVSPTQDSRPNMSRPLITRSPASPLNNCGIPTPAQLTKSN APVHIDVGGHNYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ HYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQL QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK SLIEEVPPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQEPLD 7002 1043 498 PMPSSTRWITS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRITCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRITCTWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRITTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG/YYCRVRPLGFPDQRCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMTFNSIGSF QAKRYVFKSNDRNSMDLQCEVDALLERQKREAMPNPKTSSSKRQ VDPEPADMITVQEFFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPPDPINPNLHNLNCFYKIKHNMYVAGCTEVEVKSTEEAFE				TERVEL CIPREFUNDAVAVAVSVKHDPLPLLPEANGHRSTNSPTI
APVHIDVGGHMYTSSLATLTKYPESRIGRLFDGTEPIVLDSLKQ HYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQL QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK SLIEEVFPEIGDWCNSVNAGWNHDSTHVIRFPLMGYCHLMSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQEPLD 7002 1043 498 PMFSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPFWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVQVIRQRWWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTOLG/YYCRVRPLGFPDOBCCIEVINTTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QARRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSKSKQ VDPEFADMITVQBFCKAEEVUDEDSVYGVFVSYIEIYNNYIYDLL EEVPFDPINDHNILNCFVKIKNHMYVAGGTEVEVKSTEBAFE				TSPARECTRESE VDAVVVOVIGEDE ET EN ELETTE PAOLTKSN
HYFIDRDGQMFRYILNFLRTSKLLIPDDFKDYTLLYEEAKYFQL QPMLLEMERWKQDRETGRFSRCECLVVRVAPDLGERITLSGDK SLIEEVFPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQEPLD 7002 1043 498 PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKWPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG/YYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKAEEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPPDPINPNLHNLNCFVKIKHNMYVAGCTEVEVKSTEBAFE	ì			VSPATVSPIQUSKPRIUSKFUI IKSPASI DIRGGIP IVI.DSLKO
QPMLLEMERWKQDRETGRFSRPCECLVVRVAPDLGERITLSGDK SLIEEVFPEIGDVMCNSVNAGMNHDSTHVIRFPLNGYCHLNSVQ VLERLQQRGFEIVGSCGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQEPLD 7002 1043 498 PMPSSTRWTTS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIBWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG\/YYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKAEEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPEDD INPNLHNLNCFYKIKNHMYVAGCTEVEVKSTEEAFE	Ì		1	APVHIDVGGHMIISSIMIBIRIFEBRIORBI DOILL VEFAKVEOL
SLIEEVFPEIGDVMCNSVNAGWNHDSTHVIRFPLNGYCHLNSVQ VLERLQQRGFEIVGSCGGGVDSSQFSEYVLRRELRRTPRVPSVI RIKQEPLD 7002 1043 498 PMPSSTRWITS*TYTDTSSAWACRPTTGTCT*TAAPGPTVRWWP TPCSRHQSRRRLTCWCSTSRPCGR*GGLCVRTAPTRPTTSASSS SWTSAGTSWPAGRRTGTATSGTATTTSVWPGCGTRMWSTQWSSV PRSRSCCSRPATTPPSKPGAPHAPCASSRHLAHGLAPSSPGLPA RGAEVC 7003 818 61 QGRFRAFCWQRDFLQPPGMRLSALLALASKVTLPPHYRYGMSPP GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILBGKDA GKQGKVVQVIRQRMWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG\TYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEPADMITVQBFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPRDPINPNLHNLNCFYKIKNHMYVAGCTEVEVKSTEEAFE	-		1	HYKIDKDGQMFKIILMFEKISKEELFDDFKDIIHELEEFKLIQU
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GKQGKVVQVIRQRNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKFTVKK G\PKRTLKTQLG/YYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKAEEVDEDSVYGVFVSYIEIYNNYIVDLL EEVPFDDINPNLHNLNCFYKIKNHMYVAGCTEVEVKSTEBAFE	/ / / / /	0.0		GSVADKRKNPPWIRRRPVVVEPISDEDWYLFCGDTVEILEGKDA
LLHRQVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNPCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQIG\/YYCRVRPLGFPDQBCCIEVINTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEPADMITVQBFCKAEEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPPDPINPNLHNLNCFYKIKNHMYVAGCTEVEVKSTEBAFE	1		}	GKOGKVVOVIRORNWVVVGGLNTHYRYIGKTMDYRGTMIPSEAP
FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM GIKETR\NTRRSIGIEPGABQLLPNPCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG\YYCRVRPLGFPDDBCCIEVINNTTVQLHTPE GYRLNRRGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEPADMITVQBFCKAEEVDEDSVYGVFVSYIBIYNNYIYDLL EEVPPDPINPNLHNLNCFYKIKNHMYVAGCTEVEVKSTEBAFE	1		ļ	LLHROVKLVDPMDRKPTEIEWRFTEAGERVRVSTRSGRIIPKPE
GIKETR\NTRRSIGIEPGABQLLPNFCPSLEG 7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG\TYCRVRPLGFFDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEPADMITVQBFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPPDPINPNLHNLNCFYKIKNHMYVAGCTEVEVKSTEBAFE				FPRADGIVPETWIDGPKDTSVEDALERTYVPCLKTLQEEVMEAM
7004 121 2285 FLLPVLTSRSLRQPAVPHARLGGVEPAAMKSARAKTPRKPTVKK G\PKRTLKTQLG\TYCRVRPLGFFDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEPADMITVQBFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPPDPINPHNLNCFYKIKNHMYVAGCTEVEVKSTEBAFE	ļ.		1	GIKETR\NTRRSIGIEPGAEOLLPNFCPSLEG
G\PKRTLKTQLG\YYCRVRPLGFPDQBCCIEVINNTTVQLHTPE GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRISMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEPADMITVQBFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPPDPINPHNLNCFYKIKNHMYVAGCTEVEVKSTEBAFE			2205	FLL.DVI.TSPSI.ROPAVPHARI.GGVEPAAMKSARAKTPRKPTVKK
GYRLNRNGDYKETQYSFKQVFGTHTTQKELFDVVANPLVNDLIH GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRINGHDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPFDPINPNLHNLNCFYKIKNHMYVAGCTEVEVKSTEBAFE	7004	121	2285	CARPTLYTOLG AVYCRURPLGFPDORCCIEVINNTTVOLHTPE
GKNGLLFTYGVTGSGKTHTMTGSPGEGGLLPRCLDMIFNSIGSF QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHMYVAGCTEVEVKSTEEAFE	1			CADI NENCHAREAGA LECAME TO LEGACOTE AND LANDITH
QAKRYVFKSNDRNSMDIQCEVDALLERQKREAMPNPKTSSSKRQ VDPEFADMITVQBFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHMYVAGCTEVEVKSTEEAFE	}		1	CANCIL PROCURE CONTURNICE DERCEIL DROLDMI FINSIGSF
VDPEFADMITVQBFCKAEEVDEDSVYGVFVSYIEIYNNYIYDLL EEVPFDPINPNLHNLNCFVKIKNHNMYVAGCTEVEVKSTEEAFE	- 1	l	1	GYNDRIEL I IGA I GOGYTUTHI GOLGGODDI YGCDYLL HOTGOL
		1		QAKKIVEKSNDKNSMDIQUEVDALDEKQAKBAHEREKISSSKAQ
VFWRGQKKRRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNVL				ADARKADWIIAARKACKARRAARRAARAA COMMINING COMMIN
VFWRGQKKRRIANTHLNRESSRSHSVFNIKLVQAPLDADGDNVL				EEAbad Indurance Akt Kuhumi Angere Araz Erula
	1	<u> </u>		VFWRGQKKRRIANTHLNKESSKSHSVFNIKUVQAFDDALGDNVD

		Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning	nucleotide	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	nucleotide	location	Giutamic Acid, Fernenyiaianine, George Melyaine
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence	-	\=possible nucleotide insertion)
	1001		QEKEQITISQLSLVDLAGSERTNRTRAEGNRLREAGNINQSLMT
İ			LRTCMDVLRENOMYGTNKMVPYRDSKLTHLFKNYFDGEGKVRMI
1			VCVNPKAEDYEENLQVMRFAEVTQEVEVARPVDKAICGLTPGRR
1			YRNQPRGP\IGNEPLVTDVVLQSFPPLPSCEILDINDEQTLPRL
			IEALEKRHNLROMMIDEFNKQSNAFKALLQEFDNAVLSKENHMQ
	ļ		GKLNEKEKMISGQKLEIERLEKKNKTLEYKIEILEKTTTIYEED
1	1		KRNLQQELETQNQKLQRQFSDKRRLEARLQGMVTETTMKWEKEC
1			ERRVAAKQLEMONKLWVKDEKLKQLKAIVTEPKTEKPERPSRER
ļ			DREKVTQRSVSPSPVPVSYL
7005	63	876	RNMALYQRWRCLRLQGLQACRLHTAVVSTPPRWLAERLGLFEEL
		İ	WAAQVKRLASMAQKEPRTIKISLPGGQKIDAVAWNTTPYQLARQ
		1	ISSTLADTAVAAQVNGEPYDLERPLETDSDLRFLTFDSPEGKAV
			FWHSSTHVLGAAABQFLGAVLCRGPSTEYGFYHDFFLGKERTIR
		1	GSELPVLERICQELTAAARPFRRLEASRDQLRQLFKDNPFKLHL
1			IEEKVTGPTATVYGCGTLVDLCQGPHLRHTGQIGGLKLLSNSSS
1	1		LWRSSG
7006	22	898	NAFGRHSTAVKMAAAAWLQVLPVILLLLGAHPSPLSFFSAGPAT
/006	22	""	VAAADRSKWHIPIPSGKNYFSFGKILFRNTTIFLKFDGEPCDLS
			LNITWYLKSADCYNEIYNFKAEEVELYLEKLKEKRGLSGKYQTS
			SKLFQNCSELFKTQTFSGDFMHRLPLLGBKQEAKENGTNLTFIG
			DKTAMHEPLQTWQDAPYIFIVHIGISSSKESSKENSLSNLFTMT
[
			VEVKGPYEYLTLEDYPLMIFFMVMCIVYVLFGVLWLAWSACYWR
1			DLLRIQFWIGAVIFLGMLEKAVFYAGFQ
7007	2	1001	AMTVSGPGTPEPRPATPGASSVEQLRKEGNELFKCGDYGGALAA
1		}	YTQALGLDATPQDQAVLHRNRAACHLKLEDYDKAETEASKAIEK
ĺ			DGGDVKALYRRSQALEKLGRLDQAVLDLQRCVSLEPKNKVFQEA
			LRNIGGQIQEKVRYMSSTDAKVEQMFQILLDPEEKGTEKKQKAS
		1	QNLVVLAREDAGAEKIFRSNGVQLLQRLLDMGETDLMLAALRTL
1			VGICSEHQSRTVATLSILGTRRVVSILGVESQAVSLAACHLLQV
j	1	1	MFDALKEGVKKGFRGKEGAIIVGEWKQVWGLLDVTVMEGMGLSQ
İ		-	PGQFFGDQTCSCRLFGIRFGDIILL
7008	70	1478	CRSALGHERPPPAHLPAGGRRLQTCPRSCRWLGRPPSGLPPGPR
/000	/ /	14,0	SPPPLAGPGQKMVQKKPAELQGFHRSFKGQNPFELAFSLDQPDH
			GDSDFGLQCSARPDMPASQPIDIPDAKKRGKKKKRGRATDSFSG
1	1	1	RFEDVYQLQEDVLGEGAHARVQTCINLITSQEYAVKIIEKQPGH
1		1	IRSRVFREVEMLYQCQGHRNVLELIEFFEEEDRFYLVFEKMRGG
			SILSHIHKRRHFNELEASVVVQDVASALDFLHNKGIAHRDLKPE
			NILCEHPNQVSPVKICDFDLGSGIKLNGDCSPISTPELLTPCGS
			AEYMAPEVVEAFSEEASIYDKRCDLWSLGVILYILLSGYPPFVG
			RCGSDCGWDRGEACPACQNMLFESIQEGKYEFPDKDWAHISCAA
1			KDLISKLLVRDAKQRLSAAQVLQHPWVQGCAPENTLPTPMVLQR
			WDSHFLLPPHPCRIHVRPGGLVRTVTVNE
7009	1	626	ARQLRNSWVDDFVAAPLIPLSQQIPTGNSLYESYYKQVDPAYTG
			RVGASEAALFLKKSGLSDIILGKIWDLADPEGKGFLDKQGFYVA
1		1	LRLVACAQSGHEVTLSNLNLSMPPPKFHDTSSPLMVTPPSAEAH
ì		1	WAVRVEEKAKFDGIFESLLPINGLLSGDKVKPVLMNSKLPLDVL
			GRVWDLSDIDKDGHLVRDEFAVAMHLVYRALE
7010	79	571	SHTRRAVVPETLLSPLCPLLGGGTAMSGGEQKPERYYVGVDVGT
1 ,010	''	3,2	GSVRAALVDQSGVLLAFADQPIKNWEPQFNHHEQSSEDIWAACC
1	1		VVTKKVVQGIDLNQIRGLGFDATCSLVVLDKQFHPLPVNQEGDS
	i		HRNVIMWLDHRAVSQVNRINETKHSVLQYVGG
		<u> </u>	RIOTLPHONOSOTOPLLKTPPAVLQPIAPOTTFGVQTQPQPQSL
7011	3	994	KIOITPNONOSOIONPERINAS SANOS S
			LQAQISAASITPLLQTQPQPLLQQPQQKAGLLQPPVRIVSQPQP
		1	ARRLDPPSRFSGRNDRGDQVPNRKDDRSRERERERRRSRERSPQ
		1	RKRSRERSPRRERBRSPRRVRRVVPRYTVQFSKFSLDCPSCDMM
			ELRRRYQNLYIPSDFFDAQFTWVDAFPLSRPFQLGNYCNFYVMH

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	Amino acid begment containing signal peptide
1			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
		sequence	codon, / possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
ì			REVESLEKNMAILDPPDADHLYSAKVMLMASPSMEDLYHKSCAL
			AEDPQELRDGFQHPARLVKFLVGMKGKDEAMAIGGHWSPSLDGP
	•		DPEKDPSVLIKT\AIRCCKALTG
7012	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
1	1		AAAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
			WCEDTDDWYEDDDAGDDGGG ADDDGGAGDOAGDGAGAGAGAGAGAGAGAGAGAGAGAGAG
			VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
1	1	}	TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
	1	1	NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
			DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL
1	1		TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
I	1		PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
1	1		ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP
1			LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
1	\		
1			VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV
1			NLKEKIKBLHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKB
1			YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE
1			FANATPLSTLSLKHWDQDDDFBFTGSHLTVRNGYSCVPVALAEG
1	1	ļ	LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
			PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
	[FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
	i	•	IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
1			RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
[•		
			HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
			AQQSPSM
7013	1	2661	RRAGSVKRGEARLFGPTERQSERPLRPSAARRPEMLSGKKAAAA
			AAAAAAATGTEAGPGTAGGSENGSEVAAQPAGLSGPAEVGPGA
	•		VGERTPRKKEPPRASPPGGLAEPPGSAGPQAGPTVVPGSATPME
	{		TGIAETPEG\RRTSRRKRAKVEYREMDESLANLSEDEYYSEEER
1	}		NAKAEKEKKLPPPPPQAPPEEENESEPEEPSGVEGAAFQSRLPH
1			DRMTSQEAACFPDIISGPQQTQKVFLFIRNRTLQLWLDNPKIQL
	1		TELYLOOLEY DANGED AND AND AND AND AND AND AND AND AND AN
1			TFEATLQQLEAPYNSDTVLVHRVHSYLERHGLINFGIYKRIKPL
			PTKKTGKVIIIGSGVSGLAAARQLQSFGMDVTLLEARDRVGGRV
ł			ATFRKGNYVADLGAMVVTGLGGNPMAVVSKQVNMELAKIKQKCP
1			LYEANGQAVPKEKDEMVEQEFNRLLEATSYLSHQLDFNVLNNKP
1			VSLGQALEVVIQLQEKHVKDEQIEHWKKIVKTQEELKELLNKMV
1			NLKEKIKELHQQYKEASEVKPPRDITAEFLVKSKHRDLTALCKE
1			YDELAETQGKLEEKLQELEANPPSDVYLSSRDRQILDWHFANLE
J	j		FANATPLSTLSLKHWDQDDDFEFTGSHLTVRNGYSCVPVALAEG
1			LDIKLNTAVRQVRYTASGCEVIAVNTRSTSQTFIYKCDAVLCTL
1			
1			PLGVLKQQPPAVQFVPPLPEWKTSAVQRMGFGNLNKVVLCFDRV
1	1	·	FWDPSVNLFGHVGSTTASRGELFLFWNLYKAPILLALVAGEAAG
1		1	IMENISDDVIVGRCLAILKGIFGSSAVPQPKETVVSRWRADPWA
1			RGSYSYVAAGSSGNDYDLMAQPITPGPSIPGAPQPIPRLFFAGE
1			HTIRNYPATVHGALLSGLREAGRIADQFLGAMYTLPRQATPGVP
I			AQQSPSM
7014	3	3950	DFEVGDKIRILATLEDGWLEGSLKGRTGIFPYRFVKLCPDTRVE
	, and the second		ETMALPQEGSLARIPETSLDCLENTLGVEEQRHETSDHEAEEPD
1			
1			CIISEAPTSPLGHLTSEYDTDRNSYQDEDTAGGPPRSPGVEWEM
1	ĺ		PLATDSPTSDPTEVVNGISSQPQVPFHPNLQKSQYYSTVGGSHP
1			HSEQYPDLLPLEARTRDYASLPPKRMYSQLKTLQKPVLPLYRGS
I			SVSASRVVKPRQSSPQLHNLASYTKKHHTSSVYSISERLEMKPG
			PQAQGLVMEAATHSQGDGSTDLDSKLTQQLIEFEKSLAGPGTEP
1			DKILRHFSIMDFNSEKDIVRGSSKLITEQELPERRKALRPPPPR
1	I		PCTPVSTSPHLLVDQNLKPAPPLVVRPSRPAPLPPSAQQRTNAV
1			
			SPKLLSRHRPTCETLEKEGPGHMGRSLDQTSPCPLVLVRIEEME
			SPELLSKHRPTCETLEKEGPGHMGRSLDQTSPCPLVLVRIEEME RDLDMYSRAQEELNLMLEEKQDESSRAETLEDLKFCESNIESLN

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ļ	sequence		\=possible nucleotide insertion)
	 		MELQQLREMTLLSSQSSSLVAPSGSVSAENPEQRMLEKRAKVIE
1			BLLQTERDYIRDLEMCIERIMVPMQQAQVPNIDFEGLFGNMQMV
Ì			IKVSKQLLAALEISDAVGPVFLGHRDELEGTYKIYCQNHDEAIA
			LLEIYEKDEKIQKHLQDSLADLKSLYNEWGCTNYINLGSFLIKP
ļ	ļ.		VQRVMRYPLLLMELLNSTPESHPDKVPLTNAVLAVKEINVNINE
			YKRRKDLVLKYRKGDEDSLMEKISKLNIHSIIKKSNRVSSHLKH
	1		LTGFAPQIKDEVFEETEKNFRMQERLIKSFIRDLSLYLQHIRES
			ACVKVVAAVSMWDVCMERGHRDLEQFERVHRYISDQLFTNFKER
			TERLVISPLNQLLSMFTGPHKLVQKRFDKLLDFYNCTERAEKLK
1		·	DKKTLEELQSARNNYEALNAQLLDELPKFHQYAQGLFTNCVHGY
			AEAHCDFVHQALEQLKPLLSLLKVAGREGNLIAIFHEEHSRVLQ
			QLQVFTFFPESLPATKKPFERKTIDRQSARKPLLGLPSYMLQSE
İ			ELRASLLARYPPEKLFQAERNFNAAQDLDVSLLEGDLVGVIKKK
Į.	· .		DPMGSQNRWLIDNGVTKGFVYSSFLKPYNPRRSHSDASVGSHSS
			TESEHGSSSPRFPRQNSGSTLTFNPN\S\MAVSFTSGSCQKQPQ
	l i		DASPPPKEWDQGTLSASLNPSNSESSPSRCPSDPDSTSQPRSGD
Ì			SADVARDVKQPTATPRSYRNFRHPEIVGYSVPGRNGQSQDLVKG
1			CARTAQAPEDRSTEPDGSEAEGNQVYFAVYTFKARNPNELSVSA
			NQKLKILEFKDVTGNTEWWLAEVNGKKGYVPSNYIRKTEYT
7015	1842	513	RQAWHE\VAAPSWRGARLVQSVLRVWQVGPHVARERVIPFSSLL
1			GFQRRCVSCVAGSAFSGPRLASASRSNGQGSALDHFLGFSQPDS
1			SVTPCVPAVSMNRDEQDVLLVHHPDMPENSRVLRVVLLGAPNAG
1			KSTLSNQLLGRKVFPVSRKVHTTRCQALGVITEKETQVILLDTP
			GIISPGKQKRHHLELSLLEDPWKSMESADLVVVLVDVSDKWTRN
			QLSPQLLRCLTKYSQIPSVLVMNKVDCLKQKSVLLELTAALTEG
			VVNGKKLKMRQAFHSHPGTHCPSPAVKDPNTQSVGNPQRIGWPH
ł			FKEIFMLSALSQEDVKTLKQYLLTQAQPGPWEYHSAVLTSQTPE
]		EICANIIREKLLEHLPQBVPYNVQQKTAVWEEGPGGELVIQQKL
ł			LVPKESYVKLLIGPKGHVISQIAQEAGHDLMDIFLCDVDIRLSV
l			KLLK
7016	167	2513	ILNAPKPPPPRDSVEAVAAKRDTGGGSWGTGMDVSGQETDWRST
			AFRQKLVSQIEDAMRKAGVAHSKSSKDMESHVFLKAKTRDEYLS
}			LVARLIIHFRDIHNKKSQASVSDPMNALQSLTGGPAAGAGIGM
	j		PPRGPGQSLGGMGSLGAMGQPMSLSGQPPPGTSGMAPHSMAVVS
			TATPQTQLQLQQVAAAAAATARSSSSSSRRYSSSSSSSSSKQ
1			FQAQQSAMQQ\QFQA\VVQQQQQL\QQQQQQQQQHLIKLHHQNQQ
			QIQQQQQLQRIAQLQLQQQQQQQQQQQQQQQQQALQAQPPIQQP
1	1		PMQQPQPPPSQALPQQLQQMHHTQHHQPPPQPQQPPVAQNQPSQ
1	1		LPPQSQTQPLVSQAQALPGQMLYTQPPLKFVRAPMVVQQPPVQP
			QVQQQQTAVQTAQAAQMVAPGVQVSQSSLPMLSSPSPGQQVQTP
	1		QSMPPPPQPSPQPGQPSSQPNSNVSSGPAPSPSSFLPSPSPOPF
	1		\QSPVTARTPQNFSVPSPGPLNTPVNPSSVMSPAGSSQAEEQQY
			LDKLKQLSKYIEPLRRMINKIDKNEDRKKDLSKMKSLLDILTDP
			SKRCPLKTLQKCBIALEKLKNDMAVPTPPPPPVPPTKQQYLCQP
']	,	LLDAVLANIRSPVFNHSLYRTFVPAMTAIHGPPITAPVVCTRKR
			RLEDDERQSIPSVLQGEVARLDPKFLVNLDPSHCSNNGTVHLIC
		ļ	KLDDKDLPSVPPLELSVPADYPAQSPLWIDRQWQYDANPFLQSV
	}	1	HRCMTSRLLQLPDKHSVTALLNTWAQSVHQACLSAA
7017	1	1785	INLGNTCYMNSVI*ALFMATDFRRQVLSLNLNGCNSLMKKLQHL
			FAFLAHTQREAYAPRIFFEASRPPWFTPRSQQDCSEYLRFLLDR
			LHEEEKILKVQASHKPSEILECSETSLQEVASKAAVLTETPRTS
	1		DGEKTLIEKMFGGKLRTHIRCLNCRSTSQKAEAFTDLSLAFWPS
	İ		YSLEYMSCPDCSQSPSIQDGGLMQASVPGPSEEPVVYNPTTAAF
			ICDSLVNEKTIGSPPNEFYCSENTSVPNESNKILVNKDVPQKPG
(l			GETTPSVTDLLNYFLAPEILTGDNQYYCENCASLQNAEKTMQIT
[EEPEYLILTLLRFSYDQKYHVRRKILDNVSLPLVLELPVKRITS
	L	· —	VIDENTOIDENTANTEDNANDEDBAKKIIS

Predicted Predicted en Incleotide In				
No: nuclectice corresponding to first maino acid residue of maino acid residue of maino acid residue of maino acid sequence sequ	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first amino acid amino acid residue of amino acid amino acid sequence Proline, Q-Glutamine, R-Arginine, Proline, Q-Glutamine, R-Arginine, Captur	ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
corresponding to first amino acid anino acid residue of amino acid residue of amino acid sequence anino ac	NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
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to first amino acid residue of amino acid residue of amino acid sequence #TYPYTOPHAN, Y-TYYTOPHAN, Y-UNITOP, COGN, Y-POSSIBLE nucleotide deletion, V-POSSIBLE nucleotide deletion, V-POSSIBLE nucleotide insertion) ##TYPYTOPHAN, Y-TYYTOPHAN, Y-TYYTOPHAN, Y-STOP COGN, Y-POSSIBLE nucleotide deletion, V-POSSIBLE nucleotide insertion) ##TYPYTOPHAN, Y-TYYTOPH		corresponding		· · · · · · · · · · · · · · · · · · ·
amino acid residue of amino acid sequence with the property of the proposable nucleotide deletion, "stop codon, "spossible nucleotide deletion, "south common acid sequence "FSILSESMSYDDFTDLSENLANKLKESGTDEASCTKLUPYLLS." FSILSESMSYDDFTDLSENLANKLKESGTDEASCTKLUPYLLS. SVVNISGISESSGIVTY SYARNITSTDESYDWYHGSENLALIASSQ SHILGREDSPSAYFEQDLENKEMSKEWFLFNDERVTFTSPGSVOK, ITSRFFKDTAYVLLIVKGDISTOLSSTVGWHGSENLALIASSQ SHILGREDSPSAYFEQDLENKEMSKEWFLFNDERVTFTSPGSVOK, ITSRFFKDTAYVLLIVKGDISTOLSGIVTY SYAWRITSTDESYDWHIGSENLALIASSQ SHILGREDSPSAYFEQDLENKEMSKEWFLFNDERVTFTSPGSVOK, ITSRFFKDTAYVLLIVKGDISTOLSGIVTHSPGILTSPGDIVD PGSCOPPTOGGGGGGFTVGARLVF 7018 464 1066 SILVFRGNTSGERGHKGSLENLANKGLFVGATRYBE DELECTION OF SILVFRGNTSGERGHKGSLENLANKGLFVGATRYBE DELECTION OF SILVFRGNTSGERGHKGSLENLANKGLFVGATRYBE DELECTION OF SILVFRGNTSGERGHKGSLENLANKGLFVGATRYBE DELECTION OF SILVFRGNTSGERGHKGSLENLANKGLFVGATRYBE DELECTION OF SILVFRGNTSGERGHKGSLENLANKGLFVGATRYBE DELECTION OF SILVFRGNTSGERGHKGSLENLANKGLFVGATRYBE DELECTION OF SILVFRGNTSGERGHKGSLENLANKGLFVGATRYBE DELECTION OF SILVFRGNTSGERGHKGSLENLANKGLFVGATRYBE DELECTION OF SILVFRGNTSGERGHKGSLENLANGGAT D				,
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GRIEREHQIS PGDFPNLKRMQDQLQAQDFSKFQPLKSKLLEVVD DMLAHDIAQLMVLVRQEESQRPIQMVKGGAFEGTLHGPFGHGYG EGAGEGIDDAEWVVARDKPMYDEI FYTLSPVDGKITGANAKKEM VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH ELPPHELPAHLLPPSKRKVAE 7023 2 748 AMVFGGVVPVPQPXDIRRTQNADGFSTYVCLVLLVANILRILF WFGRR FESPLLWGSAIMILTMLLMLKLCTEVRVANELNARRRSF TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG VAGYITYLS IDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA ILGGAYAFARHPQKPAPHAVHPTGTKAL 7024 1207 190 RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV	7022	2	856	
DMLAHDIAQLMVLVRQEESQRPIQMVKGGAFEGTLHGPFGHGYG EGAGEGIDDAEWVVARDKPMYDEIFYTLSPVDGKITGANAKKEM VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH ELPNELPAHLLPPSKRKVAE 7023 2 748 AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSF TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA ILGQAYAFARHPQKPAPHAVHPTGTKAL 7024 1207 190 RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV	1			
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VRSKLPNSVLGKIWKLADIDKDGMLDDDEFALANHLIKVKLEGH ELPNELPAHLLPPSKRKVAE 2 748 AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSF TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA ILGQAYAFARHPQKPAPHAVHPTGTKAL 7024 1207 190 RTGVTGVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV SSRRGSPGTVLGLPFWLLTDVLVSRSIRSMLLLTRSPTAWHRLS QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV	j	1		
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WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSF TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA ILGQAYAFARHPQKPAPHAVHPTGTKAL 7024 1207 190 RTGVTGVVAQVWMFGGGVLSSGEQLQMPVKPERGLGPSDGWLV SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS QLKPPVLPGTLGGQALHLRSWLLSRQOPAETGGQGQPQGFGLRT RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV	<u></u>			·
TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA ILGQAYAFARHPQGFVLSGEQLQMPVKPERGLGPSDGWLV 1207 190 RTGVTGVVAQVWMFGGGGVLSGEQLQMPVKPERGLGPSDGWLV SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS QLKPPVLPGTLGGQALHLRSWLLSRQQPAETGGQGQPQGPGLRT RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV	7023	2	748	AMVFGGVVPYVPQYRDIRRTQNADGFSTYVCLVLLVANILRILF
VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA ILGQAYAFARHPQKPAPHAVHPTGTKAL 7024 1207 190 RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV				WFGRRFESPLLWQSAIMILTMLLMLKLCTEVRVANELNARRRSF
VAGYITYLSIDSALFVETLGFLAVLTEAMLGVPQLYRNHRHQST EGMSIKMVLMWTSGDAFKTAYFLLKGAPLQFSVCGLLQVLVDLA ILGQAYAFARHPQKPAPHAVHPTGTKAL 7024 1207 190 RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV		}		TAADSKDEEVKVAPRRSFLDFDPHHFWQWSSFSDYVQCVLAFTG
EGMSIKMVLMWTSGDAFKTAYFILKGAPLQFSVCGLLQVLVDLA ILGQAYAFARHPQKPAPHAVHPTGTKAL 7024 1207 190 RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQQQPQGPGLRT RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV				
ILGQAYAFARHPQKPAPHAVHPTGTKAL 7024 1207 190 RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQQQPQGPGLRT RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV				
7024 1207 190 RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV				· · · · · · · · · · · · · · · · · · ·
SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV			<u> </u>	
QLKPPVLPGTLGGQALHLRSWLLSRQGPAETGGQGQPQGPGLRT RLL1TGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV	7024	1207	190	RTGVTGVVAQVWMFGGGGVLSSGEQLQMPVKPERGLGPSDGWLV
RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV				SSRRGSPGTVLGLPFWLLTPVLVSRSIRSMLLLTRSPTAWHRLS
RLLITGLFGAGLGGAWLALRAEKERLQQQKRTEALRQAAVGQGD FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV				OLKPPVLPGTLGGOALHLRSWLLSROGPAETGGOGOPOGPGLRT
FHLLDHRGRARCKADFRGQWVLMYFGFTHCPDICPDELEKLVQV				<u> </u>
VRQLEAEPGLPPVQPVFITVDPERDDVEAMARYVQDFHPRLLGL				_ · · · · · · · · · · · · · · · · · · ·
	L		<u></u>	VKOLEAEPGLPPVQPVFTTVDPERDDVEAMARYVQDFHPRLLGL

ID beg	edicted ginning	Predicted end nucleotide	Amino acid segment containing signal peptide (A=Alanine, C=Cysteine, D=Aspartic Acid, E=
	ginning	nucleotide	
NO: nue			
	cleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	cation	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	rresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
to	first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
am	ino acid	residue of	S=Serine, T=Threonine, V=Valine,
re	sidue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	ino acid	sequence	Codon, /=possible nucleotide deletion,
	quence	204	\=possible nucleotide insertion)
	quence		TGSTKOVAOASHSYRVYYNAGPKDEDQDYIVDHSIAIYLLNPDG
			LFTDYYGRSRSAEQISDSVRRHMAAFRSVLS
		832	ERNSPIGNNENL*K\HSLDCLCFRGDWEGNTQFQTLQDNQEECF
7025	232	832	KOVIRTCEKRPTFNQHTVFNLHQRLNTGDKLNEFKELGKAFISG
}			
			SDHTQHQLIHTSEKFCGDKECGNTFLPDSEVIQYQTVHTVKKTY
			ECKECGKSFSLRSSLTGHKRIHTGEKPFKCKDCGKAFRFHSQLS
			VHKRIHTGEKSYECKECGKAFSCG
7026	328	1146	NPNPSIGDIKDIKKAAKSMLDPAHKSHFHPVTPSLVFLCFIFDG
			LHQALLSVGVSKRSNTVVGNENEERGTPYASRFKDMPNFIALEK
)			SSVLRHCCDLLIGVAAGSSDKICTSSLQVQRRFKAMMASIGRLS
			HGESADLLISCNAESAIGWISSRPWVGELMFTFLFGDFESPLHK
		1	LRKSS*LPRKHR*QPINAVRMFLDQCMDGSIALRAIVSEIPVFE
		1	EKKNNG*KGIGEIF*VWGCTLPPHYWGAVTTNVPKLSNSGKLLG
1		1	
		 	QDEQPHIFG GRRLQQQQRPEDAEDGAEGGGKRGEAGWEGGYPEIVKENKLFEH
7027	43	954	
,			YYQELKIVPEGEWGQFMDALREPLPATLRITGYKSHAKEILHCL
l			KNKYFKELEDLEMDGQKVEVPQPLSWYPEBLAWHTNLSRKILRK
1		1	SPHLEKFHOFLVSETESGNISRQEAVSMIPPLLLNVRPHHKILD
			MCAAPGSKTTQLIEMLHADMNVPFPEGFVIANDVDNKRCYLLVH
		,	QAKRLSSPCIMVVNHDASSIPRLQIDVDGRKEILFYDRILCDVP
ł Į			CSGDGTMRKNIDVWKKWTTLNSLQLHGLQLRIATRGAEQL
7028	189	608	SRPPPEPEPGTMVEKGSDSSSEKGGVPGTPSTQSLGSRNFIRNS
1 /020	205		KKMQSWYSMLSPTYKQRNEDFRKLFSKLPEAERLIVDYSCALQR
}			EILLQGRLYLSENWICFYSNIFRWETTISIQLKEVTCLKKEKTA
			KLIPNAIO
		40	VLESNTEAKOATGTSSKLRHGTGQEKGREGPRCPSGLAQLRLWG
7029	1343	40	/PCPHAGRETGPRASAPIPGS*GHGWHW*RKDGRGERSEGPSAL
1		1	SPHSPSLLNMQQAPTHVGPGMGSQRPRSSVVPEQVGVGSQLSRE
1 1			SPHSPSILINMQQAPIHVGPGMGSQAPKSSAVPEQVGVGSQASKE
1		ļ	RWRA*RSLPGAAASERTEMTKERSP/RPCQGYDSSNWFTQPGKK
1			TRKRNSRRNTMVSRGGGCLLYPLQSIMPE*QLR*GAHASPPTQG
1		ì	R*GKGGPRSPLTKASGTTHIPTPFFGSIP/RPTRDSGPGTDNS\
1 1		ţ.	AAPGQKRGHREA*QGPEPV/WGRVTTHLQGPAG*TKPLGS\RNW
1			VPGPAEGEQGEGAGLEGRP*PLKGCRSTLTFSPQLSIPMVGKKP
}		ì	PEGTTASFFP\RSCHSE*RKPPPSCPHAPALSLPHPLPLPLPLPL
		Į.	PLPLPGAGT*HSARSGRPGQSETGSLCHNCHHCPPHCPKCSPGG
			T
7030	<u>2</u>	521	FVCFSAPGSGQGGKRRVNMELSAVGERVFAAEALLKRRIRKGRM
1030	٠	1 224	EYLVKWKGWSQKYSTWEPEENILDARLLAAFEEREREMELYGPK
			KRGPKPKTFLLKAQAKAKAKTYEFRSDSARGIRIPYPGRSPQDL
		1	ASTSRAREGLRN\RVCPRQRAAPAPAAP\PRRGPSGPGPRPG*G
1		1.	POLITICADO CANO CANO CANO CANO CANO CANO CANO CAN
[]·			PGLHFPGPGGPSKHGFVPASEQHQHQQHLPRRGPSGPGPRPG
7031	960	59	HCSVPGAEWPRKPPAQICPQLTSRPHLSSPRSLSPGCGHSPGPG
			/CKPS/RHCDELHEGPSRTAALPCGKPQPKHGVEECG/PCPCLA
		1	PRRLTEPPALTVSPVGRAAPSGAL*PSGRACSACSHRLAPEAAL
			SAAAPRPSLGSGQNASGLPAASLPPQDSSQPHKTVPSPARSVPP
		1	LGAQARAAPPRLWCPRALVSG*EASPEAVSVAAGPPVPGPTPST
			SGSTASHSRRGC*SPR*TPAPPRRDHGRSAAFEVLTAAASAQPC
1		1	ASOGGPRPTGAGRTPSPLGLPFSRGPPAASARPFCRHPSL
7072	1303	3104	RRPGRTEPVEPPPVPPPPRASNSKSRCR*RNLHLAPL*QSPLRK
7032	1393	2104	SRQIGTSSLPFGRSAGERPRPAATFCLSRGGSSPVFL*PSSSSL
1			
1			EPWMKRQFGRLHSLFWKSWQKMNSFLLTPKLDTSLMSGWRYRQR
1			LPRLHTFLKKSLQMASELAPPLPTPAPLASSLPPPPGPPPLLPV
1 1		i .	PLA*LSRSGILVPPNSGFSLSC\PLGDH*GSSGEVRGSCGSPPP
		I.	
			HHCWVLPPPP*LLLPPR RSRDCLSSSATSNRARRSKCSGPKRATPLDSGPGP*APPGPSSA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
<u> </u>	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
[to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
1	amino acid	sequence	Codon, /=possible nucleotide deletion,
ſ	sequence		\=possible nucleotide insertion)
			LMMPSSCPWRTGALGPSPAGSRALGRCTSSVGPGSRWLTRTSSP
		ł	GCATRTWRTMRMEPRPLRSRMGESAPGIPAELPSAAPSGPSAPS
į		}	AAAPSAPTTPAAAGPNTL*SRRTAEWCWPPSCSCCWGWC*SWSA
			WDWRRPPLQVSPAPSSSCRASCCWCLESIT*SSSTARSRATGAS
			SSSTCPTSRSDRGAAWTP\SPMGAPLLPCSVPLISREEALQDPR
I			NPSP*GVCSGSSGHAGLALGKPPVACSVP
7034	92	1942	EDTSSMPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYRERV
			KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
			TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
			RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
	1		FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
		1	TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
Ì		1	IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
		1	YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
		1	TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
i			GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
ł	į		FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
1			FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ
			KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
			QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
Ì		1	. K
7035	92	1942	EDTSSMPFRLLIPLGLLCALLPOHHGAPGPDGSAPDPAHYRERV
l			KAMFYHAYDSYLENAFPFDELRPLTCDGHDTWGSFSLTLIDALD
Ì			TLL\TLFYFQILGNVSEFQRVVEVLQDSVDFDIDVNASVFETNI
			RVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKLLPA
Į.			FQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSL
			TGDPVFEDVARVALMRLWESRSDIGLVGNHIDVLTGKWVAQDAG
	1		IGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNKAIRNYTRFDDW
		,	YLWVQMYKGTVSMPVFQSLEAYWPGLQSLIGDIDNAMRTFLNYY
Į			TVWKQFGGLPEFYNIPQGYTVEKREGYPLRPELIESAMYLYRAT
			GDPTLLELGRDAVESIEKISKVECGFATIKDLRDHKLDNRMESF
}		}	FLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGYI
1			FNTEAHPIDPAALHCCQRLKEEQWEVEDLMREFYSLKRSRSKFQ
			KNTVSSGPWEPPARPGTLFSPENHDQARERKPAKQKVPLLSCPS
			QPFTSKLALLGQVFLDSS*PLDNFFIFIFLRLNYNKLLLAIIKK
			K
7036	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
1			RNW*BRKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
	<u> </u>		PPPPPPPPPRRPPRNRRPG
7037	442	761	CLAPLFSCFQIINLHLAPSGRLRWAWLRGPGRN*LPGEGPSIPT
			RNW+ERKAGCSQPC/PAQQHHGRPPGVSPLPRDPHPTTLRPLPP
1		_	PPPPPPPPPRRPPRNRRPG
7038	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
			QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
			LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
			QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
1		}	LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
1			LQEAASPAAERACRSSKGTSTSRTG
7039	155	891	GAGAASDMSSGLRAADFPRWKRHISEQLRRRDRLQRQAFEEIIL
			QYNKLLEKSDLHSVLAQKLQAEKHDVPNRHEISPGHDGTWNDNQ
-	1	1	LQEMAQLRIKHQEELTELHKKRGELAQ\RVIDLNNQMQRKDREM
	4		QMNEAKIAECLQTISDLETECLDLRTKLCDLERANQTLKDEYDA
	1		LQITFTALEGKLRKTTEENQELVTRWMAEKAQEANRLNARE*KR
			LQEAASPAAERACRSSKGTSTSRTG
7040	34	789	KITPPRRPHRCSSGHGSDNSSVLSGELPPAMGKTALFYHSGGSS
	1		GYESVMRDSEATGSASSAQDSTSENSSSVGGRCRSLKTPKKRSN
			

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	
1			(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
ł		Bequence	\=possible nucleotide insertion)
ļ	sequence		
			PGSQRRRLIPALSLDTSSPVRKPPNSTGVRWVDGPLRSSPRGLG
			EPFEIKVYEIDDVERLQRRRGGASKEAMCFNAKLKILEHRQQRI
			AEVRAKYEWLMKELEATKQYLMLDPNKWLSEFDLEQVWELDSLE
ļ	1		YLEALECVTERLESRVNFCKAHLMMITCFDIT
7041	1	567	SGRVAMGRRRAPAGGSLGRALMRHQTQRSRSHRHTDSWLHTSEL
1	, -	1	NDGYDWGRLNLOSVTEOSSLDDFLATAELAGTEFVAEKLNIKFV
ļ	1	1	
		1	PAEARTGLLSFEBSQRIKKLHEENKQFLCIPRRPNWNQNTTPEE
	1	1	LKQAEKDNFLEWRRQL\VRLEEEQKLILTPFERNLDFWRQLWRV
ļ	}	1	IERSDIVVQIVDA
7042	7	345	PIHMAAAALRADI\ISPLFPHIQGYLLLSASHG\ATSLHTKGAL
	1	Ì	PLETVTMYTVIPKSKYVLVKPDTQYPYSENLDEFKRLAENSASN
			DDLLMAEVAISDYGDKLTLELREKY
7043	2	2170	ARGMAARDSDSEEDLVSYGTGLEPLEEGERPKKPIPLQDQTVRD
1 ,043	1	21/0	
1			EKGRYKRFHGAFSGGFSAGYFNTVGSKEGWTPSTFVSSRQNRAD
	1	1	KSVLGPEDFMDEEDLSEFGIAPKAIVTTDDFASKTKDRIREKAR
Į.	1	i	QLAAATAPIPGATLLDDLITPAKLSVGFELLRKMGWKEGQGVGP
l l	1		RVKRRPRRQKPDPGVKIYGCALPPGSSEGSEGEDDDYLPDNVTF
1			APKDVTPVDFTPKDNVHGLAYKGLDPHQALFGTSGEHFNLFSGG
]	1	1	SERAGDLGEIGLNKGRKLGISGQAFGVGALEEEDDDIYATETLS
			KYDTVLKDEEPGDGLYGWTAPRQYKNQKESEKDLRYVGKILDGF
	1	1	SLASKPLSSKKIYPPPELPRDYRPVHYFRPMVAATSENSHLLOV
			LSESAGKATPDPGTHSKHQLNASKRAELLGETPIQGSATSVLEF
	į .		
	1		LSQKDKERIKEMKQATDLKAAQLKARSLAQNAQSSRAQPSPAAA
			AGHCSWNMALGGGTATLKASNFKPFAKDPEKQKRYDEFLVHMKQ
			GQKDALERCLDPSMTEWERGRERDEFARAALLYASSHSTLSSRF
1	1	1	THAKEEDDSDQVEVPRDQENDVGDKQSAVKMKMFGKLTRDTFEW
	1		HPDKLLFQ/RLVGLPRVKRDKYSVFNFLTLPETASLPTTQASSE
į			KVSQHRGPDKSRKPSRWDTSKHEKKEDSISEFLRLARSKAEPPK
]	1		QQSSPLVNKEEEHAPELSAN
7044	276	734	
/044	276	/34	EVYLTDEFAKGRKVADLYELVQYAGNIIPRLYLLITVGVVYVKS
			FPQSRKDILKDLVEMCRGVQHPLRGLFLRNYLLQCTRNILPDEG
ŀ	İ		EPTDEETTGDISDSMDFVLLNFAEMNKLWVRMQHQGHSRDREKR
{	}	1	ERERQELRILVGTNLVRLSQV
7045	3	513	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP
	1		KANOWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK
	1	1	DLEFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
			ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEOSQG
7046		F13	
/046	3	513	LGFKMEALSRAGQEMSLAALKQHDPYITSIADLTGQVALYTFCP
		1	KANQWEKTDIEGTLFVYRRSASPYHGFTIVNRLNMHNLVEPVNK
		1	DLBFQLHEPFLLYRNASLSIYSIWFYDKNDCHRIAKLMADVVEE
	1	I	ETRRSQQA/RSGQTESQPGQWLQRPQAHRHPGDAEQSQG
7047	103	486	QMKIEKCGWSEGLTSIKGNCHNFYTAISKDVTYKELKNLLNSKN
			IMLIDVREIWEILEYQKIPESINVPLDEVGEALQMNPRDFKEKY
			NEVKPSKSDS/IVFSYLAGVRSKKALDTAISLGFHSYYER
7048	92	627	FFCLTLLSSWDYRHHATRRVISSPVFTMEDSGKTFSSEEEEANY
,040	1 34	02/	
1	1	<u> </u>	WKDLAMTYKQRAENTQEELREFQEGSREYEAELETQLQQIETRN
			RDLLSENNRLRMELETIKEKFEVQHSEGYRQISALEDDLAQTKA
			IKDQLQKYIRELEQANDDLERAKRATDHGLSKTFE\QRLN\QAI
			EKKW
7049	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL
1	1		VPVFEAVGRIYELRLMMDFDGKNRGYAFVMYCHKHEAKRAVREL
1	1	1	NNYEIRPGRLLGVCCSVDNCRLFIGGIPKMKKREEILEEIAKVT
}			EGVLDVIVYASAADKMKNRGLRLRGVREPPRGCHWLGRKLIAWX
	L		ASSLWG
7050	393	938	KRTGSASYGGPPPGLGGPATXASVAGRCSSVGKIPARRCYEDEL

Predicted Pred		15-31-5	T	
Note nucleotide corresponding to first maino acid residue of maino acid residue of maino acid residue of maino acid sequence very colon,	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
corresponding to first amino acid amino acid residue of amino acid residue of amino acid sequence seq				(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
to first amino acid residue of seidue of seidue of amino acid residue of amino acid sequence Popoline, U-Gultamine, N-Arghanje, SSERINE, T-Threonine, V-Valine, Manino acid sequence	NO:			
to first amino acid residue of amino acid aresidue of security of the control of		_		
### amino acid residue of amino acid sequence whitphophan, Y-Tyropine, X-Winknown, *=stop Codon, /=possible nucleotide deletion, \	ĺ			
maino acid sequence W-Tryptophan, Y-Tyxcoine, X-Unknown, *=Stop Coden, /=possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide deletion, A-possible nucleotide insertion) V-VPERVORTYSELEM/POPURDER/SERVE/PVWYCHERAXE/NUREL NYSIR PGRILDVICYSARD/PMWRRCBILES/ARVYYCHERAXE/NUREL NYSIR PGRILDVICYSARD/PMWRRCBILES/ARVYYCHERAXE/NUREL NYSIR PGRILDVICYSARD/PMWRRCBILES/ARVYYCHERAXE/NUREL NYSIR PGRILDVICYSARD/PMWRRCBILES/ARVYYCHERAXE/NUREL NYSIR PGRILDVICYSARD/PMWRRCBILES/ARVYYCHERAXE/NUREL NYSIR PGRILDVICYSARD/PMWRRCBILES/ARVYYCHERAXE/NUREL NYSIR PGRILDVICYSARD/PMWRYYCHARVYYCH/MCO/PMC/PMC/PMC/PMC/PMC/PMC/PMC/PMC/PMC/PMC		1	1	
amino acid sequence Codon, /-possible nucleotide deletion, \p	ì	amino acid	residue of	
Sequence N-possible mucleotide insertion		residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
VPVPEAVORTYPELRIMMPDTGSNINGYAFWYCHKHEAKRANGE NYTER PORTLIQUCCS VUNCENT FEGT TRYMKKER LIBETARYT EGYLDVI VYASAADEMKNINGERLIGGYREPPRGCHMLGRKLIAWX ASSEM'G KEMMLABE CONTAKKOREYALLGNYDSSNIVYYGOVMQOI GOHCOS. VRDPAI KOKWQOVRQELLEEYEQVKS IVGTLESFKILKPEP PIP PV SCQDEPFEDPAWP PPVPAEHRAPPOIRR / RQSRSKYSEERINGR SRSPGTCFFST\F15KSBKPSTSRDKDVRARGGEDKKRNKNMPD ASSOCIAMPRFGAGATOKDLVEALERED VSRMS I HANDOLADLEGA KKLLREAGVILPMM** SCCRORKMSKLUMPEEMTSCHYVSTDSYNHFHAHDOLADLEGA KKLLREAGVILPMM** KKLLREAGVILPMM** 7052 467 715 SCCRORKMSKLUMPEEMTSCHYVSTDSYNHFHHEMIKDEVRTL TYRNSMYSHNKHVPKDKVVLDVGSGTGILSMPAARGGERR 7053 467 715 SCCRORKMSKLUMPEEMTSCHYVSTDSYNHFHHEMIKDEVRTL TYRNSMYSHNKHVPKDKVVLDVGSGTGILSMPAARGGERR 7054 1 1036 GTSGORKMSKLUMPEEMTSCHYVSTSYNHHAMRGOPERR 7054 1 1036 GTSGORKMSKLUMPEEMTSCHYVSTSYNHHAMRGOPERR 7056 1 1036 GTSGORKMSKLUMPEEMTSCHYVSTSYNHHAMRGOPERR 7057 1036 GTSGORKMSKLUMPEEMTSCHYVSTSYNHHAMRGOPERR 7058 2 GTSCORKMSKLUMPEEMTSCHYVSTSYNHHAMRGOPERR 7059 2 SCREWSWSSHANEYNHAMSCHYLLIFIKING 7057 1368 1036 GTSGORKMSKLUMPEEMTSCHYTHAMRGOPERR 7058 2 SCREWSWSSHLANE/WGKHLCLIFIKLSHIVLIFWHT 7057 1368 431 GTYLINMSKYLERALDESTLLIPMCRTLLAYING SCREWSWSSHLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP EYHYLHQMLG/ALCISBASSVUNLGSLLILPMCRTLLAYING SCREWSWSSHLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP EYHYLHQMLG/ALCISBASSVUNLGSLLILPMCRTLLAYING SCREWSWSSWLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP EYHYLHQMLG/ALCISBASSVUNLGSLLILPMCRTLLAYING SCREWSWSSWLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP EYHYLHQMLG/ALCISBASSVUNLGSLLILPMCRTLLAYING SCREWSWSSWLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP EYHYLHQMLG/ALCISBASSVUNLGSLLILPMCRTLLAYING SCREWSWSSWLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP EYHYLHQMLG/ALCISBASSVUNLGSLLILPMCRTLLAYING SCREWSWSSWLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP SYNYSEDFVLUNARYROPP PTRILEFTSTSJOPSHKNTILDMCRTLLAYING SCREWSWSSWLANE/WGKHLGGSTNJBLAGSLILLDMCRTLLAYING SCREWSWSSWLANGAGAR SCREWSWSSWLAN		amino acid	sequence	
VPVPEAVORTYPELRIMMPDTGSNINGYAFWYCHKHEAKRANGE NYTER PORTLIQUCCS VUNCENT FEGT TRYMKKER LIBETARYT EGYLDVI VYASAADEMKNINGERLIGGYREPPRGCHMLGRKLIAWX ASSEM'G KEMMLABE CONTAKKOREYALLGNYDSSNIVYYGOVMQOI GOHCOS. VRDPAI KOKWQOVRQELLEEYEQVKS IVGTLESFKILKPEP PIP PV SCQDEPFEDPAWP PPVPAEHRAPPOIRR / RQSRSKYSEERINGR SRSPGTCFFST\F15KSBKPSTSRDKDVRARGGEDKKRNKNMPD ASSOCIAMPRFGAGATOKDLVEALERED VSRMS I HANDOLADLEGA KKLLREAGVILPMM** SCCRORKMSKLUMPEEMTSCHYVSTDSYNHFHAHDOLADLEGA KKLLREAGVILPMM** KKLLREAGVILPMM** 7052 467 715 SCCRORKMSKLUMPEEMTSCHYVSTDSYNHFHHEMIKDEVRTL TYRNSMYSHNKHVPKDKVVLDVGSGTGILSMPAARGGERR 7053 467 715 SCCRORKMSKLUMPEEMTSCHYVSTDSYNHFHHEMIKDEVRTL TYRNSMYSHNKHVPKDKVVLDVGSGTGILSMPAARGGERR 7054 1 1036 GTSGORKMSKLUMPEEMTSCHYVSTSYNHHAMRGOPERR 7054 1 1036 GTSGORKMSKLUMPEEMTSCHYVSTSYNHHAMRGOPERR 7056 1 1036 GTSGORKMSKLUMPEEMTSCHYVSTSYNHHAMRGOPERR 7057 1036 GTSGORKMSKLUMPEEMTSCHYVSTSYNHHAMRGOPERR 7058 2 GTSCORKMSKLUMPEEMTSCHYVSTSYNHHAMRGOPERR 7059 2 SCREWSWSSHANEYNHAMSCHYLLIFIKING 7057 1368 1036 GTSGORKMSKLUMPEEMTSCHYTHAMRGOPERR 7058 2 SCREWSWSSHLANE/WGKHLCLIFIKLSHIVLIFWHT 7057 1368 431 GTYLINMSKYLERALDESTLLIPMCRTLLAYING SCREWSWSSHLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP EYHYLHQMLG/ALCISBASSVUNLGSLLILPMCRTLLAYING SCREWSWSSHLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP EYHYLHQMLG/ALCISBASSVUNLGSLLILPMCRTLLAYING SCREWSWSSWLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP EYHYLHQMLG/ALCISBASSVUNLGSLLILPMCRTLLAYING SCREWSWSSWLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP EYHYLHQMLG/ALCISBASSVUNLGSLLILPMCRTLLAYING SCREWSWSSWLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP EYHYLHQMLG/ALCISBASSVUNLGSLLILPMCRTLLAYING SCREWSWSSWLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP EYHYLHQMLG/ALCISBASSVUNLGSLLILPMCRTLLAYING SCREWSWSSWLANE/WGKHLCLIFIKLSHNVLLFWKTFLLYNGGP SYNYSEDFVLUNARYROPP PTRILEFTSTSJOPSHKNTILDMCRTLLAYING SCREWSWSSWLANE/WGKHLGGSTNJBLAGSLILLDMCRTLLAYING SCREWSWSSWLANGAGAR SCREWSWSSWLAN		sequence		\=possible nucleotide insertion)
NNYSIEPGRILGVCSVUDNCH.PIGGIPRMKKRERILEZIAVT GUVLOVIVASALWKNGRENGENERPRGCHMLGRKLIAMX ASSLWG		<u> </u>		
ROYLDVIVYASAADEMKNRGLELRGVREPRGCHMLGRKLIAMX ASSLWG	ľ			_
ASSLING ***REMILABE IODNAKKGREVALLGNYDSSNYTYGOVNGOIGRHCGS** ***VRDPAIKGKWQOVRQELLEEYEQVKSIVGTLESPKIDKPPDPPV** SCQDEPFRDPAIWP PPVPAEHRAPPGIRR/FGGRENTSERRIGR SRSFGTCRPST\PISKSERSFSTERDKDYRARGDDKGRKNMCDGA ASOGEMPKFCAGYDKDLVEALERDIVSRPPSIHMDIADLEA KKLIREAGVIJEMMM** ***7052** 467** 715***SCPGRGKMSKLLAPEEMTSRDYTPDSYAHFGIHEMIKDEVKTL TYRNSMYINKHVYEKKVVLDVGSGTGILSMPAARGGPRR** 7053** 467** 715**SCPGRGKMSKLLAPEEMTSRDYYFDSYAHFGIHEMIKDEVKTL TYRNSMYINKHVYEKKVVLDVGSGTGILSMPAARGGPRR** 7054** 1 1036**CTSGRSFTDARRSAGEPFAALEPPAALEEMDLKDEVKTL TYRNSMYINKHVYEKKVVLDVGSGTGILSMPAARGGPRR** 7054** 1 1036**CTSGRSFTDARRSAGEPFAALEPPAALEEMDLEGDESEVDIJ TYRNSMYINKHVYEKKVVLDVGSGTGILSMPAARGGPRR** 7054**CTSGRSFTDARRSAGEPFAALEPPAALEEMDLEGDESEVDIJ TYRNSMYINKHVYEKKVVLDVGSGTGILSMPAAGGPRR** 7056**CTSGRSFTDARRSAGEPFAALEPPAALEEMDLEGDESEVDIJ VQLRQAIEBCKQVILEBRPYKESKSVKGTCDKTINGLGDGSEVDIJ TYRNSMYINKHLEBRPYKESKSKVKGTCDKTINGLGDGSEVDIJ VQLRQAIEBCKQVILEBRPYKESKSVKGTCDKTINGLGDGSEDUJ VQLRQAIEBCKQVILEBRPYKESKSVKVGTCDKTINGLGDGSEDUJ TYRCACCARPI/CS/JDAVVSBARGCDYTGGYCSHCHNDLAV VQLRQAIEBCKQVILEBRPYKESKSVKVGTCDKTINGLGDKGD TYRCACCARPI/CS/JDAVVSBARGCDYTGGYCSHCHNDLAV TERRIVANDELGERGENDAVARLINGLIDERGTELLSTURG PSYNTYSEDFVELINARYTDEDEPKLLFTTVGGITGCMEVVLFL M ***SERVSWSSELTABLDKSRTFHITTCGATICTFSCHVAAHLVVALIN FSVNYSEDFVELINAARYNDEDPRKLLFTTVGLTGVCMEVVLFL M ***SERVSWSSELTABLDKSRTFHITTCGATICTFSCHVAAHLVVALIN FSVNYSEDFVELINAARYNDEDPRKLLFTTVGLTGVCMEVVLFL M ***SUNYSEDFVELINAARYNDEDPRKLLFTTVGLTGVCMEVVLFL M ***SUNYSEDFVELINAARYNDEDPRKLLFTTVGLTGVCMEVVLFL M ***SUNYSEDFVELINAARYNDEDPRKLLFTTVGLTGVCMEVVLFL M ***SUNYSEDFVELINAARYNDEDPRKLLFTTVGLTGVCMEVVLFL M ***SUNYSEDFVELINARRYNDEDPRKLLFTTVGLTGVCMEVVLFL M ***SUNYSEDFVELINAARYNDEDPRKLLFTTVGLTGVCMEVVLFL SSDFVKIGKTTTGKTTTCGATICTFSCHVAAHLVVALIN SSDFVKIGKTTTTGKTTTCGATICTFSCHVAAHLVVALIN FSVNYSEDFVELINAARYNDEDPRKLLFTTVGLTGVCMEVVLFL SSDFVKIGKTTTTGKTTCGATICTFSCHTTAARTYNDEDPRTLARGCATTLARYNDELGGATARTYNDELGTTTGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	ļ	•		
Total	Į.		}	
VRDPATKKKMQOVRGELLEEYEQVISTUGILESFKIDKPPDPP SCQDEFFEDPAVPPPPVPAHRAPPOTRER, PGSKTSERNGEN SCRSPGTCRPST\LISKSEKPSTSKROKRARGEN SCRSPGTCRPST\LISKSEKPSTSKROKPARGENDKGRKOMADG ASDGEMFKFDGAGYDKDLVEALERDIVSRNPSIHMODIADLEA KKLIREAGVLDMMM 7052 467 715 SCPGGKMSKLLNPEEMTSKDYYFDSYAHFGIHEMLKDEVRTL TYRNSMYHNKHVFKOKVULDVGGGTGILSMPAARGEPR 7053 467 715 SCPGGKMSKLLNPEEMTSKDYYFDSYAHFGIHEMLKDEVRTL TYRNSMYHNKHVFKOKVULDVGGGTGILSMPAARGEPR 7054 1 1036 GTSGSSFETDAERESAGEPTSALDPYSBAHFGIHEMLKDEVRTL TYRNSMYHNKHVFKOKVULDVGGGTGILSMPAARGEPR 7054 1 1036 GTSGSSFETDAERESAGEPTSALDPYBAARGEPRSCPCEPLGFG RCCRNDAMEYDEKLARPRQAHLNPFNKGSGRQHCQTDGEVPD VTPERALPELDPGEFFRCPERVMDLGISSDEVSTEPLGFG RCCRNDAMEYDEKLARPRQAHLNPFNKGSGRQHCQTDGEVPD VTPERALPELDPGEFFRCPERVMDLGISSDEVSRCHGLOPGEVPD VTPERALPELDPGSEKGKDAVVRLIHHRIKLQELKD PNEDEPNIRVLLBHRPYKERSKVKVCTCOKTGHSARGOVTGLEKD DYRCASCRAPI-CS/DGVVPSKVSHQASYSLNICPETGLDSQ DYRCASCRAPI-CS/DGVVPSKRVGKVCTCHMDLAV IPARVVHNNDEPRKVSRCSMRVLALMVSRPVLRIRSIN PNEXASEAGCCYTTGYCHGHNDLAV IPARVVHNNDEPRKVSRCSMRVLALMVSRPVLRIRSIN FSVNYSEDFVELHAARVXRDEDPRKLLFTTVPGLTGVCMBVVLFJ M 7055 2 527 DSRRVSWRSKLANE/WGKHLCLFIWLSMVLLFWKTFLLYNGOF EYHYLMQMG/ALCLSRASASVLNINGSLILLPMCRTLLAYLRG SQKVPSRRTRRLLDKSRFFHITTGATICISSGVHVAAHLVNALN FSVNYSEDFVELNAARVXRDEDPRKLLFTTVPGLTGVCMBVVLFJ M 7056 2 527 DSRRVSWRSKLANE/WGKHLCLFIWLSMVVLLFWKTFLLYNGOF EYHYLMQMG/ALCLSRASASVLNINGSLILLPMCRTLLAYLRG SQKVPSRTRELLDKSPFHITTGATICISSGVHVAAHLVNALN FSVNYSEDFVELNAARVXRDEDPRKLLFTTVPGLTGVCMBVVLFJ M 7057 1368 431 GIYLHVNEKIPRTCIGDRQENDKENINLENHRQELLHASCQA SGEVPSQASLRGFFTEDEPGCFGGGRNIPFALQNIQDEGTGGL SPQGKISSGNGGNGFTTTEDEPGCTGGGGGGRAFTYPQCTCKKAPLR SSDFVLNGGTTTGERCYCCXGFSPFSKSSSI DRKGGGGGGGFFTTGENGAGGGGGGAFTYPGGGGGGGRAFTYPQCTCKKAPLR SSDFVLNGGTTGSFTSGAGGFFTTGEFGCCTGCGRNTHLFKKKYBFYQCGGGGGFFTHAERTHTGKSSI CYLSFFDEMSGCGGGGGFFTMADGGGGGGGGAFTTGGGGGGGGAFTTGAGL SSDFVLNGGTTGGGGGGGGAFTTGAGGGGGGGAFTTGAGGGGGGGAFTGAGGGGGGGAFTGAGGGGGGGAFTGAGGGGGGAFTGAGGGGGGGAFTGAGGGGGGGAFTGAGGGGGGGAFTGAGGGGGGAFTGAGGGGGGGAFTGAGGGGGGAFTGAGGGGGGAFTGAGGGGGGGAFTGAGGGGGGAFTGAGGGGGGGAFTGAGGGGGGAFTGAGGGGGGAFTGAGGGGGGAFTGAGGGGGGA	7051	119	816	
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7059 1 1178 WPAFPRQPAAAAMDALLGTGPRRARGCLGAAGPTSSGRAARTPA APWARPSAWLECVCVVTFDLBLGQALELVYPNDFRLTDKEKSSI CYLSFPDSHSGCLGDTQFSFRMRQCGGQRSPWHADDRHYNSRAP VALOREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL FQALLSLIAPEYPDKLAPCLEAVCSEIDQWPAPAPGQTLNLPVM GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL QPLRFCCDFRPYFTIHDSEFKBFTTRTQAPPNVVLGVTNPFFIK TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP 7060 90 1670 SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ	1			ARN*SCTQLLQHPQLCTLPFLILA
APWARPSAWLECVCVVTFDLELGQALELYYPNDFRLTDKEKSSI CYLSFPDSHSGCLGDTQFSFRMRQCGGQRSPWHADDRHYNSRAP VALQREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL FQALLSLIAPEYFDKLAPCLEAVCSEIDQWPAPAPGQTLNLPVM GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL QPLRFCCDFRPYFTIHDSEFKBFTTRTQAPPNVVLGVTNPFFIK TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP 7060 90 1670 SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ	7059	1	1178	
CYLSFPDSHSGCLGDTQFSFRMRQCGGQRSPWHADDRHYNSRAP VALQREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL FQALLSLIAPEYFDKLAPCLEAVCSEIDGWPAPAPGQTLNLPVM GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL QPLRFCCDFRPYFTIHDSEFKBFTTRTQAPPNVVLGVTNPFFIK TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP 7060 90 1670 SVNLPPSLWFWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ	1			17
VALQREPAHYFGYVYFRQVKDSSVKRGYFQKSLVLVSRLPFVRL FQALLSLIAPEYFDKLAPCLEAVCSEIDQWPAPAPGQTLNLPVM GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL QPLRFCCDFRPYFTIHDSEFKBFTTRTQAPPNVVLGVTNPFFIK TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP 7060 90 1670 SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ		ļ		_
FQALLSLIAPEYFDKLAPCLEAVCSEIDQWPAPAPGQTLNLPVM GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL QPLRFCCDFRPYFTIHDSEFKBFTTRTQAPPNVVLGVTNPFFIK TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP 7060 90 1670 SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ		1		
GVVVQVRIPSRVDKSESSPPKQFDQENLLPAPVVLASVHELDLF RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL QPLRFCCDFRPYFTIHDSEFKBFTTRTQAPPNVVLGVTNPFFIK TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP 7060 90 1670 SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ				1
RCFRPVLTHMQTLWELMLLGEPLLVLAPSPDVSSEMVLALTSCL QPLRFCCDFRPYFTIHDSEFKEFTTRTQAPPNVVLGVTNPFFIK TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP 7060 90 1670 SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ			1	1
QPLRFCCDFRPYFTIHDSEFKBFTTRTQAPPNVVLGVTNPFFIK TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP 7060 90 1670 SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ				The state of the s
TLQHWPHILRVGEPKMSGDLPKQVKLKKPFKV*RPWDTKP 7060 90 1670 SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ			J	·-
7060 90 1670 SVNLPPSLWPWEEAMDSTKSEPLKGSPEAEDGNIEYKKLVNPSQ	1			I -
YRFEHLVTQMKWRLOEGRGEAVYOIGVEDNGLLVGLAEEEMRAS	7060	90	1670	- 1
	L			YRFEHLVTQMKWRLQEGRGEAVYQIGVEDNGLLVGLAEEEMRAS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
		l .	
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	1 '		
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
Į	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Ì	amino acid	sequence	Codon, /=possible nucleotide deletion,
1	sequence	l *	\=possible nucleotide insertion)
<u> </u>	bequence		1
	1	!	LKTLHRMAEKVGADITVLREREVDYDSDMPRKITEVLVRKVPDN
)	j	}	QQFLDLRVAVLGNVDSGKSTLLGVLTQGELDNGRGRARLNLFRH
	1	1	LHEIQSGRTSSISFEILGFNSKGEVHGINGTQWGOTLRMGW***
ì	1	i .	RT*DGGRVWRLFEIV*MNALRGL*TSSAPLRKSMGNQLN*IKNG
ł	1	1	VKIKRQGHPGNGLGPGNSEGVGRAGRRH*GPWALGQVVNYSDSR
1			
	1	,	TAEEICBSSSKMITFIDLAGHHKYLHTTIFGLTSYCPDCALLLV
1			SANTGIAGTTREHLGLALALKVPFFIVVSKIDLCAKTTVERTVR
1	i		QLERVLKQPGCHKVPMLVTSEDDAVTAAQQFAQSPNVTPIFTLS
]	1	ļ	SVSGESLDLLKVFLNILPPLTNSKEQEELMQQLTEFQVDEIYTV
	1		·
		<u> </u>	PEVGTVVGGTLSR*IDLLATLPTQPSPIYSKTSWPKGGDPGI
7061	364	710	ARMPSPLGPPCLPVMDPETTLEEPETARLRFRGFCYQEVAGPRE
1			ALARLRELCCQWLQPEAHSKEQMLEMLVLEQFLGTLPPEIQAWV
]		1	RGQRPGSPEEAAALVEGLQHDP*ARMPSPLGPPCLPVMDPETTL
i			EEPETARLRFRGFCYQEVAGPREALARLRELCCQWLQPEAHSKE
J	1		QMLEMLVLEQFLGTLPPEIQAWVRGQRPGSPEEAAALVEGLQHD
1		i	PGQLLG
7062	71	744	AKAGTNLERLHWLSYFFCIPKHKLKSSQKDKVROFMACTOAGER
		1	TAIYCLTONEWRLDEATDSFFONPDSLHRESMRNAVDKKKLERL
i			The state of the s
ĺ	(1	YGRYKDPQDENKIGVDGIQQFCDDLSLDPASISVLVIAWKFRAA
1	1		TQCEFSRKEFLDGMTELGCDSMEKLKALLPRLEQELKDTAKFKD
1	1	j	FYQFTFTFAKNPGQKGLDL*MAGAYWKLVLSGRFKFLYLWNTFL
1 .	1		менн
7063	2	562	LRTVPDLPGRRFRAMRTGORR*PELPPDMNSLEOAEDLKAFERR
7003	1 2	302	
ì	1		LTEYIHCLQPATGRWRMLLIVVSVCTATGAWNWLIDPETQKVSF
	1		FTSLWNHPFFTISCITLIGLFFAGIHKRVVAPSIIAARCRTVLA
1	1		EYNMSCDDTGKLILKPRPHVQ*QSSLIVMGLKIAFLRISDTAKS
1		1	HKGFLLRLDM
7064	300	884	RDTGSDPSSTRRLCSTCCTGH*PAEPIASPHPSRGTCPPASSAS
/064	300	004	
1	1		SRRTGCWTCPPESGHAQARRSRRASASRWGARGAVRSAVAARGC
i	(SSRAGRWLETPGRRRGPPACAAAAGRLRGPAP*AAPPTASVPAR
1			CRCPAARTGAPAAATWLRRRLSGLRAPALGRRRSPGPSPKSAAP
	j]	PLLTPLGAGRAGGSRANS
7065	 		
['005	1	555	ATTTHSARRSGRGAAAEAAASAAGGRQKGFDRKAWEGRRTTPGG
1	1 .		RSQSEPKAPPPQKRSEAAFASMAHSPVAVQVPGMQNNIADPEEL
1	1		FTKLERIGKGSFGEVFKGIDNRTQQVVAIKIIDLEEARDEIEDI
			QQEITVLSQCDSSYVTKYYGSYLKGSKLWIIMEYLGGGSALDLL
1	1		RAGPFDEFO
	 		
7066	356	676	PGPQRGPWRAREGGHPLDPADHPRAPASLRSNVRAATMMQICDT
1			YNQKHSLFNAMNRFIGAVNNMDQTVMVPSLLRDVPLADPGLDND
1	1	1	VGVEVGGSGGCLEERTPP
7067	152	973	KENITMATEIGSPPRFFHMPRFQHQAPRQLFYKRPDFAQQQAMQ
1		1 -73	OLTFDGKRMRKAVNRKTIDYNPSVIKYLENRIWORDORDMRAIO
1	,		PDAGYYNDLVPPIGMLNNPMNAVTTKFVRTSTNKVKCPVFVVRW
J			TPEGRRLVTGASSGEFTLWNGLTFNFETILQAHDSPVRAMTWSH
Į.			NDMWMLTADHGGYVKYWQSNMNNVKMFQAHKEAIREARFIHNIP
1			FSVVPIVMVKLFSKCILGAEMHGLCQFLGNFLHPINTIFFFVFT
	ľ		·-
	ļ	<u> </u>	HSPFCWAPF
7068	222	816	DTMKEYVLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDD
			DDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDDD
1			VHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGLTSLY
1	1		GLILNNNKLTKIHPKAFLTTKKLRRLYLSHNQLSEIPLNLPKSL
i			1
		<u> </u>	AELRIHENKVKKIQKDTFKKK
7069	1147	1765	FRDHRRYFYVNEQSGESQWEFPDGEBEEEESQAQENRDETLAKQ
1			TLKDKTGTDSNSTESSETSTGSLCKESFSGQVSSSSLMPLTPFW
j			TLLQSNVPVLQPPLPLEMPPPPPPPPPPESPPPPPPPPPPPAPKMPPP
L		L	

SEQ Fredicted Fredicted In uncleotide location location corresponding to first mino acid sequence location corresponding to first mino acid sequence ence Secuence				
NO: nucleotide	SEQ		Predicted end	Amino acid segment containing signal peptide
Coration Corresponding Lo first amino acid residue of Common	ID		nucleotide	
to first amino acid residue of residue of amino acid residue of amino acid sequence Perfoline, Q=Glutamine, R=Arginine, S=Serine, T=Threonine, V=Vallne, amino acid sequence Refrequence Perfoline, Q=Glutamine, V=Vallne, S=Serine, T=Threonine, V=Vallne, S=Serine, T=Threonine, V=Vallne, S=Serine, T=Threonine, V=Vallne, T=Threonine, V=Vallne, S=Serine, T=Threonine, V=Vall	NO:		(1
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amino acid sequence sequence (amino acid sequence sequence (amino acid sequence (amino acid sequence (amino acid sequence) (am	1		1	
residue of amino acid sequence				, -
amino acid sequence Sequence Sequence Sepassible nucleotide insertion SETEXCARRIDAKKSKTEMPSLVKKWGSIQARELDEEDNSSSSED RETEXCARRIDAKKSKTEMPSLVKKWGSIQARELDEEDNSSSSED RETEXCARRIDAKKOGOLVSWARERNANPEA SETEXCARRIDAKKOGOLVSWARERNANPEA SOTTEDSSEAVGRATALIEGRIAGEEDNSKISGEDREITEKLIDGALOKUL LEDREKHAGOSALOKVKGGERVKSTSLILREITUVGGIQKLI LERKEKOKKEDALASHEPPEDERITIPVDEETFIKAAVEGK MYVIPPO ARGTIRALETAKVCKKUGALAGSKARPSBADSVEREKUGSPFETF ARGTIRALETAKKVCKVGANGOKAAPESBADSTERITUVGATOKUL ARGTIRALETAKKVCKVGANGOKAAPESBADSTERITUSPAPPISENIOV FODERTOLTERVEYPOTOTOTTPPPTVAGAAPECHKUTSCEPE PEGMTAPVIDSRITMFPHYRGDIITASSIPPHYPSININ PESSLEPASMPIADHISTSFSREDMISSPYQPPPQTOTOPPP PEGMTAPVIDSRITMFPHYRGDIITASSIPPHYPSININ PESSLEPASMPIADHISTSFSPEDMISSPYQPPTPTOTOPPPP PEGMTAPVIDSRITMFPHYRGDIITASSIPPHYPSININ PESSLEPASMPIADHISTSTSPEDMISSPYQPPTPTPTAVAGAPCHKITSCEPE TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDOMAQYHTOKAPLUSSTLEVATOSPTPSTLARGGES TRIKEPDO	1			
Sequence Septimic mucleotide insertion	,	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
RETRICATIONAL SILVENGES LORGILDEEDINSSISSEE RVSTAQKE IEEMKOQOLUSGMARENINTER 7070 1 547 DOTMEDSESVORATALIEGRIAGEENREKUEGDAGOKLEMOLUSGULI LEDEKHHGAGSAALGKVKGGENVEKTSLÜLERELIDVGGIQHLI ELKKRKQKERGALAASHEPPPPEPET NGVUEGTPILKAAVEGK MKVIRKFLAGGGATOTOOFRETALHRASLEGHMEILEKLLDVA ATVUPO 7071 2 921 ARGTLEALETAKVGKVGAGGKAAGPSADSVTENKIGSPPRTF VSNVAATSAGGENVOTELMSVPGKSSPELTRVPAYPPHSENIQY PODERTOI PEEVEQY POTGYTYPPPPTVPAQVADEVOPPTVERNIQY PODERTOI PEEVEQY POTGY YPPPPTVPAQVADEVOPPTVERNIQY PESSLEPASMPVADUTSTSTSROUMSSSPYQPPDPYGGVDVPV PEGMYAPVYDSRRIMPPMYGRDDI TRSNSLPPMOVHISSVYQT SLERENVISLOGYYSVACOPPSETTIVPLPERECHIKKTGSEP TRKPDOMAGYHTOKAPLVSSTLEVATGSPTPPSTLANGEGS TRKPDOMAGYHTOKAPLVSSTLEVATGSPTPPSTLANGEGS TRKPDOMAGYHTOKAPLVSSTLEVATGSPTPPSTLANGEGS TRKPDOMAGYHTOKAPLVSSTLEVATGSPTPPSTLANGEGS TRKPDOMAGYHTOKAPLVSSTLEVATGSPTPPSTLANGEGS SLERENVISLOGYYSVACOPPSEPRTTVPLPERECHIKKTGSEPKTP VSNVAATSAGDSNVOTELMSVEKSSPFLTRVSAYPPPSENINY PESSLEPASMPVADHYSTSPPDEMMSSPYQPPPGYGFVSPVDV PSGMYAPVYDSRRIMPPMYGRDDI TRSNSLPPMOVHRSVVOY SLERENVISLOGYYSVACOPPSEPRTTVPLPERECHIKKTGSEPKTP VSNVAATSAGDSNVOTELMSVEKSSPFLTRVSAYPPPSENINY PESSLEPASMPVADHYSTSPPDEMMSSPYQPPPGPGVGVPVPVV PSGMYAPVYDSRRIMPPMYGRDI TRSNSLPPMOVHRSVVOY SLERENVISLOGYYSVACOPPSEPRTTVPLPREPGGHLKTISCEEQ TRKPDOMAGYHTOKAPLVSSTLEVATGSPTPPSTLANGEGS SLERENVISLOGYYSVACOPPSEPRTTVPLPREPGGHLKTISCEEQ TRKPDOMAGYHTOKAPLVSSTLEVATGSPTPPSTLANGEGS VPLESTRYAPVYLGARGENSTATTSPSGSLSTOPTRFTSTLANGERS VPLESTRYAPVYLGARGENSTATTSPSGSLSTOPTRFTSTLANGENS VPLESTRYAPVYLGARGENSTATTSPSGSLSTOPTRFTSTRAGENS VPLESTRYAPVYLGARGENSTATTSPSGSLSTOPTRFTSSTNILLFYPP VLDEMOMONYFLIFYSSULTENSTITLISSNILVKRDITTSSNILLFYPP VLDEMOMONYFLIFYSSULTENSTITLISSNILVKRDITTSSNILLFYPP VLDEMOMONYFLIFYSSTLEREDTSSNILLFYPP VLDEMOMONYFLIFYSSTHUELSTLANGERVGORGONARAL AGVEFPORTSLIDRKELIFTTSTHVEI 7076 279 1049 LQSESSNABGRREGERARGEVPPPDITSRAGKKRKKPLRDSNAP SPLITGYVERMBERGOLGARGREVPPPDITSRAGKKRKKPLRDSNAP ROLGAGGNOTHAPTHARSTENSTANGENSKLUPTROGROKAR ROGGRAFFELERANGERVERTENSTANGENSKLUPTROGROKAR ROGGRAFFELERANGERVERTENSTANGENSKLUPTROGROKAR ROGGRAFFELERANGERVERTENSTANGENSKLUPTROGROKAR	İ	amino acid	sequence	
RVSTACKS IERKKOOLUSGABERNANPER	1	sequence		· •
Total				
LEDEXHHGAGSALIGNYEGGERVERTSLDLRERITUNGGIONLI BLRKEKGKKRADLAASHER PEP BET GTGYDESTPILKAAVEGK MKVIEKFLADGSADTCDQFRRTALHRASLEGHMEILEKLLDNG ATTOPO 7071 2 921 ARGTLERALETAKKVGKVGANGGRAAGPSADSVTENKIGSPPKTP VSNVAATSAGSSNVGTELNSVPGKSSPFLIRVPAYPPHEBRIGY FODPRTQTPEPEVQYPGTGYTYPPFTVPAAVJAPCVPEFVESNNV PESSLEPASMPYADHYSTFSPBDRNNSSPYQDPPDGYPGVPEV SGRYAPAVDSRFINEPPMYADHYSTFSPBDRNNSSPYQDPPDGYPGVPUP PSGMYAPAVDSRFINEPPMYADHYSTFSPBDRNNSSPYQDPPDGYPGVPUP PSGMYAPAVDSRFINEPPMYADHYSTFSPBDRNNSSPYQDPPDGYPGVPUP PSGMYAPAVDSRFINEPPMYADHYSTFSPBDRNNSSPYQDPPDGYPGVPUP PSGMYAPAVDSRFINEPPMYADHYSTFSPBDRNNSSPYQDPPDGYPGVPUP PSGNYAPANSAGSSNVGTELNSVPGKSSPPLTEVSTNGGES PSGNYAPAVDSRFINEPPMYADHYSTFSPBDRNNSSPYQDPPDGYPGVPUP PSGNYAPANSAGSSNVGTELNSVPGKSSPPLTEVSTNGGES PSGNYAPAVDSRFINEPPMYADHYSTFSPBDRNNSSPYQDPPDGYPGVPUP PSGNYAPANSAGSSNVGTELNSVPGKSSPPLTEVSTNGGES PSGNYAPANSAGSSNVGTELNSVPGKSSPPLTEVSTNGGES SERNYADHYADHYSTFSPBDRNNSSPYQDPPDGYPGVPUP PSGNYAPAVDSRFINEPPMYADHYSTFSPBDRNNSSPYQDPPDGYPGVPUP PSGNYAPAVDSRFINEPPMYADHYSTFSPBDRNNSSPYQDPPDGYPGVPUP PSGNYAPAVDSRFINEPPMYADHYSTFSPBDRNNSSPYQDPPDGYPGVPUP PSGNYAPAVDSRFINEPPMYADHYSTFSPBDRNNSSPYQDPPDGYRAPMP LVRYKVVLLGKROVERSVNINGERSKENDGESGYDPTVENTYSKI VTLGKDSPHLHILVDTNGGDFYSTLPYSFIGHTANGEGES TRENDONACHYGKNINGENGAGGAGGAGGTANTANGEGE LVRYKVVLLGKDSPHLHILVDTNGGDFYSTLPYSFIGHGHTANGEGE THERETOLLDVGRYTLGENGRKMMGCKLKKGNEVSRAM CALINSGGVIKABISHDSYTKOGIGLDLENSFSNILLFYBE TLDEMGNORYFILIFYKSMSINTSGLRITTLSSNIYKRDITSAKV MNATAALEFILIDVGRYTLGENGRKKMGCKKKKGNEVSRAM CALINSGGVIKABISHDSYTKOGIGLDLENSFSNILLFYBE TLDEMGNORYFILIFYKSMSINTSGLRITTLSSNIYKRDITSAKV MNATAALEFILITSTSHOSGGVIKKKGNEKKMGNERVSKAM CALINSGGVIKABISHDSYTKOGIGLDLENSFSNILLFYBE TLDEMGNATHALINGTHANGAGAGNAGAGGAGNGGAGGGNGGAGGAGGAGGAGGAGG	1			RVSTAQKRIEEWKQQQLVSGMAERNANFEA
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7078 483 767 FQGQRMAGEQKPSSNLLEQFILLAKGTSGSALTALISQVLEAPG VYVFGELLELANVQBLAEGANAAYLQLLNLFAYGTYPDYIANKE SLPELY 7079 2 376 SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ	1			
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SLPELY 7079 2 376 SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ	7078	483	767	
7079 2 376 SVVEFKRPKEPSGSDGESDGPIDVGQEGQLSQMARPLSTPSSSQ	1			**
	L		<u> </u>	
MQARKKRRGIIEKRRKDRINSSLSELKKLVPTAFEKQGSSKLEK	7079	2	376	- - - - - - - - - -
		1	1	MQAKKKRGITEKKKUKINSSLSELKKUVPTAFBKQGSSKLEK

SEO Predicted Predicted end Amino acid segment	containing signal peptide
SEQ Predicted Predicted end Amino acid segment ID beginning nucleotide (A=Alanine, C=Cyste	ine, D=Aspartic Acid, E=
	enylalanine, G=Glycine,
No: Macroscrae	
1 200002011	
collesponding to the	
20 11180	
amino acid residue of S=Serine, T=Threoni	ne, vevailne,
	osine, X=Unknown, *=Stop
	nucleotide deletion,
sequence \=possible nucleoti	
AEVLQMTVDHLKMLHATGG	
7080 200 595 VQLPLEAPCLSLLSCRDHS	GGNRDLSRRHRDCRVYGSPQDG1PY
LTHPLCHQDVVSVGRLQIR	RALATPGHTQGHLVYLLDGEPYKGPS
CLFSGDLLFLSGCGEFPRK	REELGEEGETEVRAATVPWRALKP
7081 213 506 AVTEEEMILNSLSLCYHNK	LILAPMVRVGTLPMRLLALDYGADI
	EVLSTVDFVAPDDRVVFRTCEREQN
RVVFOMGTS	
	LROGLGTNSFLHGLGOEPFEGARSL
7082 3 1137 APSRNTMLMAWCRGPVLLC	DRUGIGINSF INGLOURFE GARSI
CCRSSPRDLRDGEREHEAA	AQRKAPGAESCPSLPLSISDIGTGCL
SSLENLRLPTLREESSPRE	ELEDSSGDQGRCGPTHQGSEDPSMLS
QAQSATEVEERHVSPSCST	rsrerpfQageLilaetgegetkfkk
LFRLNNFGLLNSNWGAVPF	GKIVGKFPGQILRSSFGKQYMLRRP
	CDINMILSMMDINPGDTVLEAGSGSG
	FEVRKDHHDLAKKNYKHWRDSWKLSH
	TEDIKSLTFDAVALDMLNPHVTLPVF
YPHLKHGGVCPVYVVNITC	
	LLYPKSLSRHVSVRTSVVTQQLLSEP
7083 115 541 RSNAVQLTRMEYAMKSLSI	VRKGIMAYSLEDLLLKVRDTLMLADK
DEEL UI DEDOUMIEMENT	FOALAGDTVFMVLQKGQKWQPPSEQG
· · · · · · · · · · · · · · · · · · ·	ONTHOD I ALM ADDING KING I SOUGO
TRHPLSLSHK	CHOP CARA DWAR CORA ACTION I DVIJAV
	GVQRSAAADMAASTAAGKQRIPKVAK
VKNKAPAEVQITAEQLLRE	EAKERBLELLPPPPQQKITDEEELND
	VISNWIKYAQWBESLKEIQRARSIYE
RALDVDYRNITLWLKYAE	MEMKNRQVNHARNIWDRAITTL
7085 243 1499 RQLARLRRRGWRSPFGGAI	PMAHITINQYLQQVYEAIDSRDGASC
AELVSFKHPHVANPRLQM/	ASPEEKCQQVLEPPYDEMFAAHLRCT
YAVGNHDFIEAYKCQTVI	VQSFLRAFQAHKEENWALPVMYAVAL
	SKVGDMLEKAAELLMSCFRVCASDTR
	FKIYFKINKLHLCKPLIRAIDSSNLK
	amfdsdfkqaeeylsfafehchrssq
	HMPTVELLKKYHLMQFAEVTRAVSEG
	CGIFLILEKLKIITYRNLFKKVYLLL
	VEDVDIDEVQCILANLIYMGHVKGYI
SHQHQKLVVSKQNPFPPL	
7086 256 525 ILAARMGKQNSKLRPEVM	QDLLESTOFTEHBIQEWYKGFLRDCP
SGHLSMEEFKKIYGNFFP	YGDASKFAEHVFRTFDANGDGTIDFR
EF	
	HELVPITTENAPKNVVDKGEGASRGG
NTRKSLEDNGSTRVTPSV	QPHLQPIRNMSVSRTMEDSCELDLVY
	FRSNLREVAQMLKSKHGGNYLLFNLS
	PDLHTPALEKICSICKAMDTWLNAHP
HRCRVLHNKG	
	ETGELYSSYVGLVYMFNLIVGTGALT
	FLGFMSFMTTTFVIEAMAAANAQLHW
	DSDVLIRDNYERABKRPILSVQRRGS
	FFNKVGVNLFYFCIIVYLYGDLAIYA
	SCGVEADTKYNDTDRCWGPLRRVD
	SRAPSRGGVNFLNVARTYIPNTKVEC
HYTLPPGTMPSASDWIGI	FKVEAACVRDYHTFVWSSVPESTTDG
SPIHTSVOFOASYLPKPG	AQLYQFRYVNRQGQVCGQSPPFQFRE
PRPMDELVTLERADGGSD	ILLVVPKATVLQNQLDESQQERNDLM
OLKI OLEGOVTELESEVO	ELERALATARQEHTELMEQYKGISRS
\Quad \Qua	
עמקותקפקות פפססמקט	WARTLELEDDIOTISEKVITKEVELD
HGEITEERDILSRQQGDH	VARILELEDDIQTISEKVLTKEVELD
HGEITEERDILSRQQGDH RLRDTVKALTREQEKLLG	VARILELEDDIQTISEKVLTKEVELD QLKEVQADKEQSEABLQVAQQENHHL QRLKDKVAQMKDTLGQAQQRVABLEP

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
No.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
1			
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
]	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
]]	LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR
			LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK
1		}	LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKRER
1			TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
			EDATTEDERAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ
			ASLLLGLE
7090	33	1775	SVCWEDRYLKARMEESPLSRAPSRGGVNFLNVARTYIPNTKVEC
			HYTLPPGTMPSASDWIGIFKVEAACVRDYHTFVWSSVPESTTDG
1	1		SPIHTSVOFQASYLPKPGAQLYQFRYVNRQGQVCGQSPPFQFRE
1			PRPMDELVTLEEADGGSDILLVVPKATVLQNQLDESQQERNDLM
			OLKLOLEGOVTELRSRVQELERALATARQEHTELMEQYKGISRS
		1	HGEITEERDILSROOGDHVARILELEDDIQTISEKVLTKEVELD
1			RLRDTVKALTREQEKLLGQLKEVQADKEQSEAELQVAQQENHHL
}			NLDLKEAKSWQEEQSAQAQRLKDKVAQMKDTLGQAQQRVAELEP
		1	LKEQLRGAQELAASSQQKATLLGEELASAAAARDRTIAELHRSR
			LEVAEVNGKLAELGLHLKEEKCQWSKERAGLLQSVEAEKDKILK
			LSAEILRLEKAVQEERTQNQVFKTELAREKDSSLVQLSESKREL
			TELRSALRVLQKEKEQLQEEKQELLEYMRKLEARLEKVADEKWN
			EDATTEDERAAVGLSCPAALTDSEDESPEDMRLHPMAFVSVETQ
L			ASLLLGLE
7091	186	1076	EGMLTREHRCGRSEEQELEPWPSPKKARSGRWLRNGFKRKMEEP
1			EEPADSGQSLVPVYIYSPEYVSMCDSLAKIPKRASMVHSLIEAY
			ALHKQMRIVKPKVASMEEMATFHTDAYLQHLQKVSQEGDDDHPD
			SIEYGLGYDCPATEGIFDYAAAIGGATITAAQCLIDGMCKVAIN
}			WSGGWHHAKKDEASGFCYLNDAVLGILRLRRKFERILYVDLDLH
1			HGDGVEDAFSFTSKVMTVSLHKFSPGFFPGTGDVSDVGLGKGRY
ŀ	Į		YSVNVPIQDGIQDEKYYQICERYEPPAPNPGL
7092	522	809	KQGINEDQEESQKPRLGEGCEPISKRQMKKLIKQKQWBEQRELR
			KQKRKEKRKKKLERQCQMEPNSDGHDRKRVRRDVVHSTLRLII
1			DCSFDXLM
7093	454	655	NFGVSGVELAQQASMVRMSFVIAACQLVLGLLMTSLTESSIQNS
	1		ECPOLCVCEIRPWFTPOSTYREA
7094	1 2	508	FVRSMHWGVGFASSRPCVVDLSWNQSISFFGWWAGSEEPFSFYG
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,	1	300	DIIAFPLODYGGIMAGLGSDPWWKKTLYLTGGALLAAAAYLLHE
1	i		LLVIRKQQEIDSKDAIILHQFARPNNGVPSLSPFCLKMETYLRM
	1		ADLPYQNYFGGKLSAQGKMPWIEYNHEKVSGTEFII
7005	 	43.7	
7095	1	411	IASSLPKMASLLQSDRVLYLVQGEKKVRAPLSQLYFCRYCSELR
			SLECVSHEVDSHYCPSCLENMPSAEAKLKKNRCANCFDCPGCMH
	1		TLSTRATSISTQLPDDPAKTTMKKAYYLACGFCRWTSRDVGMAD
		<u> </u>	KSVGE
7096	224	2067	ETRSLAVQEKPSQAGRRRSSRISFAGALFLTRFLLQELLLNNFC
			SAMSPAPDAAPAPASISLFDLSADAPVFQGLSLVSHAPGEALAR
		1	APRTSCSGSGERESPERKLLQGPMDISEKLFCSTCDQTFQNHQE
			QREHYKLDWHRFNLKQRLKDKPLLSALDFEKQSSTGDLSSISGS
1	1		EDSDSASEEDLQTLDRERATFEKLSRPPGFYPHRVLFQNAQGQF
			LYAYRCVLGPHQDPPEEAELLLQNLQSKGPRDCVVLMAAAGHFA
1	1		GAIFQGREVVTHKTFHRYTVRAKRGTAQGLRDARGGPSHSAGAN
			LRRYNEATLYKDVRDLLAGPSWAKALEEAGTILLRAPRSGRSLF
	1	1	FGGKGAPLQRGDPRLWDIPLATRRPTFQELQRVLHKLTTLHVYE
			EDPREAVRLHSPOTHWKTVREERKKPTEEEIRKICRDEKEALGO
		1	NEESPKQGSGSEGEDGFQVELELVELTVGTLDLCESEVLPKRRR
		-	RKRNKKEKSRDQEAGAHRTLLQQTQEEEPSTQSSQAVAAPLGPL
		1	LDEAKAPGOPELWNALLAACRAGDVGVLKLOLAPSPADPRVLSL
			LSAPLGSGGFTLLHAAAAAGRGSVVRLLLEAGADPTVQCQDH
7097	256	1228	IRTKSAATWEAWPQCGREGSRIITEPCEANAGSRQELQTERISS
,037	000	1440	1
	<u> </u>		FLAAQGDQAFHSGLETNINSNSELPLRVGLKVAQGSPLMGGQVSA

SEQ Predicted beginning nucleotide location nucleotide location corresponding to first amino acid residue of amino acid segment containing signal personal p	DTMTYC LIDVTEQ LITEISE MLCPRG WGNRVK VMRLQT THPSLEA
NO: nucleotide location corresponding to first amino acid residue of amino acid sequence No: nucleotide location corresponding to first amino acid residue of amino acid sequence No: nucleotide location corresponding to first amino acid residue of amino acid sequence No: nucleotide location corresponding to first to first amino acid residue of amino acid sequence No: nucleotide location corresponding to first t	=Stop DTMTYC LIDVIEQ LITEISE MLCPRG WGNRVK WMRLQT THPSLEA
corresponding to first amino acid residue of residue of amino acid residue of amino acid sequence code code code code code code code co	=Stop DTMTYC LDVTEQ LTTEISE MLCPRG WGNRVK VMRLQT THPSLEA
to first amino acid residue of amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, w=Tryptophan, Y=Tyrosine, X=Unknown, * Codon, /=possible nucleotide deletion, \ -possible nucleotide insertion) SNSFSRLHCRNANEDWMSALCPRLWDVPLHHLSIPGSH LNKKSPISHEESRLLQLLNKALPCITRPVVLKWSVTQA LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTALVEDT WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGD EVPTLRQLWSRGQQVIVSYEDESSLRRHHELWPGVPYW TEALIRYLETMKSCGR 7098 82 956 SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYC EARSGFWAPNNFPVNICRMTAVDGDRGGSSRETCRCHHE LVLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLP LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFL LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAE AIHFFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPV	=Stop DTMTYC LDVTEQ LTEISE MLCPRG WGNRVK VMRLQT THPSLEA
amino acid residue of amino acid sequence S=Serine, T=Threonine, V=Valine, W=Tryptophan, Y=Tyrosine, X=Unknown, * Codon, /=possible nucleotide deletion, \	IDTMTYC LLDVTEQ LLTEISE MLCPRG WGNRVK VMRLQT THPSLEA
residue of amino acid sequence	IDTMTYC LLDVTEQ LLTEISE MLCPRG WGNRVK VMRLQT THPSLEA
amino acid sequence Codon, /=possible nucleotide deletion, -possible nucleotide insertion	IDTMTYC LLDVTEQ LLTEISE MLCPRG WGNRVK VMRLQT THPSLEA
*possible nucleotide insertion	DTMTYC LDVTEQ LTEISE MLCPRG WGNRVK VMRLQT THPSLEA
SNSFSRLHCRNANEDWMSALCPRLWDVPLHHLSIPGSH LNKKSPISHEESRLLQLLNKALPCITRPVVLKWSVTQA LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTALVEDT WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGD EVPTLRQLWSRGQQVIVSYEDESSLRRHHBLWPGVPYW TEALIRYLETMKSCGR 7098 82 956 SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYC EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHP LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLP LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFL LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAE AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPV	LDVTEQ LTEISE MLCPRG WGNRVK VMRLQT THPSLEA
LNKKSPISHEESRLLQLLNKALPCITRPVVLKWSVTQA LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTALVEDT WLERHPREVVILACRWFEGLSEDLHEYLVACIKNIFGD EVPTLRQLWSRGQQVIVSYEDESSLRRHHBLWPGVPYW TEALIRYLETMKSCGR 7098 82 956 SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYC EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHP LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLP LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFL LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAE AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPV	LDVTEQ LTEISE MLCPRG WGNRVK VMRLQT THPSLEA
LDAGVRYLDLRIAHMLEGSEKNLHFVHMVYTTALVEDT WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGD EVPTLRQLWSRGQQVIVSYEDESSLRRHHBLWPGVPYW TEALIRYLETMKSCGR 7098 82 956 SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYC EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHF, LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLP LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFL LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAE AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPV	TLTEISE MLCPRG WGNRVK TVMRLQT THPSLEA
WLERHPREVVILACRNFEGLSEDLHEYLVACIKNIFGD EVPTLRQLWSRGQQVIVSYEDESSLRRHHELWPGVPYW TEALIRYLETMKSCGR 7098 82 956 SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYC EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHF LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLP LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFL LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAE AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPV	MLCPRG WGNRVK VMRLQT 'HPSLEA
EVPTLRQLWSRGQQVIVSYEDESSLRRHHBLWPGVPYW TEALIRYLETMKSCGR 7098 82 956 SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYC EARSGFWAPNRFVNICRMTAVDGDRGSSRETCRCHF LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLP LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFL LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAE AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPV	WGNRVK VMRLQT THPSLEA
TEALIRYLETMKSCGR 7098 82 956 SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYC EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHF LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLP LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFL LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAE AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPV	VMRLQT HPSLEA
7098 82 956 SSFLKRCRKVLGCWGIPSEQSLFSTLEEPRDKEIDNYC EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHF LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLP LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFL LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAE AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPV	HPSLEA
EARSGFWAPNRFPVNICRMTAVDGDRGGSSRETCRCHF LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLP LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFL LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAE AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPV	HPSLEA
LVLLLQDWQPGGVGICTSFLGISWALLDYHRALRTCLP LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFL LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAE AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPV	
LGSSVIYFLWNLLLLWPRVLAVALFSALFPSYVALHFL LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAE AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPV	SKPLLG
LLWVWLQGTDFMPDPSSEWLYRVTVATILYFSWFNVAE AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPV	
AIIHFAFLLSDSILLVATWVTHSSWLPSGIPLQLWLPV	
TOTAL BE UNVERSE EDUCATION OF THE PROPERTY OF	
LGLALRLVYYHWLHPSCCWKPDPDQVD	
7099 992 210 LFRLAPGFLRSLARQGYHQTWAFFFLPSGATATWPAAS	RSRSLA
ARSLPRSPARPGPNDALLGEHDFRGQGVRAQRFRFSEE	PGPGAD
GAVLEVHVPQIGAGVSLPGILAAKCGAEVILSDSSELP	HCLEVC
RQSCQMNNLPHLQVVGLTWGHISWDLLALPPQDIILAS	DVFFEP
EDFEDILATIYFLMHKNPKVQLWSTYQVRSADWSLEAL:	
KCVHIPLESFDADKEDIAESTLPGRHTVEMLVISFAKD	
7100 205 671 ANGGFWEAAPGSEVSLPLWVPTASHSKTTALGIGSAPP	
FLFSFPPQLGDPLEAFPVFKKYDRNGLNVSIECKRVSG.	
DWAFDLTKTNMQTMYEQSEWGWKDREKREEMTDDRAWY:	LIAWEN
SSVPVAFSHFRFDVERGDEVLYW 7101 2 503 WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRA	3 D)(****
VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITI	
ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNN	
VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR	KHSIDK
7102 2 503 WRGGPRRAKRLAGGAVGWVLLVRGVHSVRAGGGRPPRA	ADMKKD
VRILLVGEPRVGKTSLIMSLVSEEFPEEVPPRAEEITT	
ERVPTHIVDYSEAEQSDEQLHQEISQANVICIVYAVNNI	
VTSRWIPLINERTDKDSRLPLILGGNKSDLVEYSR	
7103 119 438 GSQSSVAVNIRSGTDEESMDLMNGQASSVNIAATASEK	SSSSES
LSDKGSELKKSFDAVVFDVLKVTPBEYAGQITLMDVPV	FKAIQP
DELSSCGWNKKEKYSSAP	
7104 1670 795 RLWEHRSVSAGASGWGLSSPGCLLLHPSLPEEERVDIL	INNAGV
MRCPHWTTEDGFEMQFGVNHLGEAWAGAAPWVQAILPRI	
GF*V*VKSDLFIILNPGHFLLTNLLLDKLKASAPSRIIN	
HVAGHIDFDDLNWQTRKYNTKAAYCQS\KLAIVLFTKEI	
GSGVTVNALHPGVARTELGRHTGIHGSTFLOHHN\WAH	
KSPRSWPAPAQHNTLAVAEELA\VISGKYFDGLKQKAP	APEAED
EEVARRLWAESARLVGLRAPSVREQPLPR 7105 765 143 GOMCRRPSPKSTSCLSMTCDLP/RGLODPOCLALFRVA	UDWITE -
7105 765 143 GQMCRRPSPKSTSCLSMTCDLP/RGLQDPQCLALFRVAV LLKAAMSGQGVDRHLFALYIVSRFLHLQSPFLTOVHSEC	
SQIPVQQMHLFDVHNYPDYVSSGGFGPADDHGYGVSY)	~ ~
MITFHISSKKSSTKTDSHRLGQHIEDALLDVASLFQAG(
FRGSGKENSRHRCGFLSROTGASKASMTSTDF	ZITE KKK
7106 14 1064 GLQAGHPHPRSASRIPEADTH\YSKLQRAFDSIVNKDHF	KRMFGT
YFRVGFFGSKFGDLDEQEFVYKEPAITKLPEISHRLEAF	
GAEFVEVIKDSTPVDKTKLDPNKAYIQITFVEPYFDEYF	
TYFEKNFNLRRFMYTTPFTLEGRPRGELHEQYRRNTVLT	
PYIKTRISVIQKEEFVLTPIEVAIEDMKKKTLQLAVAIN	
AKMLQMVLQGSVGATVNQGPLEVAQVPLAEIPADPKLYF	- 1
RLCFKEFIMRCGEAVEKNKRLITADQREYQQELKKNYNY	
RPMIERKIPELYKPIFRVESQKRDSFHRSSFRKCETQLS	1000 I
7107 1145 591 *I*WLQTGKKK	SUUS

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
•	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
1	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
	sequence		\=possible nucleotide insertion)
7108	1	942	VKVALLLTNLEQPRTESEWENSFTLKMFLFQFVNLNSSTFYIAF
1			FLGRFTGHPGAYLRLINRWRLEECHPSGCLIDLCMQMGIIMVLK
Ţ			QTWNNFMELGYPLIQNWWTRRKVRQEHGPERKISFPQWEKDYNL
			QPMNAYGLFDEYLEMILQFGFTTIFVAAFPLAPLLALLNNIIEI
			RLDAYKFVTQWRRPLASRAKDIGIWYGILEGIGILSVITNAFVI
			AITSDFIPRLVYAYKYGPCAGQGEAGQKCMVGYVNASLSVFRIS
1		į	DFENRSEPESDGSEFSGTPLKYCRYRDYRDPPHSLVPYGYTLQF
	l		WHVLAW
7109	964	102	WDQRKRNSLVPGPAHGPAQEEPWEKKESLGAAQEALSIQLQPKE
			TOPFPKSEQVYLHFLSVVTEDGPEPKDKGSLPQPPITEVESQVF
			SEKLATOTSTFEATSEGTLELQQRNPKAERLRWSPAQEESFRQM
	1		VVIHKEIPTGKKDHECSECGKTFIYNSHLVVHQRVHSGEKPYKC
	1		SDCGKTFKQSSNLGQHQRIHTGEKPFECNECGKAFRWGAHLVQH
1	1		QRIHSGEKPYECNECGKAFSQSSYLSQHRRIHSGEKPFICKECG KAYGWCSELIRHRRVHARKEPSH
7330	0.0	607	RLDNFSGFLVEVTKEERHIVKPLYDRYRLVKQMLTRASITPVLG
7110	96	697	SPSTKRRGOMLOPIIEGETAHFFEEIKEEEEDGVNLSSELGDML
]		KTAVOVOSSLKNSESDVEENOEKLALDLRLSSSRAASMPELLEO
İ			LWKARAEKKKLRKTLREFEEAFYQQNGRNAQKEDRVPVLEEYRE
			YKKIKAKLRLLEVLISKQDSSKSI
7111	2	414	GSGLYRGPTPGGOCIWKPNSMPPDHERNFGFTOFALELNELTAE
/+++		314	LKRSLPSTDTRLRPDQRYLEEGNIQAAEAQKRRIEQLQRDRRKV
ļ			MEENNIVHCARFFRRCTDSSGKEWWVTNNTYWRLRAEPGYGNMD
1			GAVLW
7112	103	495	PRCFPVADRGRLIGGLPDVVTIMEGKTLNLTCTVFGNPDPEVIW
/	1	1	FKNDODIOLSEHFSVKVEQAKYVSMTIKGVTSEDSGKYSINIKN
1			KYGGEKIDVTVSVYKHGEKIPDMAPPQQAKPKLIPASASAAGQ
7113	1	824	KCLRQAWHEAPSSLAFTRWCSREERAEGGGNLHRSITRDPKPPG
			LRPSQRPMDDKKKKRSPKPCLAQPAQAPGTLRRVPVPTSHSGSL
İ			ALGLPHLPSPKQRAKFKRVGKEKCRPVLAGGGSGSAGTPLQHSF
1			LTEVTDVYEMEGGLLNLLNDFHSGRLQAFGKECSFEQLEHVREM
			QEKLARLHFSLDVCGEEEDDEEEEDGVTEGLPEEQKKTMADRNL
1			DQLLSNLGSCLGALVPGGMRGGEGTYSQSHSWALGEKVGVHGSK
	}		SSGPLNLPRR
7114	3	1492	VWEVDEQIDHYKESQDKFLWQAAFIGKETLKDBSGQECKICRKI
	1		IYLNTDFVSVKQRLPKYYSWERCSKHHLNFLGQNRSYVRKKDDG
			CKAYWKVCLHYNLHKAQPAERFFDPNQRGKALHQKQALRKSQRS
			QTGEKLYKCTECGKVFIQKANLVVHQRTHTGEKPYECCECAKAF
1			SQKSTLIAHQRTHTGEKPYECSECGKTFIQKSTLIKHQRTHTGE
1.]	KPFVCDKCPKAFKSSYHLIRHEKTHIRQAFYKGIKCTTSSLIYQ
			RIHTSEKPQCSEHGKASDEKPSPTKHWRTHTKENIYECSKCGKS
1		1	FRGKSHLSVHQRIHTGEKPYECSICGKTFSGKSHLSVHHRTHTG
		1	EKPYECRRCGKAFGEKSTLIVHQRMHTGEKPYKCNECGKAFSEK
		1	SPLIKHORIHTGERPYECTDCKKAFSRKSTLIKHORIHTGEKPY
			KCSECGKAFSVKSTLIVHHRTHTGEKPYECRDCGKAFSGKSTLI
51.5		0.5	KHORSHTGDKNL
7115	1	947	NAAHGYNWGLWCMYIIPPQDWLDRGDESAPIRTPAMIGCSFVVD
			REYFGDIGLLDPGMEVYGGENVKLGMRVWQCGGSMEVLPCSRVA
		1	HIERTRKPYNNDIDYYAKRNALRAAEVWMDDFKSHVYMAWNIPM
			SNPGVDFGDVSERLALRQRLKCRSFKWYLENVYPEMRVYNNTLT
			YGEVRNSKASAYCLDQGAEDGDRAILYPCHGMSSQLVRYSADGL
			LQLGPLGSTAFLPDSKCLVDDGTGRMPTLKKCEDVARPTQRLWD
		1	FTQSGPIVSRATGRCLEVEMSKDANFGLRLVVQRCSGQKWMIRN WIKHARH
7116	866	95	RVRMRRNAEVIEEKLSMKSWAKFRPGEPWKGYPNIDPETDPYVT
,110	1	, , ,	PGSVINNLSINTVREVDHLRDRNSGSSSSLNTTLPSTSAWSSIR
L		L	ALCONYLIA TOTALIA DILIMINA DILIMINA TATALIA DE L'ANTONIA

SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
110.	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
			S=Serine, T=Threonine, V=Valine,
1	amino acid	residue of	=
1	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
i	amino acid	sequence	Codon, /=possible nucleotide deletion,
l	sequence		\=possible nucleotide insertion)
			ASNYNVPLSSTAQSTSARNSDSKLTWSPGSVTNTSLAHELWKVP
			LPPKNITAPSRPPPGLTGQKPPLSTWDNSPLRIGGGWGNSDARY
			TPGSSWGESSSGRITNWLVLKNLTPQIDGSTLRTLCMQHGPLIT
			PHLNLPHGNALVRYSSKEEVVKAQKSLHISDLFLLTL
7117	695	1261	LLISTPGGCHPPPSSIEFTYTGAWGKALPAPHMPCAPGALPQGA
			FVSQAARAIPLLQPSQAAQAEGLSQPARACGALCSLPWPLRNWG
Į.	}		SPILRLPGGLRTPTNDRKTRTRSAMACWARAQWDTLGPLKLSHR
į	ł		GKVCLRHPRPTGVRGGPGAAGRQGGMGTRRRGTFTSGARDPGGL
			RVKHRCQPTGHLP
7777	40	1063	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE
7118	49	1863	
	1		ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR
			LLLETHLPSKKKKVLLGVGDPKIGAAIQEBLGYNCQTGGVIAEI
1		1	LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD
ļ			NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT
ĺ	ĺ		YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG
			MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS
Į			ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT
1	}	}	RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF
,			SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE
1	1		EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE
l		j	EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL
i			MSSDLEETAGSTSIPKRKKSTPKEETVNDPBEAGHRSGSKKKRK
	ŀ	ļ	FSKEEPVSSGPEEAAGKSSSKKKKKFHKASQED
7119	49	1863	PHCEPNPGAGAMVLLHVLFEHAVGYALLALKEVEEISLLQPQVE
1 ,113	""	1003	ESVLNLGKFHSIVRLVAFCPFASSQVALENANAVSEGVVHEDLR
ł	i	ĺ	LLLETHLPSKKKKVLLGVGDPKIGAAIQEELGYNCOTGGVIAEI
1			LRGVRLHFHNLVKGLTDLSACKAQLGLGHSYSRAKVKFNVNRVD
			NMIIQSISLLDQLDKDINTFSMRVREWYGYHFPELVKIINDNAT
			YCRLAQFIGNRRELNEDKLEKLEELTMDGAKAKAILDASRSSMG
			MDISAIDLINIESFSSRVVSLSEYRQSLHTYLRSKMSQVAPSLS
ŀ		ŀ	ALIGEAVGARLIAHAGSLTNLAKYPASTVQILGAEKALFRALKT
		l.	RGNTPKYGLIFHSTFIGRAAAKNKGRISRYLANKCSIASRIDCF
1		ł	SEVPTSVFGEKLREQVEERLSFYETGEIPRKNLDVMKEAMVQAE
		ĺ	EAAAEITRKLEKQEKKRLKKEKKRLAALALASSENSSSTPEECE
			EMSEKPKKKKKQKPQEVPQENGMEDPSISFSKPKKKKSFSKEEL
1		[MSSDLEETAGSTSIPKRKKSTPKEETVNDPEEAGHRSGSKKKRK
1			fskeepvssgpeeaagkssskkkkkfhkasqed
7120	1991	64	QLGTRRCLRGDKVTNAMQDFLVTNLEPRFIEPQTANLSVVFKDS
1	1	ļ	NSTTPLIFVLSPGTDPAADLYKFAEEMKFSKKLSAISLGQGQGP
1			RAEAMMRSSIBRGKWVFFQNCHLAPSWMPALERLIEHINPDKVH
1			RDFRLWLTSLPSNKFPVSILQNGSKMTIEPPRGVRANLLKSYSS
1			LGEDFLNSCHKVMEFKSLLLSLCLFHGNALERRKFGPLGFNIPY
			EFTDGDLRICISQLKMFLDEYDDIPYKVLKYTAGEINYGGRVTD
.			DWDRRCIMNILEDFYNPDVLSPEHSYSASGIYHQIPPTYDLHGY
		[LSYIKSLPLNDMPEIFGLHDNANITFAQNETFALLGTIIQLQPK
		1	SSSAGSOGREEIVEDVTONILLKVPEPINLOWVMAKYPVLYEES
1		1	MNTVLVQEVIRYNRLLQVITQTLQDLLKALKGLVVMSSQLELMA
1		1	ASLYNNTVPELWSAKAYPSLKPLSSWVMDLLQRLDFLQAWIQDG
1		1	IPAVFWISGFFFPQAFLTGTLQNFARKFVISIDTISFDFKVMFE
1		1	APSELTQRPQVGCYIHGLFLEGARWDPEAFQLAESQPKELYTEM
}		1	AVIWLLPTPNRKAQDQDFYLCPIYKTLTRAGTLSTTGHSTNYVI
	<u> </u>	<u> </u>	AVEIPTHQPQRHWIKRGVALICALDY
7121	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK
1			LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV
1			SVPLTLAETVASLWPALQELARCGNLACRSDLQVAAKALEMGVF
	1 .		GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCL
	·	·	<u> </u>

SEO	Predicted	Predicted end	Amino acid segment containing signal peptide
ID	beginning	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
Ì	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
ł	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
ł	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
ł	amino acid	sequence	Codon, /=possible nucleotide deletion,
}	sequence	201101101	\=possible nucleotide insertion)
	55400.00		ETRQE
7122	2	546	RPLRPWVLSLGSMVGLMTYGRRQFQSLDTTMRRLIPPFREASAK
1	1 -	3.0	LTTLVDADAEAFTAYLEAMRLPKNTPEEKDRRTAALQEGLRRAV
			SVPLTLAETVASLWPALQELARCGNLACRSDLOVAAKALEMGVF
	1		GAYFNVLINLRDITDEAFKDQIHHRVSSLLQEAKTQAALVLDCL
			ETRQE
7123	1	1092	KPAVPEARSAGTSEAGRSGAEEVSCGSVSGDGAAMRLTPRALCS
1 /123	1	1072	AAQAAWRENFPLCGRDVARWFPGHMAKGLKKMQSSLKLVDCIIE
1		ł	VHDARIPLSGRNPLFQETLGLKPHLLVLNKMDLADLTBQQKIMQ
1			HLEGEGLKNVIFTNCVKDENVKQIIPMVTELIGRSHRYHRKENL
		·)
			EYCIMVIGVPNVGKSSLINSLRRQHLRKGKATRVGGEPGITRAV MSKIQVSERPLMFLLDTPGVLAPRIESVETGLKLALCGTVLDHL
1	1	1	i e e e e e e e e e e e e e e e e e e e
			VGEETMADYLLYTLNKHQRFGYVQHYGLGSACDNVERVLKSVAV
			KLGKTQKVKVLTGTGNVNVIQPNYPAAARDFLQTFRRGLLGSVM LDLDVLRGHPRV
7124	2	382	LPLTLLLAAPFAHLILPPGHDOSPCWHPGPALSPGTLGPLSWAM
/124	4	.382	ANSGLQLLGYFLALGGWVGIIASTALPQWKQSSYAGDASIQLRS
1		1	-
L	ļ <u> </u>		KVFVLESEWGGDSLGLPRDCGWSCLLHSAVRSEKGFWS
7125	166	1127	NCISEKRNYSFSMQKGKGRTSRIRRRKLCGSSESRGVNESHKSE
			FIELRKWLKARKFQDSNLAPACFPGTGRGLMSQTSLQEGQMIIS
j			LPESCLLT\RDTVIRSYLGAYITKWKPPPSPLLALCTFLVSEKH
			AGHRSLLEA\YLEILPKAYTCPVCLEPEVVNLLPKSLKAKAEEQ
*			RAHVQEFFASSRDFFSSLQPLFAEAVDSIFSYSALLWAWCTVNT
ļ	ļ		RAVYL\SPGSGNAFLQSRTPVQLAPYLDLLNHSPHVQVKAAFNE
i			ETHSYEIRTTSRWRKHEEVFICYGPHDNQRLFLEYGFVSVHNPH
7156	ļ		ACVYVSRGWNQLCS
7126	1	733	CRDMAAFIVPSPARRCSQKGSLGHLPTQPWLWAAMSPRGQERGT
			SHSQAREPQRPGRWLLGSLQSSPGTLGQAGTASRRRGCMVQRWV
			QVATGRRAVQVPKGALGLALGETSPGASRGMSGGAGGCWALGWA
]	PSPVLPSWLLEGPPPWLSIISDSGTQRPSPRRCPARPSPWGPQC
			WRGGRIASAEASST*TPGSGSRARSGRRSPGSRRRSASAPSPTP
7127	1222	277	PTDACA+SCVARPAGSRSSRPAAA
/12/	1311	2//	GLPAMCST*KAGYYEETEGDCIPKDR*IEKRPFKEI*RRIPRIF
			AKQKQI*S*NSQKIGASEIDRGRKEADCSDAPAAARIGAVSVFR
1	1	1	RSTQEARVSPRSNAKSANLRAVRAD*WEHFVLLFHTPEQFLAEC
	1		ICRST**K*WHQLC*PLSSL*TGLKRKLLL*VLFRI*WLKDCDV
			*FCQKIFATNFCNWQNLIQ*EE*KPVEYSVEN*HIMNLLLPM*L
	ļ	1	CQSSLRDQTIVTWRM*RNYSMFRINMISSL*DGSIHIPLKLHFY
[Į.	PALIFTLTVPINSCCQRPLPLFAHQSIKTLASSGSPMLACLRFL
7100	 		LVKKRAFIHTPRSPGCSV*CKHVLVKDNKNNCVGSEV
7128	2	5228	GRVDLWTILLGRSALRELSQIEAELNKHWRRLLEGLSYYKPPSP
			SSAEKVKANKDVASPLKELGLRISKFLGLDEEQSVQLLQCYLQE
		!	DYRGTRDSVKTVLQDERQSQALILKIADYYYEERTCILRCVLHL
		j	LTYFQDERHPYRVEYADCVDKLEKELVSKYRQQFEELYKTBAPT
			WETHGNLMTERQVSRWFVQCLREQSMLLEIIFLYYAYFEMAPSD
			LLVLTKMFKEQGFGSRQTNRHLVDETMDPFVDRIGYFSALILVE
			GMDIESLHKCALDDRRELHQFAQDGLICQDMDCLMLTFGDIPHH
			APVLLAWALLRHTLNPEETSSVVRKIGGTAIQLNVFQYLTRLLQ
1		1	SLASGGNDCTTSTACMCVYGLLSFVLTSLELHTLGNQQDIIDTA
			CEVLADPSLPELFWGTEPTSGLGIILDSVCGMFPHLLSPLLQLL
	1	{	RALVSGKSTAKKVYSFLDKMSFYNELYKHKPHDVISHEDGTLWR
		1	RQTPKLLYPLGGQTNLRIPQGTVGQVMLDDRAYLVRWEYSYSSW
			TLFTCEIEMLLHVVSTADVIQHCQRVKPIIDLVHKVISTDLSIA
1			DCLLPITSRIYMLLQRLTTVISPPVDVIASCVNCLTVLAARNPA
İ		1	KVWTDLRHTGFLPFVAHPVSSLSQMISAEGMNAGGYGNLLMNSE
	L		QPQGEYGVTIAFLRLITTLVKGQLGSTQSQGLVPCVMFVLKEML
		· · · - · · · · · · · · · · · · · · · · · · ·	

	B 32 - 1 3	Predicted end	Amino acid segment containing signal peptide
SEQ	Predicted	nucleotide	(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
ID	beginning nucleotide	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
NO:	location	corresponding	H=Histidine, I=Isoleucine, K=Lysine,
İ		to first	L=Leucine, M=Methionine, N=Asparagine,
	corresponding	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	to first	residue of	S=Serine, T=Threonine, V=Valine,
,		amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	residue of		Codon, /=possible nucleotide deletion,
, 1	amino acid	sequence	\=possible nucleotide insertion)
	sequence		PSYHKWRYNSHGVREOIGCLILELIHAILNLCHETDLHSSHTPS
			LOFLCICSLAYTEAGQTVINIMGIGVDTIDMVMAAQPRSDGAEG
			QGQGQLLIKTVKLAFSVTNNVIRLKPPSNVVSPLEQALSQHGAH GNNLIAVLAKYIYHKHDPALPRLAIQLLKRLATVAPMSVYACLG
1 1			
į Į			NDAAAIRDAFLTRLQSK\IE\DMRIK\VMIL\EFLTVA\VETQP GLIELFLNLEVKDG\SDGSKEFSLGMW\SCLHAV/VWELIDSQQ
1			ODRYWCPPLLHRAAIAFLHALWQDRRDSAMLVLRTKPKFWENLT
1		1	, -
i l			SPLFGTLSPPSETSEPSILETCALIMKIICLEIYYVVKGSLDQP
1			LKDTLKKFSIEKRFAYWSGYVKSLAVHVAETEGSSCTSLLEYQM
			LVSAWRMLLIATTHADIMHLTDSVVRRQLFLDVLDGTKALLLV
			PASVNCLRLGSMKCTLLLILLRQWKRELGSVDEILGPLTEILEG
}	ļ	1	VLQADQQLMEKTKAKVFSAFITVLQMKEMKVSDIPQYSQLVLNV
1		1	CETLQEEVIALFDQTRHSLALGSATEDKDSMETDDCSRSRHRDQ
ļ !		j	RDGVCVLGLHLAKELCEVDEDGDSWLQVTRRLPILPTLLTTLEV
			SLRMKQNLHFTEATLHLLLTLARTQQGATAVAGAGITQSICLPL
			LSVYQLSTNGTAQTPSASRKSLDAPSWPGVYRLSMSLMEQLLKT
1 1			LRYNFLPEALDFVGVHQERTLQCLNAVRTVQSLACLEEADHTVG
1			FILQLSNFMKEWHFHLPQLMRDIQVNLGYLCQACTSFLHSRKML
1	-		QHYLQNKNGDGLPSAV\AQRV\QRPPSAASAAPSSSKQPAADTE ASEOOALHTVOYGLLKILSKTLAALRHFTPDVCQILLDQSLDLA
1 1			1
	Ì		EYNFLFALSFTTPTFDSEVAPSFGTLLATVNVALNMLGELDKKK
,	}		EPLTQAVGLSTQAEGTRTLKSLLMFTMENCFYLLISQAMRYLRD
1	}		PAVHPRDKQRMKQELSSELSTLLSSLSRYFRRGAPSSPATGVLP
		1054	SPQGKSTSLSKASPESQEPLIQLVQAFVRHMQR FRRFRWRRLH*AGPASSAGGSPGEASGTMSGELPPNINIKEPR
7129	1	1054	WDQSTFIGRANHFFTVTDPRNILLTNEQLESARKIVHDYRQGIV
	1		
j l			PPGLTENELWRAKYIYDSAFHPDTGEKMILIGRMSAQVPMNMTI
1	1]	TGCMMTFYRTTPAVLFWQWINQSFNAVVNYTNRSGDAPLTVNEL GTAYVSATTGAVATALGLNALTKHVSPLIGRFVPFAAVAAANCI
i '	1		NIPLMRQRELKVGIPVTDENGNRLGESANAAKQAITQVVVSRIL
}			MAAPGMAIPPFIMNTLEKKAFLKRFPWMSAPIQVGLVGFCLVFA
			TPLCCALFPOKSSMSVTSLEAELQAKIQESHPELRRVYFNKGL
L			HEVPSLOTSDPLPGSVQRCSVVVSQPNKENWCQDHLYNSLGRKG
7130	2	780	
1			ISAKSQPYHRSQSSSSVLINKSMDSINYPSDVGKQQLLSLHRSS
		j	RCESHQDLLPDIADSHQQGTEKLSDLTLQDSQKVVVVNRNLPLN
			AQIATQNYFSNFKETDGDEDDYVEIKSEEDESELELSHNRRRKS
			DSKFVDADFSDNVCSGNTLHSLNSPRTPKKPVNSKLGLSPYLTP
		<u> </u>	YNDSDKINDYLWRGPSPNQQNIVQSLREKFQCLSSSSFA
7131	805	573	AAAEGHIEVVKFLIEACKVNPFAKDRWGNIPLDDAVQFNHLEVV
	<u> </u>		KLLQDYQDSYTLSETQAEAAAEALSKENLESMV
7132	1420	1087	IDMLLLSGALVSGPYTLITTAVSADLGTHKSLKGNAHALSTVTA
		Ì	IIDGTGSVGAALGPLLAGLLSPSGWSNVFYMLMFADACALLFLI
		ļ	RLIHKELSCPGSATGDQVPFKEQ
7133	2	3648	QQIPGLLPAHGESGDALRKPRLQKPITGHLDDLFFTLYPSLEKF
			EBELLELHVQDHFQEGCGPLDGGALEILERRLRVGVHNGLGFVQ
	1		RPQVVVLVPEMDVALTRSASFSRKVVSSSKTSSGSQALVLRSRL
			RLPEMVGHPAFAVIFQLEYVFSSPAGVDGNAASVTSLSNLACMH
			MVRWAVWNPLLEADSGRVTLPLQGGIQPNPSHCLVYKVPSASMS
			SEEVKQVESGTLRFQFSLGSEEHLDAPTEPVSGPKVERRPSRKP
	1		PTSPSSPPAPVPRVLAAPQNSPVGPGLSISQLAASPRSPTQHCL
}	1		ARPTSQLPHGSQASPAQAQEFPLEAGISHLEADLSQTSLVLETS
			IAEQLQELPFTPLHAPIVVGTQTRSSAGQPSRASMVLLQSSGFP
1			EILDANKQPAEAVSATEPVTFNPQKEESDCLQSNEMVLQFLAFS
		i c	concordant and a second control of the DEACODE
		1	RVAQDCRGTSWPKTVYFTFQFYRFPPATTPRLQLVQLDEAGQPS
			RVAQDCRGTSWPKTVYFTFQFYRFPPATTPRLQLVQLDDAGQFS SGALTHILVPVSRDGTFDAGSPGFQLRYMVGPGFLKPGERRCFA RYLAVQTLQIDVWDGDSLLLIGSAAVQMKHLLRQGRPAVQASHE

Deginning Coation Co	SEQ	Predicted	Predicted end	Amino acid segment containing signal peptide
Notation Corresponding	-	1		/A-Nomine C. Green D. B. B. S.
Cortesponding	1	-		(A=Aranine, C=Cysteine, D=Aspartic Acid, E=
to first amino acid residue of amino acid residue of amino acid sequence Seserine, T-Threonine, V-Valine, amino acid sequence Sequence Leythophan, Y-Tyrosien, K-Wukhown, *-Stop Codon, /-possible nucleotide deletion, V-p	NO:	1	t .	Glutamic Acid, F=Phenylalanine, G=Glycine,
to first amino acid residue of amino acid sequence sequen	i		,	H=Histidine, I=Isoleucine, K=Lysine,
### amino acid sequence	1		i e	L=Leucine, M=Methionine, N=Asparagine,
residue of amino acid sequence (Codon, /-possible nucleotide deletion, IGRGGTSVIAQOSVETOLIR.DLOYTANT BETTARSIASLISLAITEHTLIANIQUESPEPELINEN PENTON TUTVELINBELSVIVINGOPROBERGAAGLIFTYSEENDHADA APOLYTHEISMERSTERSTAISLAITTEHTLIANIQUESPEPELINEN PENTON PERSENSEN PERSENSEN PERSENSEN PERSENSEN PERSENSEN PERSENSEN PERSENSEN PERSENSEN PERSENSEN PERSENSEN PENTON PERSEN PENTON PERSENSEN PERSENSEN PERSENSEN PERSENSEN PERSENSEN PERSENSEN PERSENSEN PERSENSEN PERSENSEN PERSEN PENTON PERSENSEN PERSEN				P=Proline, Q=Glutamine, R=Arginine,
### amino acid ### sequence Codon, /-possible nucleotide deletion,	1		1	S=Serine, T=Threonine, V=Valine,
### amino acid ### sequence Codon, /-possible nucleotide deletion,	ì	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
Apossible nucleotide insertion	1	amino acid	sequence	Codon, /=possible nucleotide deletion.
LEWNATEYEDDNINVISIONLIGIGRYNFIOVISVWKGELHITLAN VGHPCEOKVRGCTIPPSSRSVIDNOASRYSGETTYGSSR KHYVQAQKLADVDSELAAMLITHARQGKCPDVSRSEDATRAK LERMESVELQEAGGLGRRGTSTVLAQOSVRTOHLOVTANYR ERTKARSIASLISLAITTEHTLHATIGVARPFPFVLINPHYNCH TVTVELDMPLESVUTVSGORNPROFAAALHTPUENDHLAGSL APOLVLRHETANVPYKPOSPSAQOLAWVQASPGLSEKKOMDAV SPMKSSAVPTKHAKVIFRASGGRIAVICLITYELDPHVVCUSDNAV ICETONVGFGERDITHKVASGESPSIKOFFVILTYSDRWLAFPY QTKQVYLHSIQAVVQKSVAGGITELSLULKGTQTYGKVARPTSH PQELKTDRKAVFVLPRGVQDLHVGVGELGEDPVVTQKSDRNY ICETONVGFGERDITHKVASGESPSIKOFFVILTYSDRWLAFPY QTKQVYLHSIQAVVQKSVAGGITELSLULKGTQTYGKVARPTSH PQELKTDRKAVFVLDFRGVQOLHVGVRELARGSRFVLHAUVDCY CHQUASMIVLCLGCOPPLISKAFS HILAAGGGKGVANKRITYTND YPSRRTFHILISDHEPELLRFREDSFQVGGGTYTIGLGPASPCV GEBELILIYINDHEDNEAFCVKUTYO THE GGGGFSYPFRVGLSIGFTLDPHYVLLEVHYDNFTYEGLIDNS GEGFSYPFRVGLSIGFTLDPHYVLLEVHYDNFTYEGLIDNS LRFYTMDIRKYDAGVILAGVHANDVALLHAHLAGGGIRLRIFRKGENKL LAVDDPFDFFFGFGYLKEGTILDFDALTHEFORMFFGSFGHTL ECLERALBAKPSGIHVPAVLLHAHLAGGGIRLRIFRKGENKL LAVDDPFDFFFGFGYLKEGTILDFDALTHEFORMFFGSFGHTL ECLERALBAKPSGIHVPAVLLHAHLAGGGIRLRIFRKGENKL LAVDDPFDFFFGFGYLKEGTILGFDALTHEFORMFFGFGFGHTL ECLERALBAKPSGIHVPAVLLHAHLAGGGIRLRIFRKGENKL LAVDDPFFFFGFGYLKEGTILGFDALTHEFORMFFGFGFGHTGL FURNVARFFTHEFTILSFFGYKLESFBUNDARSPKSTRENDFFGFGFGFTGNES SSLHABPSILLVULLLLSCTLETKSL 7135 2 2072 FVFFVFFRSLSJOGFKGBSVGSTTGPLDSSVLIFFRASSSDGF KTESGFALLBURGHTALLEGARTATERASTTTTARASTSTCH SATVHPDOLFPHAGSSLENDARSDKSRENPBEGDTFTODHSR KTESGFOKSTFDAGAVRGTTTVEVQVGSELGBLERGAPSSLGCLIPA SATVHPDOLFPHAGSSLENDARSDKSRENPBEGDTFTODHSR KTESGFOKSTFDAGAVRGTTTVEVQVGSELGBLERGAPSTVAKLGOTTUR ADLLSRAVEBDAYSRKLVULRHYLSGTYKKRGTGKFGFTHALS GSTTAKSRFTGNSLSALLLGTCTQCGARGHGFTVARKGFGTTSKAFG KTESGFOKSTFDAGATTTARARREDYTTTMPYAHCH ADLLSRAVEBDAYSRKLVULRAVLAGFFLKKTATTMPYAHCH SGSTTAKSRFTGNSLSALLLGTCTQCAAVRGTTTVERGSTSTNOT SGRTTSGERVLASUGGRGGATTGESSSALFMTGGGGRTGFTGKFAT GRGGAGARGGESLMPKRGGGGGGGTTGGGGFTGGGFTGGGFTFTGGFTFTGGGFTFTGGGFTTNOT SGRTTSGERVLASUGGGGGGGGTTGGGFTGGGFTTGGFTFTGGFTFTGGGFTTNOT GGGTTAAGSFTYDGGGGGGGGGTTGGGGGGGGGTTGGGGGGGGGGGGGG	1	sequence		\=possible nucleotide insertion)
VGHPCEQVINGCSTLPPSSRVISNOGARSGSLITTGSSTARRR KHYWOQOKLAD/USELAAMILITHAGGSKEPQDVSRSSDATRRRK LERMSVALQEAGGLIGRKGTSVLAQQSVRTQHLDLQVIANG ERTKASSIAGLIGATIGHTHATIGUARPFPSTLINPINTQH TVTVEIDMPLISVIVDSQDRRDPKGAAGLHTPVEEDMPHLRGSL APQLYLRHETSHAWPVPKPQSPSAQLAMVQASPGLISREVQDWA SPMKSSAVPTKHAKVLFRASGGKPIAVLCLITVELQPHVVDQWA SPMKSSAVPTKHAKVLFRASGGKPIAVLCLITVELQPHVVDQWA SPMKSSAVPTKHAKVLFRASGGKPIAVLCLITVELQPHVVDQWA SPMKSSAVPTKHAKVLFRASGGKPIAVLCLITVELQPHVVDQWA SPMKSSAVPTKHAKVLFRASGGKPIAVLCLITVELQPHVVDQWA CTOMVGOEPROJ HKWASSESPES IKOPFVILYSIGRMLATPY GTWQYLIASIQRVDWSCVAGQLTHELGLURGTQTVTRKVRAPSTV CTOMVGOEPROJ HKWASSESPES IKOPFVILYSIGRMLATPY GTWQYLIASIQRVDWSCVAGQLTHELGULRGTQTVTRKVRAPSTV CHQLVASSHIVCLCCRQPLISKAFFIHLAAGGGKGWINKTITYTNP YPERSTFHILISPHELBERPRUSPSGVGGGTTYTIGPASGRV CHQLVASSHIVCLCCRQPLISKAFFIHLAAGGGKGWINKTITYTNP YPERSTFHILISPHELBERPRUSPSGVGGGTTYTIGPASGRV GEBELILYINDHEDKNBERFCVKUIYO GEBETILYINDHEDKNBERFCVKUIYO GEBETILYINDHEDKNBERFCVKUIYO GEBETILYINDHEDKNBERFCVKUIYO GEBETILYINDHEDKNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO GEBETILYINDHENNBERFCVKUIYO SUURANASSAARAANASSAAGAANASSAAGAAAAAAAAAAAAA			 	LEVVATEYEODNMVVSGDMLGEGRVKDTGVHSTAKGDLULTLAN
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1937 MEMBER AND THE PROPERTY OF THE PROPERTY IN CASE	7140	1401	1057	
nmnvslekQlrpsQpwprgkcrktpgwbearpkaQdlrgdlgkt	/140	1401	1957	KASSIQVLKAWGGLIPSSFQQQHTGQYALEELFDLKVYDCPCSF
	L	L		NMNVSLKKQLRPSQPWPRGKCRKTPGWBEARPKAQDLRGDLGKT

SEQ	Predicted	Predicted end	
ID		nucleotide	Amino acid segment containing signal peptide
NO:	beginning nucleotide		(A=Alanine, C=Cysteine, D=Aspartic Acid, E=
NO:	location	location	Glutamic Acid, F=Phenylalanine, G=Glycine,
1		corresponding	H=Histidine, I=Isoleucine, K=Lysine,
1	corresponding	to first	L=Leucine, M=Methionine, N=Asparagine,
1	to first	amino acid	P=Proline, Q=Glutamine, R=Arginine,
	amino acid	residue of	S=Serine, T=Threonine, V=Valine,
}	residue of	amino acid	W=Tryptophan, Y=Tyrosine, X=Unknown, *=Stop
	amino acid	sequence	Codon, /=possible nucleotide deletion,
L	sequence	<u></u>	\=possible nucleotide insertion)
			QAGPAEAHTRGPPRLPAATGCPPHLPGLLSGISVDIDPTGLQSQ
		j	WTPKGQDPPLMFSEDYQKSLLEQYHLGLDQKLRKYVVGELIWNF
	-		ADFMTNQCG
7141	124	1073	LDSRSCWLDMEDLEEDVRFIVDETLDFGGLSPSDSREEEDITVL
Į			VTPEKPLRRGLSHRSDPNAVAPAPQGVRLSLGPLSPEKLEEILD
į			EANRLAAQLEQCALQDRESAGEGLGPRRVKPSPRRETFVLKDSP
1	ĺ		VRDLLPTVNSLTRSTPS/LKQPDASTPE***EGVSQGSPGYIWK
İ			EALQHEEGVTHLQSVPCIQKPSIFSS\SRSTPPVRGRAGPSGRA
			AASEETRAAKLRGAAAKSSCQLPIPSAIPRPASRMPLTSRSVPP
			GRGALPPDSLSTRKGLPRPSTAGHRVRESGHKVPVSORLNLPVM
		ļ	GATRSNLOPP
7142	658	839	LIFLMLHMELKMLSSVTLHIRAFLYWICLKPTSCLIFONVLNLL
			KK*SRAVGVVVVMCRT/YSSDLQVGVIKPWLLLGSQDAAHDLDT
			LKKNKVTHILNVAYGVENAFLSDFTYKSISILDLPETNILSYFP
			ECFEFIEEAKRKDGVVLVHCNA
7143	3	773	SLEMSSDGEPLSRMDSEDSISSTIMDVDSTISSGRSTPAMMNGO
1		'''	GSTTSSSKNIAYNCCWDQCQACFNSSPDLADHIRSIHVDGORGG
			VFVCLWKGCKVYNTPSTSQSWLQRHMLTHSGDKPFKCVVGGCNA
	j		SFASQGGLARHVPTHFSQQNSSKVSSQPKAKEESPSKAGMNKRR
			KLKNKRRRSLARPHDFFDAQTLDAIRHRAICFNLSAHIESLGKG
			HSVVFHSTVSILLFFQIKYKTLOKNISTIISKSLKI
7144	1	988	FRVNMQDGGPSPAEHSKAEESAGMEARFLGLPDAAGSSGPTPAR
/ ***	<u> </u>	300	RCPAPRPAGVSYVIRDEVEKYNRNGVNALQLDPALNRLFTAGRD
l			SIIRIWSVNQHKQDPYIASMEHHTDWVNDIVLCCNGKTLISASS
1			DTTVKVWNAHKGFCMSTLRTHKDYVKALAYAKDKELVASAGLDR
1			QIFLWDVNTLTALTASNNTVTTSSLSGNKDSIYSLAMNQLGTII
			VSGSTEKVLRVWDPRTCAKLMKLKGHTDNVKALLLNRDGTQCLS
1			GSSDGTIRLWSLGQORCIATYRVHDEGVWALQVNDAFTHVYSGG
	<u> </u>	<u> </u>	RDRKIYCTDLRNPDIRVLICE

TRADOCS:1416260.1(%CSK01!.DOC)

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, and complementary sequences thereof.

- 2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.
- 3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 90% sequence identity with the polynucleotide of claim 1.
- 4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.
- 5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.
- 6. A vector comprising the polynucleotide of claim 1.
- 7. An expression vector comprising the polynucleotide of claim 1.
- 8. A host cell genetically engineered to comprise the polynucleotide of claim 1.
- 9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.
- 10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

- (b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO:1-1786 and 3573-5358.
- 11. A composition comprising the polypeptide of claim 10 and a carrier.
- 12. An antibody directed against the polypeptide of claim 10.
- 13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex;
 and
- b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.
- 14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:
- a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;
- b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and
- c) detecting said product and thereby the polynucleotide of claim 1 in the sample.
- 15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.
- 16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

- b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.
- 17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and
- b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:
- a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and
- b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.
- 19. A method of producing the polypeptide of claim 10, comprising,
- a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of a polynucleotide sequence of SEQ ID NO:1-1786 and 3573-5358, a mature protein coding portion of SEQ ID NO:1-1786 and 3573-5358, an active domain of SEQ ID NO:1-1786 and 3573-5358, complementary sequences thereof and a polynucleotide sequence hybridizing under stringent conditions to SEQ ID NO:1-1786 and 3573-5358, under conditions sufficient to express the polypeptide in said cell; and
 - b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO:1787 -3572 and 5359-7144, the mature protein portion thereof, or the active domain thereof.

- 21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.
- 22. A collection of polynucleotides, wherein the collection comprising the sequence information of at least one of SEQ ID NO:1-1786 and 3573-5358.
- 23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.
- 24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.
- 25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.
- 26. The collection of claim 22, wherein the collection is provided in a computerreadable format.
- 27. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.
- 28. A method of treatment comprising administering to a mammalian subject in need thereof a therapeutic amount of a composition comprising an antibody that specifically binds to a polypeptide of claim 10 or 20 and a pharmaceutically acceptable carrier.

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INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

A. CLASSIFICATION OF SUBJECT MATTER IPC(7) : C07H 21/04; C12N 15/11, 15/63, 15/70, 15/82, 15/85; C07K 14/00 US C1 : 536/73 1: 435/370 1: 455, 468, 530/300, 350						
	US CL: 536/23.1; 435/320.1, 455, 468, 530/300, 350 According to International Patent Classification (IPC) or to both national classification and IPC					
	DS SEARCHED					
	cumentation searched (classification system followed b 36/23.1; 435/320.1, 455, 468, 530/300, 350	y classification symbols)				
Documentation	on searched other than minimum documentation to the	extent that such documents are included in	n the fields searched			
Electronic da MEDLINE, I	ta base consulted during the international search (name	e of data base and, where practicable, sear	rch terms used)			
C. DOC	UMENTS CONSIDERED TO BE RELEVANT					
Category *	Citation of document, with indication, where a		Relevant to claim No.			
A	WAJIMA et al. The cDNA cloning and transient exp hydroxysteroid dehydrogenase of chickens. Gene. 19		1-11, 13-16, and 19-26			
A	US 5,175,095 A (MARTINEAU et al) 29 December columns 3-18.	1992 (29.12.1992), see especially	1-11, 13-16, and 19-26			
A	Database PubMed, 1D No. 2393392, FREUDENSTEIN et al. mRNA of bovine tissue inhibitor of metalloproteinase: sequence and expression in bovine ovarian tissue. Biochem. Biophys. Res. Commun. August 1990. Vol.171. No. 1. pages 250-256, see Abstract.					
A,P	Database PubMed, ID No. 10919256, HENNEBOLD et al. Ovary-selective genes I: the generation and characterization of an ovary-selective complementary deoxyribonucleic acid library. Endocrinology. August 2000. Vol.141. No.8. pages 2725-2734, see Abstract.					
A	Database PubMed, ID No. 2760883, BEIL et al. Synthesis of polypeptides by the cervix of the baboon (Papio anubis). J. Reprod. Fertil. July 1989, Vol.86. No.2. pages 535-544, see Abstract.					
A,P	Database PubMed, ID No. 10830289, HINSHELWOOD et al. A 278 bp region just upstream of the human CYP19 (aromatase) gene mediates ovary-specific expression in transgenic mice. Endocrinology. June 2000. Vol.141. No.6. pages 2050-2053, see Abstract.					
	documents are listed in the continuation of Box C.	See patent family annex.				
"A" document	pecial categories of cited documents: It defining the general state of the art which is not considered to be	"T" later document published after the inte date and not in conflict with the applic principle or theory underlying the inve	ation but cited to understand the			
•	"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered novel or cannot be considered novel or cannot be considered novel or cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone					
establish :						
"O" document referring to an oral disclosure, use, exhibition or other means being obvious ") a person skilled in the art						
	"P" document published prior to the international filing date but later than the "&" document member of the same patent family priority date claimed					
Date of the actual completion of the international search Date of mailing of the international search report N 2001						
Name and mailing address of the ISA/US Commissioner of Patents and Trademarks Authorized positioner of Patents and Trademarks						
	Commissioner of Patents and Trademarks Box PCT Michael Woodward // Clarents and Trademarks					
	shington, D.C. 20231 p. (703)305-3230	Telephone No. (703) 308-0196	/)			
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Form PCT/ISA/210 (second sheet) (July 1998)

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)				
This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:				
1. Claim Nos.: because they relate to subject matter not required to be searched by this Authority, namely:				
Claim Nos.: because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:				
Claim Nos.: because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).				
Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)				
This International Searching Authority found multiple inventions in this international application, as follows: This includes 4 invention Groups and 3572 sequence species				
As all required additional search fees were timely paid by the applicant, this international search report covers all searchable claims. As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee. As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:				
4. No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: Remark on Protest The additional search fees were accompanied by the applicant's protest. No protest accompanied the payment of additional search fees.				

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US00/34263

This application contains the following inventions or groups of inventions which are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for all inventions to be searched, the appropriate additional serch fees must be paid. Group I, claims 1-11, 13-16, and 19-26, drawn to nucleic acid molecules, vector molecules and host cells containing said nucleic acids, polypeptides, methods of making said polypeptides and method of detection using said nucleic acids and polypeptides. Group II, claim 12 and 28, drawn to antibodies and method of treatment using composition comprising said antibodies. Group IV, claim 17-18, drawn to method of indentifying a binding partner to a polypeptides.

The inventions listed as Groups I-IV do not relate to a single inventive concept under PCT Rule 13.1 because, udner PCT Rule 13.2, they lack the same or corresponding special technical features for the following reasons: Group I encompasses nucleic acids, polypeptides expressed thereby, vectors and host cells containg same, respectively, and methods of making as well as the first method of use of this jubject matter. Groups II-V all are directed to different special technical features as summarized as follows: Group II is directed to an antibody and method of treatment using same, which antibody undergoes recognition and binding reactions wherein what is bound is different from what is bound by the compositions of Group I. For example, the polypeptides of Group I do not bind the polypeptides of Group I as the antibody of Group II does. Identification of binding partner and treatment are clearly different special technical features from detection. Group III is directed to the identification of a binding partner of a polypeptide, which is not identified in any of the other Groups and thus clearly contains its own special technical feature. Group IV is directed to treatment, which is a clearly different methods than the methods in the other Groups. Thus, in summary, each of Groups I-IV are directed to different special technical features and thus support this lack of unity.

Additionally, each of the claims is directed to more than one species of the generic invention. These species are deemed to lack unity of invention because they are not so linked as to form a single inventive concept under PCT Rule 13.1. In order for more than one species to be searched, the appropriate additional search fees must be paid. The species are as follows: The claims include a series of polynucleotides and the polypeptides encoded thereby as represented by the sequences of SEQ ID Nos: 1-1786, and 3573-5358. Each of these polynucleotide sequences encodes a separate polypeptide and thus represent a separate gene. Therefore, each of these genes defines its own special technical feature. In summary, one species is a gene represented by one polynucleotide sequence and one polypeptide sequence encoded thereby.

CORRECTED VERSION

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[Continued on next page]

(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

(57) Abstract: The present invention provides novel nucleic acids, novel polypeptide sequences encoded by these nucleic acids and uses thereof.





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ance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

For two-letter codes and other abbreviations, refer to the "Guid-

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